

LABORATÓRIUM MOLEKULÁRNEJ MIKROBIOLÓGIE

Výskum laboratória molekulárnej mikrobiológie je zameraný na molekulárnu analýzu mechanizmov, ktoré vedú k vzniku rezistencie eukaryotickej bunky voči antifungálnym zlúčeninám. Študujeme transkripčné siete kvasiniek *Kluyveromyces lactis* a *Candida glabrata*, ktoré zabezpečujú odpoveď bunky na chemický stres resp. vyvolávajú rezistenciu buniek voči xenobiotikám. Analyzujeme jednotlivé gény z hľadiska ich biologickej funkcie. Pripravujeme kmene kvasiniek nesúce rôzne mutácie s izogénnym genetickým pozadím a sledujeme vplyv jednotlivých mutácií ako aj ich kombinácií na rozvoj mnohonásobnej rezistencie u modelových druhoch kvasiniek. Vo výskume tiež aplikujeme celogenómové prístupy (kvantitatívna transkriptomika, funkčná genomika).

LABORATORY OF MOLECULAR MICROBIOLOGY

The overall goal of our research is to dissect the molecular mechanisms underlying clinical antifungal drug resistance development. We are interested in the transcriptional networks that control drug resistance and stress response in two model yeast species *Kluyveromyces lactis* and *Candida glabrata*. Our work stretches from functional and mechanistic studies on single genes to genome-wide approaches through quantitative transcriptomics and functional genomics (For this purpose, advanced genetic and molecular tools are used.) by creating strains containing various mutations in an isogenic background we are currently investigating the impact of different types of mutations and combinations thereof on drug resistance development in model yeast species.

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UK/161/2016 Funkčná analýza génu *ERG6* v kvasinkách *Kluyveromyces lactis*

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Publikácie:

Svrbicka A, Toth Hervay N, Gbelska Y (2016) The major facilitator superfamily transporter *Knq1p* modulates boron homeostasis in *Kluyveromyces lactis*. **Folia Microbiol** 61:101–107.

Culakova H, Dzugasova V, Valencikova R, Gbelska Y, Subik J (2015) Stress response and expression of fluconazole resistance associated genes in the pathogenic yeast *Candida glabrata* deleted in the CgPDR16 gene. **Microbiol Res** 174:17–23.

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