Workshop: Advanced Research on Pneumocystis jirovecii and Fungal Infections in Immunocompromised Individuals

Objective:
To provide researchers and PhD students with in-depth knowledge on Pneumocystis jirovecii and other fungal infections, focusing on advanced research topics, diagnosis, treatment, and prevention.

Agenda:
10:00 AM - 10:15 AM: Registration and Welcome
- Participants sign in and receive workshop materials.
- Opening remarks and introduction to the day's agenda.

10:15 AM - 11:00 AM: Lecture by Dr. Philippe HAUSER
- **Topic**: Surface Antigenic Variation of the Human Fungal Pathogenic Fungus Pneumocystis jirovecii: Possible Involvement of DNA-Triplexes
- Detailed exploration of antigenic variation mechanisms and their implications for treatment and vaccine development.

11:00 AM - 11:45 AM: Lecture by Prof. Václav Brázda
- **Topic**: Local DNA Structures in Genomes of Various Pathogens
- Examination of unique DNA structures in pathogens and their roles in infection and immune evasion.

11:45 AM - 1:00 PM: Lunch
1:00 PM - 2:00 PM: Discussion
2:00 PM - 4:00 PM: visit if Mendel's museum
Materials:
- Research papers and articles by Dr. Philippe HAUSER and Prof. Václav Brázda.

Target Audience:
- Researchers and PhD students in microbiology, immunology, and related fields.

Venue:
- Faculty of Chemistry, Brno Technical University, Purkynova 118, Brno, Czech Republic, lecture room P4

Date:
- July 15, 2025

This workshop aims to provide advanced insights and foster collaboration among researchers and PhD students.

Surface antigenic variation of the human fungal pathogenic fungus *Pneumocystis jirovecii*: possible involvement of DNA-triplexes

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Abstract

Surface antigenic variation is crucial for major pathogens that infect humans. To escape the immune system, they exploit various mechanisms to modify or exchange the proteins that are exposed on their cell surface, at the genetic, expressional, and/or epigenetic level. We studied the mechanisms used by the fungus *Pneumocystis jirovecii* that causes life-threatening pneumonia in immunocompromised individuals. Though this fungus is currently not cultivable, our detailed analysis of the subtelomeric sequence motifs and genes encoding six families of major surface glycoproteins suggests that the system relies mainly on homologous recombinations. Translocations of entire genes lead to the reassortment of the repertoire of ca. 80 non-expressed alleles of family I present in each strain. From this repertoire single genes are retrieved over time for mutually exclusive expression within subpopulations of cells. The recombinations also lead to allele mosaicism and rearrangement of the subtelomeres. In addition, imperfect mirror sequences potentially forming DNA triplexes may play a role in the system.