11TH EUROPEAN CONFERENCE

ON FUNGAL GENETICS

# PROGRAMME & ABSTRACTS

Philipps-Universität Marburg and Max Planck Institute for Terrestrial Microbiology Marburg, Germany

## Poster Category 3: Genomes and Genome Evolution

**PR3.1**

**Development of DNA Barcodes to Identify Edible Mushrooms**

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*Basidiomycetes* as one of the largest groups of edible mushrooms have become more important in recent times for their medicinal and nutritional properties. For many years, species of this family have been mainly classified by their common phenotypic traits, however, taxonomic identification based solely on morphological features can be misleading and unreliable. In contrast, DNA based identification provides a powerful and reliable method for taxonomic discrimination of fungi, it can be performed at any growth stages using parts of the fruit body, mono- and dikaryotic mycelia, or any other organic fungal. In the current study, three different DNA and c-DNA molecular markers including Internal Transcribed Spacer (ITS) I and II, Intergenic Spacer (IGS) I, and mitochondrial COXI gene were developed to identify mushroom species and individuals. Phylogenetic trees could clearly distinguish the species of Basidiomycetes by showing distinct clades. Species differentiations were re-confirmed by AMOVA analysis, nucleotide divergence, haplotyping and P values. Moreover, the designed primers were perfectly matched with the used species, can be employed in phylogenetic studies of other *Basidiomycetes*. Polymorphism occurred throughout the regions of interest due to insertion-deletion and point mutations, and can be clearly differentiated within the families as well as genera. This study proved that the three developed molecular markers can be used as the consensus DNA and/or c-DNA barcodes for taxonomic identification of *Basidiomycetes*.

**PR3.2**

**Genomic and molecular characterization of a model ascomycete that is ancestral to mutualistic and pathogen-rich fungal lineages (Strain A95 *Sarcinomyces petricola*, Chaetothyriales)**

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Melanised micro-colonial fungi (MCF) that colonise bare rock surfaces survive in extreme environments. Phylogenetically, rock-inhabiting MCF are ancestors of lichens as well as important animal and plant pathogens. MCF may thus have been a “stepping-stone” to colonisation of other extreme environments including animals. A meristematic black yeast species *Sarcinomyces petricola* (strain A95) was selected as a model strain. The estimated 29 Mbp DNA sequence is being assembled and annotated. As with all MCF that possess the characteristic stress-tolerant morphology (including thick, melanised cell-walls) disruption of the cellular structure is problematic. Nevertheless an efficient procedure for protoplast formation was developed using various hydrolytic enzymes. Protoplast formation is an important prerequisite for both the development of an appropriate transformation system for A95 and application of other tools to characterise the genome. For example, the number of chromosomes will be ascertained by pulsed-field gel electrophoresis of the protoplasts. Karyotyping A95 in this way will provide an additional check on the estimated genome size (and thus the depth of sequencing required to close the genome) and permit the isolation of mitochondrial DNA and plasmids (if A95 contains them).