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In recent years, incidence of mucormycosis (i.e., invasive fungal infections caused by members of the order Mucorales, such as *Mucor lusitanicus*) has significantly increased worldwide. Such infections are considered as the third most frequent type of invasive mycoses after candidiasis and aspergillosis in patients with hematological malignancy, haematopoietic stem cell- and solid organ transplantation and diabetes mellitus. Genome of *M. lusitanicus* contains two genes encoding survival factor 1 (SVF1), which were named as *svf1a* and *svf1b*. Aim of the present study was to examine the expression and reveal the function of these genes, first in a Mucorales fungus. We demonstrated that SVF1 proteins are required for survival under conditions of oxidative and cold stress in *Mucor*. Knock-out of *svf1a* caused increased sensitivity to oxidative stress when compared to the wild-type strain. The sphingolipid metabolism of the knock-out strains was also investigated with HPLC techniques. We found that Svf1b affects sphingolipid biosynthesis, its absence altered the accumulation of phytosphingosine and its downstream metabolites. In both *svf1a* and *svf1b* knock-out mutants, conidial germination was delayed, vegetative growth was reduced and spore forming ability was impaired. We have studied the expression of the genes after culturing the fungus under different conditions by real-time quantitative reverse transcription PCR. Macromorphology and sensitivity to different stressor chemicals (e.g., acetate, H_2O_2, Congo red and Calcofluor white) were tested. Mutants showed altered characteristics compared to the original strain suggesting that the cellular integrity may be damaged in the mutants. Furthermore, recognition and internalization of the fungal spores by macrophages were affected by the disruption of the *svf1* genes in *M. lusitanicus*.

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TRANSCRIPTIONAL RESPONSE OF *CANDIDA AURIS* BIOFILMS TO FARNESOL AND TYROSOL TREATMENT

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Candida auris is an emerging fungal pathogen that causes outbreaks in health care facilities with a high mortality rate. The conventional antifungal agents have limited effects against the majority of clinical isolates. Furthermore, multidrug-resistance is typical in case of *C. auris* biofilms; thus, innovative therapies are urgently needed. Farnesol and tyrosol are two fungal quorum-sensing molecules with opposite effect in terms of *Candida* morphogenesis. Moreover, they have a remarkable antimicrobial effect at supraphysiological concentrations. Our aim was to investigate genome-wide gene transcription changes induced by these compounds against *C. auris* biofilm using total transcriptome sequencing (RNA-Seq). We found that farnesol and tyrosol exposures significantly reduced the biofilm mass produced by *C. auris* and resulted 587 up- and 1851 down-regulated genes with significant differential expression, respectively ($P<0.05$). Following farnesol treatment, 138 and 199 genes showed increased (>1.5-fold change) or decreased (<-1.5-fold change) transcription level, respectively; while tyrosol resulted 686 up-regulated (>1.5-fold change) and 662 down-regulated (<-1.5-fold change) genes compared to control. Farnesol-induced genes involved in ribosomal small and large subunit biogenesis, RNA metabolic process and iron-sulfur cluster binding were up-regulated. Tyrosol resulted the up-regulation of genes involved in ribosomal small and large subunit biogenesis, RNA metabolic process, translation, unsaturated fatty acid biosynthesis as well as iron-sulfur cluster binding. Moreover, tyrosol decreased the expression of carbohydrate catabolic process, ergosterol biosynthesis, fatty acid beta-oxidation, response to endoplasmic reticulum stress, peroxisome and vacuole associated genes. Our study provides novel clues for future studies in terms of understanding of quorum-sensing molecules-related effect on *C. auris* biofilms.

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SEROPREVALENCE STUDY OF HUMAN POLYOMAVIRUSES

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The number of species within the Polyomaviridae family has increased since 2007. Currently, 14 human polyomaviruses are classified within the family, but only five of these viruses are associated with diseases. The human polyomaviruses do not result in obvious clinical symptoms in healthy individuals, but in immunocompromised patients they can cause disease, even severe one. Merkel cell polyomavirus, as a tumour virus is a causative agent of Merkel cell carcinoma. To reveal the significance of the other, not well known viruses, seroprevalence studies are essential. Detection of the antibodies against the viruses in different patient groups will answer some basic questions: the time of the primary infection, the rate of population infected by