land to grow on in this way do not trigger "food or fuel" conflicts. This biomass is composed of interwoven cellulose and hemicellulose, coated by anaerobically almost undegradable lignin [2]. Microbial pre-treatment utilizing the fibre degrading potentials of aerobic fungi may be a much cheaper alternative but there are some drawbacks e.g. loss of carbohydrates by respiration and biomass build-up and the requirement of long pretreatment periods [3]. Anaerobic fungi (AF) from the phylum Neocallimastigomycota are natural inhabitants of the digestive tract of herbivorous animals [4], which decompose a big share of the ingested forage. The AF attach to the plant material and crack the fibres mechanically by growth and expansion of their rhizoids or bulbous holdfasts [5]. In addition, AF possess cellulosomes which contain a multitude of lignocellulolytic enzymes. The objective of this study was the application of two newly isolated strains to the hydrolysis phase in order to improve hydrolysis of lignocellulosic biomass. The applied isolates were obtained from animals living on a high fibre diet, namely sheep (*Ovis aries*) and Asian elephant (*Elephas maximus*). The effects on biogas production of anaerobic fungi from both animal species were assessed in two step batch experiments, comprised by a hydrolytic/acidogenic stage, followed by a methane production stage. The assimilated carbohydrates were measured by HPLC. Additionally, gas composition was analized by GC during the methane production stage.

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TRANSCRIPTOMIC APPROACHES FOR THE FARNESOL EXPOSURE OF *CANDIDA AURIS*

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The threat of antifungal resistance of Candida auris necessitates bold and innovative therapeutic options. Farnesol is a quorum-sensing molecule with a potential antifungal and/or adjuvant effect; it may be a promising candidate in alternative treatment. To gain further insights into the farnesol-related effect to C. auris, genome-wide gene expression analysis was performed using RNA-Seq. Farnesol exposure resulted in 1,766 differentially expressed genes. Out of them, 447 and 304 genes with at least 1.5-fold increase or decrease in expression, respectively; were selected for further investigations. Genes involved in morphogenesis, biofilm events (maturation and dispersion), gluconeogenesis, iron metabolism, and regulation of RNA biosynthesis showed down-regulation, while genes related to antioxidative defence, transmembrane transport, glyoxylate cycle, fatty acid β-oxidation, and peroxisome process were up-regulated. In addition, farnesol treatment increases the expression of certain efflux pump genes including MDR1, CDR1 and CDR2. Growth was significantly inhibited within two hours of the addition of farnesol regarding CFU changes ($5.8\times10^7\pm1.1\times10^7$ and $1.1\times10^7\pm0.3\times10^7$ for untreated control and farnesol-exposed cells, respectively) ($p<0.001$). In addition, farnesol treatment caused a significant reduction in intracellular iron (152.2±21.1 vs. 116.0±10.0 mg/kg), manganese (67.9±5.1 vs. 18.6±1.8 mg/kg), and zinc (787.8±22.2 vs. 245.8±34.4 mg/kg) ($p<0.05$–0.001) compared to untreated control cells, whereas the level of cooper was significantly increased (274.6±15.7 vs. 828.8±106.4 mg/kg) ($p<0.001$). This is the first study analyzing the global changes in gene transcription in *C. auris* following farnesol exposure, providing important insights into the mechanism of antifungal action of farnesol and the response of *C. auris*, facilitating a better understanding of farnesol-related antifungal activity. In summary, farnesol exposure enhanced the oxidative stress response and up-regulated drug efflux pumps, while reducing zinc and manganese intracellular content as well as iron metabolism. Moreover, cellular metabolism was modulated towards β-oxidation. These results may open new directions in developing alternative therapies against *C. auris*.

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