

Abstract

The digestive tract of insects is naturally inhabited by a large number of microorganisms, including fungi. Contrary to the original assumptions, the quantitative representation of fungal species in the intestines and on the surface of the leaves that these insects feed on varies considerably. Among the representatives inhabiting both these niches, there are those whose representation is significantly higher in the intestines. However, the microorganisms living here must be able to deal with a number of inhibiting substances for them, which are taken with plant food. These phytochemicals can significantly influence the metabolism of microorganisms. At the same time, the ability to act as epigenetic modifiers of eukaryotic cells has been demonstrated for a significant part of these phytochemicals. To answer the question of whether these facts can be related and whether changes in the metabolism of fungi have a basis in changes at the epigenetic level, the methodology of transcriptomic analysis and several analyzes monitoring metabolic changes was chosen. As a model organism of the given system, this thesis focuses on the species *Aureobasidium pullulans*, in which changes are monitored after exposure to phytochemicals (quercetin, tannin and gallic acid). This is a species whose percentage representation in the guts of insects was significantly higher compared to its representation on the surface of the leaves and at the same time a biotechnologically important species. According to the results of monitoring the metabolic activity phytochemicals used in this work do not increase the biomass produced in *A. pullulans*, as was originally assumed. However, it can be seen from the results that although the effect on the change in differential gene expression is very significant, the changes in the growth rate are rather negligible. Analysis of the transcriptome of *A. pullulans* revealed a number of genes whose expression varied depending on the addition of phytochemicals used. These were not only genes responsible for epigenetic changes (methyltransferases, acetylases, deacetylases), but also genes related to the production of lytic enzymes (cellulases, lipases, xylanases, amylases). At the same time, there was a significant up-regulation of genes that can be linked to the response to environmental stress. The study of epigenetics in fungi represents an area with enormous potential, as among fungi we can find a considerable part of pathogens, symbionts or biotechnologically important producers.

Key words: *Aureobasidium pullulans*, transcriptomics, epigenetics, gut microbiome, phytochemicals