

Gene expression in lichen *Lobaria pulmonaria* in response to UV-B stress

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Lichens belong to extremophilic organisms, which survive in harsh environments. Mechanisms of their high stress tolerance include regulation at the gene expression level, however there are only few reports on the transcriptome analysis in stressed lichens. In present work we analyzed differential gene expression in the lichen *Lobaria pulmonaria* in response to UV-B exposure to learn about stress-induced defence proteins and secondary metabolites. Lichen *L. pulmonaria* was chosen due to the availability of information about sequenced genomes of photo- and mycobionts. The thalli of lichen were daily exposed to UV-B radiation for 14 days. Analysis of gene expression of photo- and mycobionts was performed by transcriptome analysis and real time PCR. Among differentially expressed genes of photobiont, the most up-regulated were the genes encoding heat shock proteins, antioxidant enzymes, glutathione dependent proteins Mss4-like and glutathione-S-transferase, thioredoxins, alpha-ketoglutarate dependent dioxygenases, genes of nitrogen and lipid metabolism. Among differentially expressed genes of mycobiont, the most up-regulated were the genes involved in protein repair, antioxidative defence, proteolysis and nitrogen metabolism, in particular genes of ornithine cycle, shikimate pathway and amino acid metabolism. Cortex of fungal symbiont of a lichen shields the most of UV radiation, that is why the stress response of mycobiont is stronger than that of photobiont. This caused by the necessity to synthesize photoprotective compounds by mycobiont. We showed that UV exposure of lichen induces the expression of genes involved in the synthesis of dark pigment melanin. Moreover, gene cluster participating in biosynthesis of prenylated xantone, a potential photoprotective metabolite, was also found. Interestingly, genes encoding alternative oxidase were highly expressed in both symbionts in UV exposed thalli suggesting the redistribution of the main respiratory pathways and energy metabolism. Taken together, our data suggest that UV response of *L. pulmonaria* is regulated by complex interplay between gene activity in photobiont and mycobiont.

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