



PlantGen2021

6th International scientific conference

Plant genetics, genomics,
bioinformatics, and biotechnology

June 14–18, 2021, Novosibirsk, Russia



GENE EXPRESSION IN LICHEN LOBARIA PULMONARIA IN RESPONSE TO UV-B STRESS

Leksin I.Y.^{1,2*}, *Minibayeva F.V.*^{1,2}

¹Kazan Institute of Biochemistry and Biophysics, FRC Kazan Scientific Center of the RAS, Kazan, Russia

²Kazan Federal University, Kazan, Russia



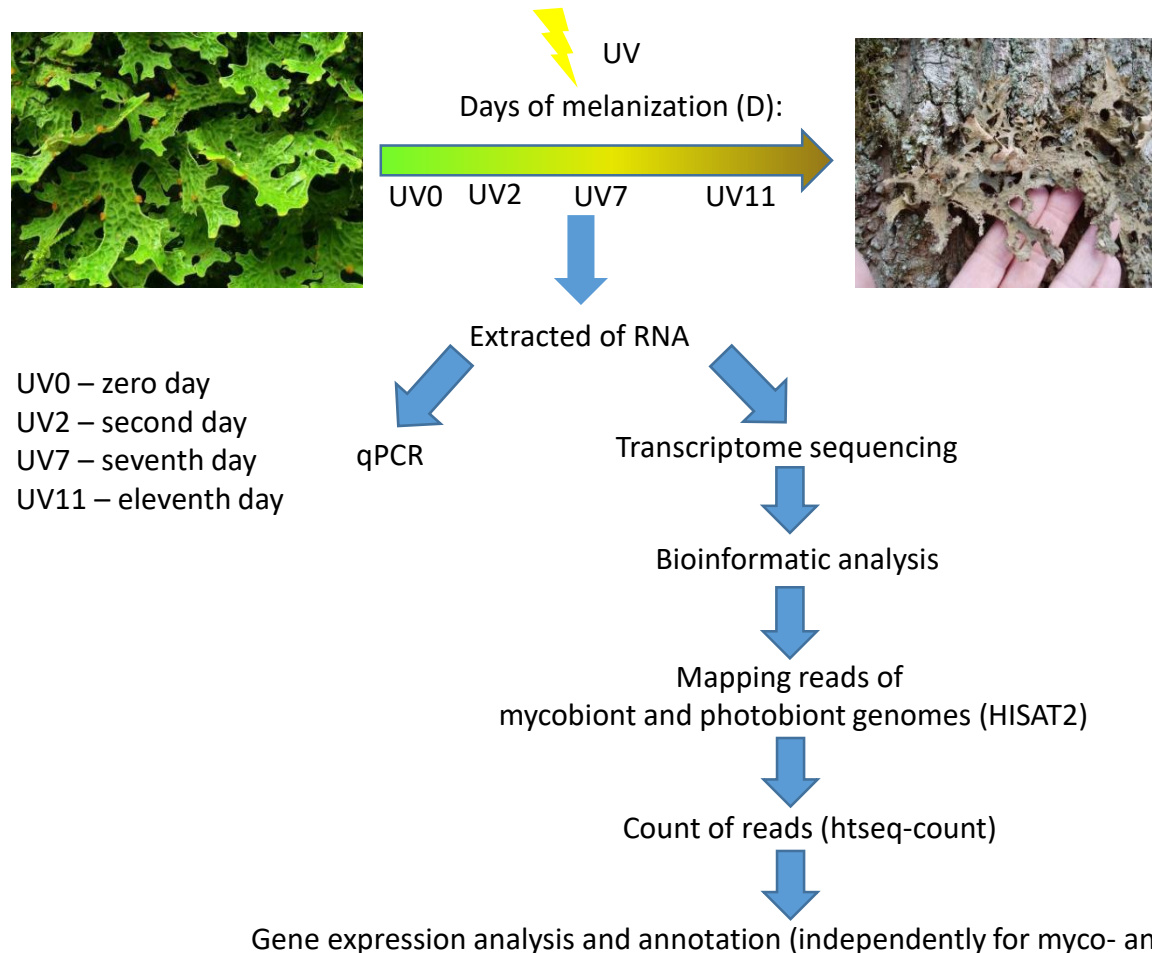
INTRODUCTION

Lichens are symbiotic photosynthesizing organisms able to 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.

AIM

In present work, we analyzed differential gene expression in the lichen *Lobaria pulmonaria* in response to UV-B exposure to learn about the stress-induced changes in defence proteins and secondary metabolites.

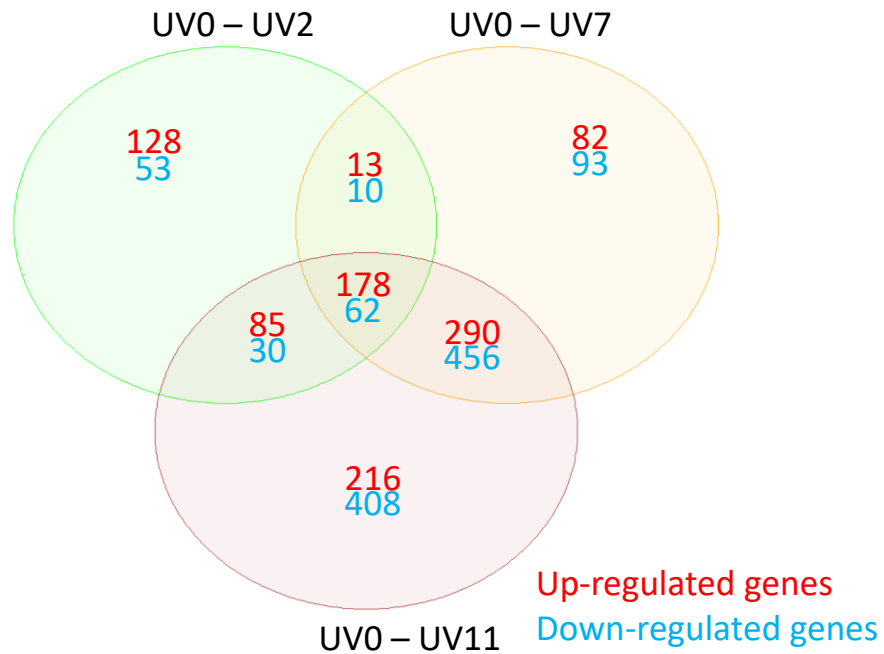
MATERIALS AND METHODS



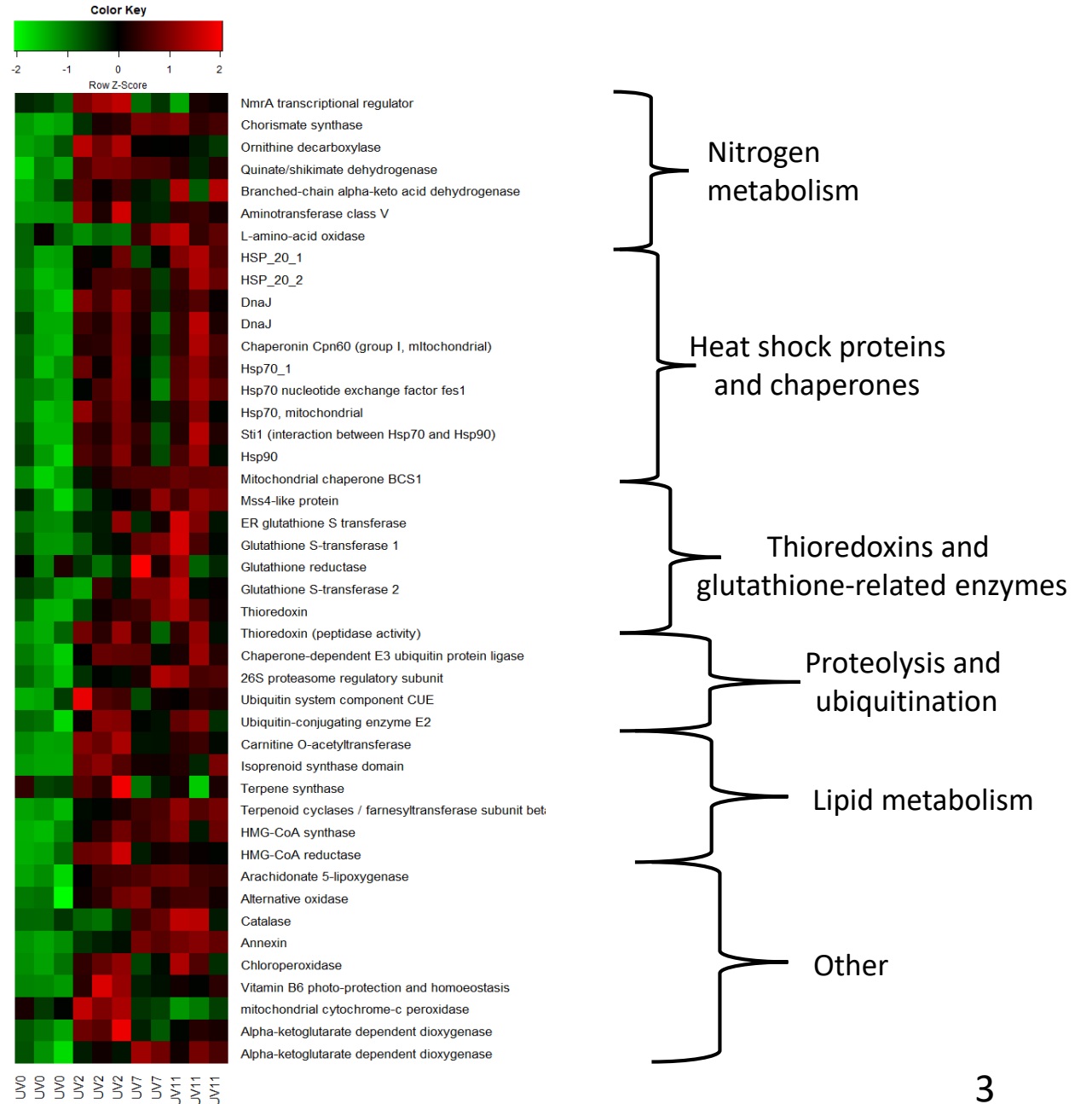
Lichen *L. pulmonaria* was chosen due to the availability of information about sequenced genomes of photo- and mycobionts. The thalli of lichen were daily exposed to UV-B radiation for 14 d. Analysis of gene expression of photo- and mycobionts was performed by transcriptome analysis and qPCR. For gene expression analysis R package edgeR was used, genes with $|\log_2FC| > 1$ and $FDR < 0.05$ were considered to be **differential expressed genes (DEGs)**.

Mycobiont DEGs

Pairwise comparisons	Number of DEGs	
	Up	Down
UV0 – UV2	404	155
UV0 – UV7	563	621
UV0 – UV11	769	956

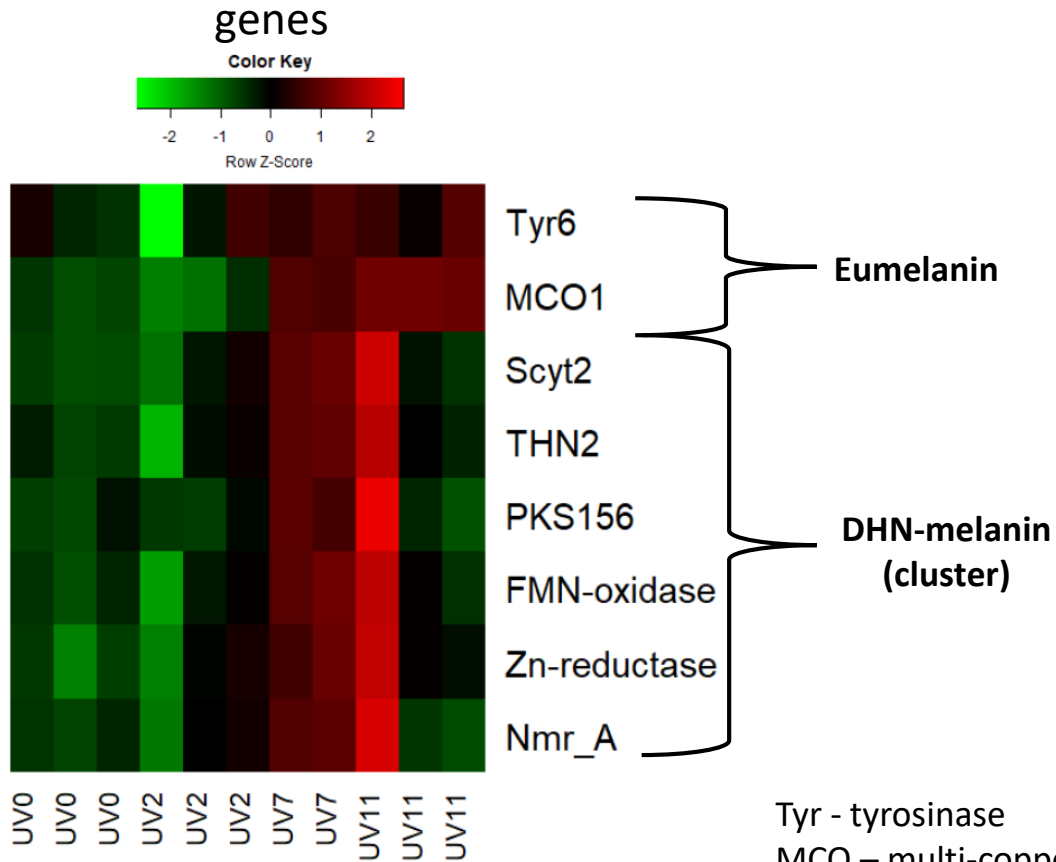


Several mycobiont DEGs related to stress tolerance



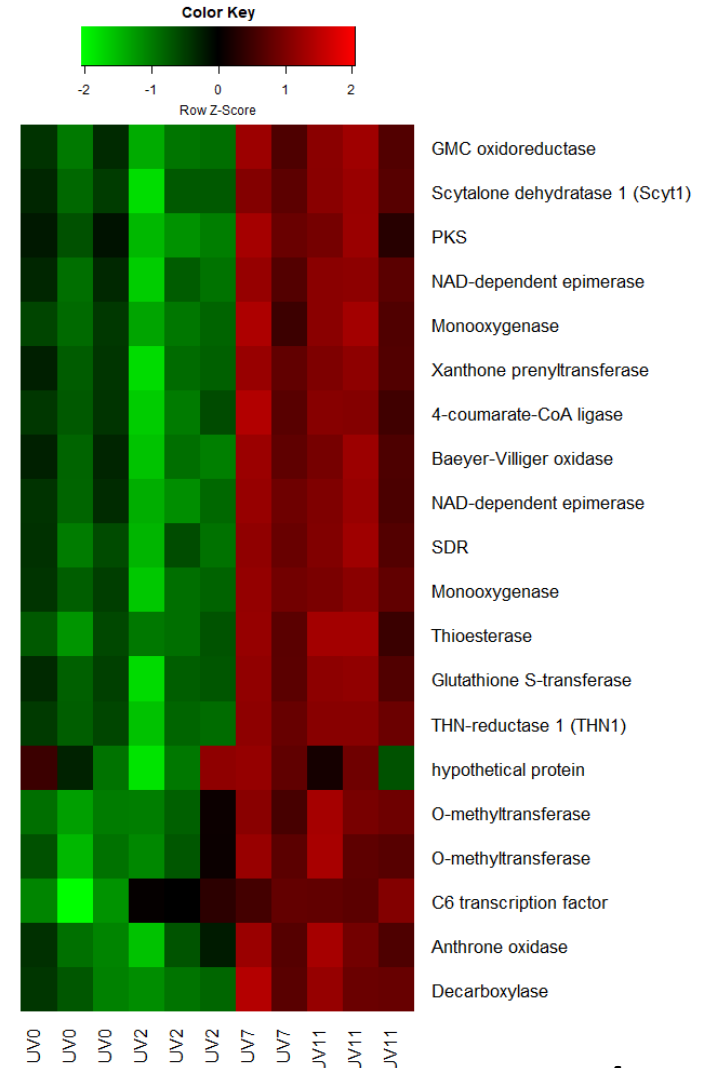
Gene expression DEGs related to the synthesis of melanins and xanthone in mycobiont

Melanin biosynthesis genes



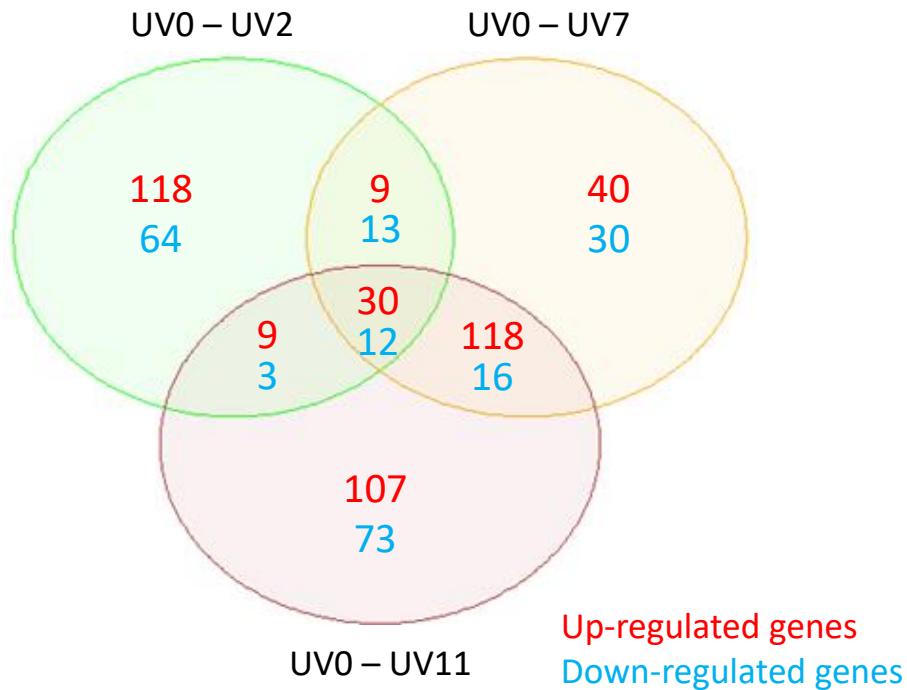
Tyr - tyrosinase
MCO – multi-copper oxidase
Scyt – scytalone dehydrogenase
THN – tetrahydroxynaphtolene dehydrogenase
PKS – polyketide synthase
Nmr_A – transcription factor NmrA
SDR – short-chain dehydrogenase
DHN - 1,8-dihydroxynaphthalene

Xanthone biosynthesis gene cluster

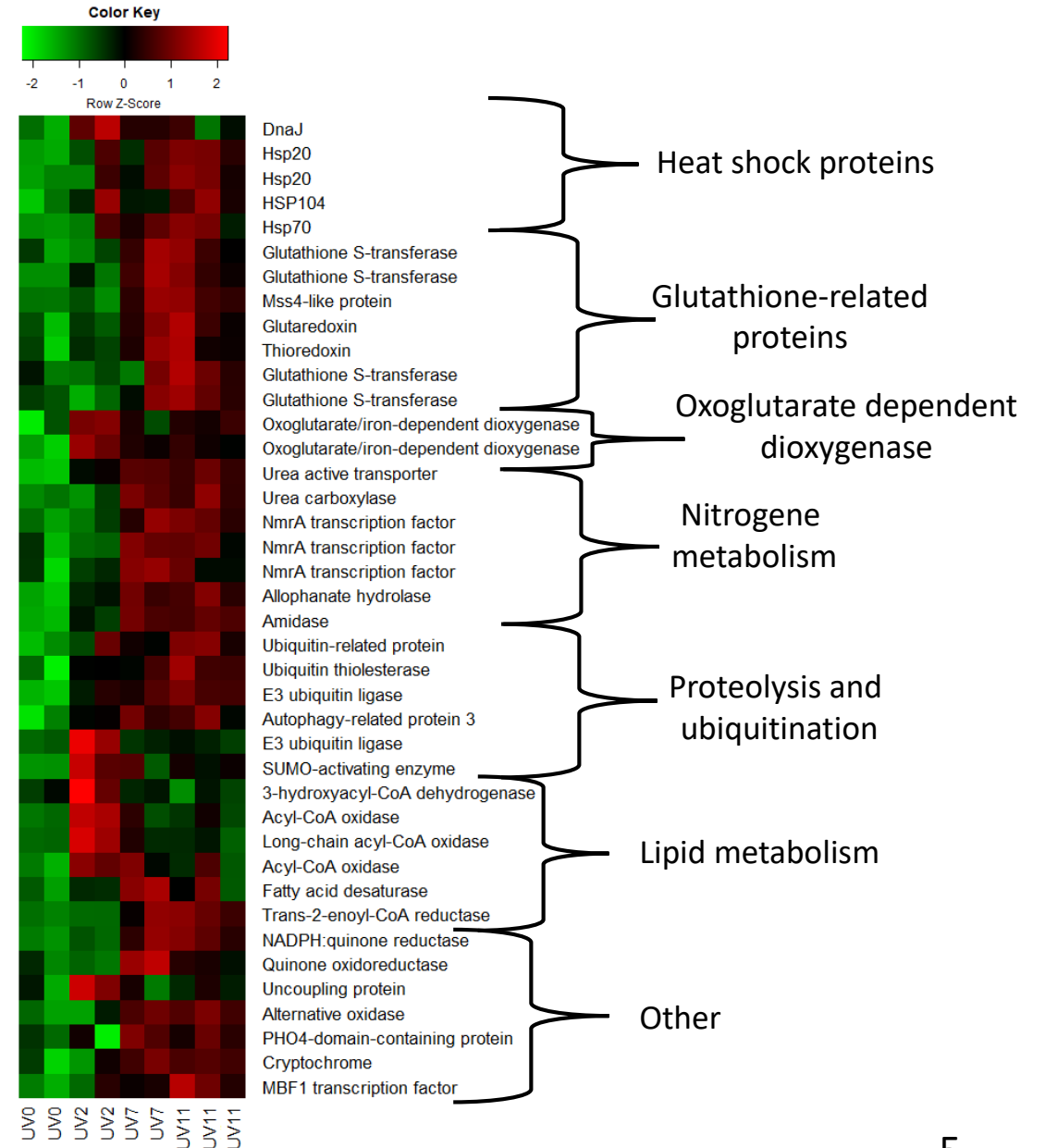


Photobiont DEGs

Pairwise comparison	Number of differential expressed genes	
	Up	Down
UV0 – UV2	166	92
UV0 – UV7	197	71
UV0 – UV11	264	104



Several photobiont DEGs related to stress tolerance



Conclusions

- 1) 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 shikimate pathway and amino acid metabolism.
- 2) Among differentially expressed genes of photobiont, the most up-regulated were the genes encoding heat shock proteins, antioxidant enzymes, alpha-ketoglutarate dependent dioxygenases, genes of nitrogen and lipid metabolism.
- 3) We showed that UV-B exposure of lichens induces the expression of genes involved in the synthesis of dark pigment melanin and prenylated xantone, the potential photoprotective metabolites. Interestingly, genes encoding alternative oxidase were highly expressed in both symbionts in UV-B exposed thalli suggesting the redistribution of the main respiratory pathways and energy metabolism.

This work was supported by RSF No. 18-14-00198.