Gene expression of a two-component regulatory system associated with sunscreen biosynthesis in the cyanobacterium Nostoc punctiforme ATCC 29133

Jacob Janssen
Indiana University - Purdue University Fort Wayne

Follow this and additional works at: http://opus.ipfw.edu/stu_symp2015

Part of the Biology Commons

Recommended Citation

This is brought to you for free and open access by the IPFW Student Research and Creative Endeavor Symposium at Opus: Research & Creativity at IPFW. It has been accepted for inclusion in 2015 IPFW Student Research and Creative Endeavor Symposium by an authorized administrator of Opus: Research & Creativity at IPFW. For more information, please contact admin@lib.ipfw.edu.
Gene expression of a two-component regulatory system associated with sunscreen biosynthesis in the cyanobacterium *Nostoc punctiforme* ATCC 29133

Jacob Janssen and Tanya Soule, Indiana University-Purdue University, Fort Wayne

**Introduction:** The cyanobacterium *Nostoc punctiforme* can cope with UVA stress by releasing a yellow-brown sunscreen pigment known as scytonemin into the extracellular sheath (Fig. 1). Based on comparative genomics, the production of scytonemin is hypothesized to be controlled by a putative two-component regulatory system (TCRS), NpF1277 and NpF1278, in *N. punctiforme* (Fig. 3). In this model, the sensor kinase (SK) senses UVA and phosphorylates the response regular (RR) to induce expression of the scytonemin biosynthetic gene cluster (Fig. 2). While expression of the genes in the scytonemin gene cluster have previously been shown to increase under UVA stress, the response of the TCRS genes has not been determined.

**Research Objectives:** The objective of this research were to determine 1) if the TCRS genes also respond to UVA and related stress conditions, and 2) the level of co-transcription between the TCRS genes.

**Materials and Methods:** *N. punctiforme* cells were exposed to either UVA ("~6 Wm⁻²), UVB ("~0.5 Wm⁻²), high light (135 mmols photons m⁻²s⁻¹), or oxidative stress (2 mM methylene blue) for 20, 40, or 60 min. Following each treatment, cells were harvested for RNA extraction. Following cDNA synthesis, the expression levels of NpF1277 and NpF1278 were measured against unstressed control samples using quantitative PCR on cDNA from cells exposed to 20 min UVA stress.

**Results and Discussion:** The TCRS genes generally had an early (20 min), up-regulated response to each treatment, with the exception of oxidative stress (Table 1). Both genes increased in expression following UVA stress for 20 min, and there with no significant difference in expression after 40 or 60 min of stress for either gene (Fig. 4).

While UVB and high light stress both resulted in the general up-regulation of the TCRS at 20 min, and no significant difference at 40 min, at 60 min cells exposed to UVB were down-regulated while those under high light stress were up-regulation. For oxidative stress, there was no significant change in expression for the duration of the experiment. These results suggest that NpF1277 and NpF1278 may regulate scytonemin biosynthesis since they respond to similar stress conditions as those that induce scytonemin. Furthermore, it appears as though the TCRS genes are co-transcribed (Fig. 5).

**Summary and Significance:** The TCRS genes, NpF1277 and NpF1278, associated with scytonemin biosynthesis respond to UVA, UVB, and high light stress. This response, however, is rapid and occurs within 20 min, much earlier than the 48 hrs required for peak expression of the biosynthetic genes. These genes are also not responsive to oxidative stress, which suggests that the TCRS is sensing UVA and not the reactive oxygen generated by UVA. Furthermore, the TCRS genes appear to be co-transcribed. This research shows how regulation occurs for the sunscreen scytonemin in cyanobacteria and how they cope with stress under certain environmental conditions.

**Acknowledgements:** We would like to thank the Indiana Academy of Sciences and the IPFW Office of Research, Engagement, and Sponsored Projects for the financial support to conduct this research as well as the IPFW Department of Biology for providing the facilities and additional support. We would also like to thank Dr. Vamsi Nalam for his assistance and expertise.

**References:**
1. Dillon, JG et al. (2002) Arch Microbiol 177(4) 322-331