Identification of cryptochrome-dependent signalling pathways in *Rhodobacter sphaeroides*

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Introduction

As all other phototrophic bacteria, *Rhodobacter sphaeroides* has to deal with photooxidative stress. Due to the formation of reactive oxygen species, when photosynthesis pigments are present together with light and oxygen, the bacterium has evolved mechanisms to tightly control the formation of its photosynthetic apparatus. AppA is a BLUF domain protein with dual abilities, sensing light and oxygen (1). AppA binds FAD and heme as cofactors and interacts with PpsR, the repressor of photosynthesis gene expression. *R. sphaeroides* contains several additional blue light photoreceptors, amongst others, a cryptochrome-like protein, named CryB (2). CryB also binds FAD as cofactor, shows a blue light-dependent, reversible photocycle and influences the amount or composition of photosynthetic apparatus. Cryptochromes, together with photolyases, belong to one superfamily. Despite CryB’s binding to ssDNA and RNA, it did not show significant photopairing of thymidine dimers in vitro (3). Here we show by transcriptome analysis that the deletion of cryB affects approximately 17% of all genes under O$_2$ stress and 32% under blue light exposure. The most and highly affected genes are part of energy production and consumption and of transport systems. The data was validated by real-time RT-PCR. The altered expression of a small RNA under O$_2$ exposure was proven by Northern Blot analysis. We could also show by pulldown and Western Blot analysis that CryB interacts with AppA which brings two blue light photoreceptors in a closer relation. A Yeast-Two-Hybrid system revealed further possible interaction partners.

1) Microarray transcriptome analysis comparing WT to ΔcryB

- **A** Overview of microarray data and validation of selected targets
- **B** Northern Blot analysis
- **C** Yeast Two-Hybrid system reveals possible interaction partners of CryB

**Fig. 1:** Transcriptome analysis of *Rhodobacter sphaeroides*. Using Agilent Technology, Inc. microarrays to compare wild type (WT) to ΔcryB deletion-extracted (ΔcryB).

**Fig. 2:** Overview of microarray data and validation of selected targets

**Fig. 3:** Yeast Two Hybrid system revealed possible interaction partners for CryB. These can be confirmed by β-galactosidase activity assay.

### References