

PhD position

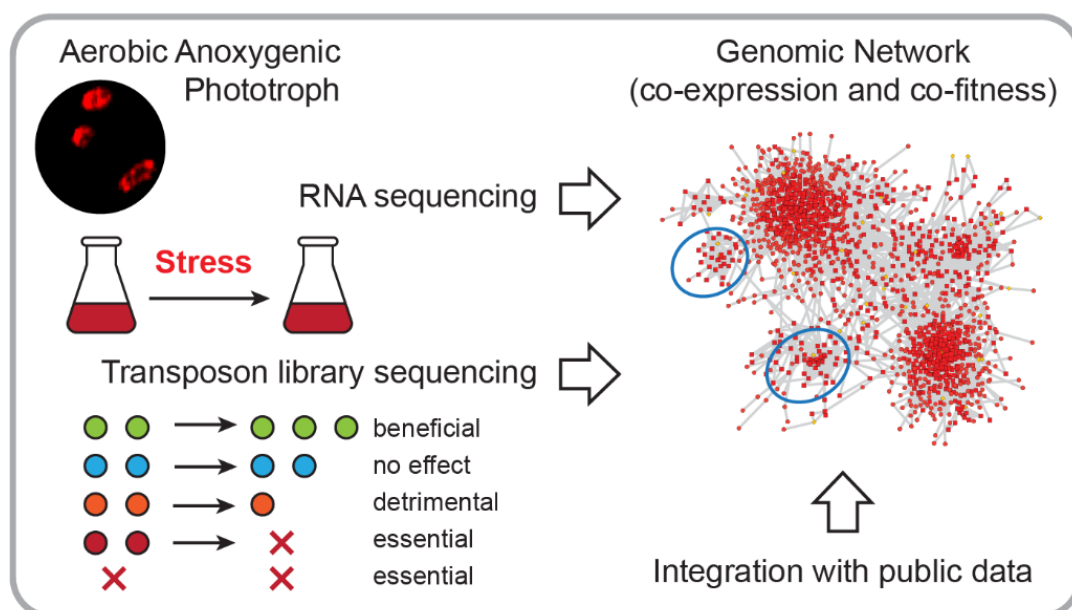
Systems Biology of the Stress Response in a Marine Anoxygenic Phototrophic Bacterium

Bacteria using aerobic anoxygenic photosynthesis (AAP) to complement their heterotrophic lifestyle are found in all sunlit habitats on earth and can account for up to 25% of the microbial communities[1]. Our model AAP bacterium *Dinoroseobacter shibae* is a representative of the *Roseobacteraceae* phylum that consists of important players in all marine ecosystems around the globe. *D. shibae* has been isolated from a dinoflagellate culture and can switch from mutualism to pathogenicity towards the algal host[2]. Various aspects of its versatile metabolism have already been characterized, including anaerobic nitrate respiration and quorum sensing. The transcriptional regulators of photosynthesis genes have been identified[3] and the physiological response to light has been studied in great detail[4–6]. To date, *D. shibae* is the best understood AAP bacterium.

The Project

The photoheterotrophic lifestyle places a constant burden on *D. shibae* as light facilitates the formation of reactive oxygen species[7]. This aspect has so far not been studied in great detail[8]. Your aim is to identify the general and specific responses of this AAP bacterium to various stress conditions, focused on, but not necessarily restricted to oxygen and light. To this end you will use physiological assays, transcriptomics (RNAseq), and a library of transposon mutants in challenging experiments (Transposon insertion sequencing, TnSeq).

You will systematically monitor the survivability of *D. shibae* with various sources and concentrations of reactive oxygen sources and light intensities. The results of these experiments will allow the determine the right conditions for the following experiments. The time-resolved transcriptional response to different stressors will help to identify shared and unique regulatory pathways. Transposon-insertion sequencing will allow to pin down genes that are essential (or detrimental) under the tested stress conditions but are not differentially expressed. You will reconstruct a genome-scale network of the *D. shibae* stress response using the generated co-expression and co-fitness data and integrate your data with the vast body of transcriptome and TnSeq data available for *D. shibae*[9]. Identified genes of interest can be selected from a library of knockouts for further characterization.



Your Profile:

You hold a master degree in a relevant biological field. You have experience with microbiological and/or molecular biological laboratory work. The employed methods require careful handling of small amounts of biological material. A robust knowledge of basic statistics is essential and previous experience in Linux shell and R or Python scripting is of great benefit, as large-scale data analysis is a big part of the project. However, we can also help you to acquire the necessary scripting skills here.

Our Profile:

Center Algatech is part of the Institute of Microbiology of the Czech Academy of Sciences. The center is located in the small spa town Třeboň in South Bohemia, Czech Republic, embedded in a beautiful landscape dominated by numerous ponds. The focus is on basic and applied science of photosynthetic microorganisms. In our group we research aerobic anoxygenic phototrophic bacteria from different angles, covering their ecology, physiology and evolution, the structure and functioning of photosynthetic protein complexes and transcriptional control of photosynthesis genes. Your project will benefit from the established routine generation of multiplexed RNAseq libraries and the already prepared library of mutant strains for TnSeq, leaving more room for you to develop own ideas.

Contact:

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References

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