

## SynChips

### **Combined microarray hybridization and transposon mutagenesis to study the impact of environmental stresses on marine *Synechococcus***

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#### **Abstract**

Marine phytoplankton which comprises all the photosynthetic organisms smaller than 2  $\mu\text{m}$ , represents more than 80 % of the chlorophyll biomass in the intertropical, nutrient-depleted (oligotrophic) regions of the world's ocean. It includes small eukaryotes phylogenetically very diverse and two main genera of cyanobacteria: *Prochlorococcus* and *Synechococcus*.

*Synechococcus* spp. cells can virtually be found in any seawater sample. Their pigmentation widely differs whether they are located in blue, nutrient-poor waters of the oceans or in green, nutrient-rich waters. However, very few *Synechococcus* strains are able to change their pigmentation and adapt to both conditions. Instead, there are ecotypes adapted for each environment. The two first *Synechococcus* strains (Wh8102 and 7803) which have been completely sequenced are representative of the two major oceanographic conditions found in the field: oligotrophic or mesotrophic. The SYNCHIPS project focusses on *Synechococcus* WH7803 which is representative of marine mesotrophic waters. The total genome sequence of this strain has been sequenced by the Genoscope in Evry/France in the course of 2004.

Comparative genome analysis shows that *Synechococcus* WH7803 has more signal transduction genes, i.e. is adapted to a more variable environment. Thus, the total genome sequence of this strain adapted to mesotrophic conditions provides a unique basis for fundamentally new insights into the molecular responses to environmental stress.

Currently, however, functions can be assigned only to about 60 % of the genes of any organism. Thus, methods that can be used to study the function of thousands of genes in parallel are needed to make efficient use of genomic information. SYNCHIPS focusses on the following aims:

- 1. Develop a partial then a full DNA microarray for *Synechococcus* sp. WH7803 to measure changes in global gene expression in response to varying environmental conditions.**
- 2. Develop a saturating random transposon mutagenesis approach for this type of marine cyanobacteria and combine the microarray hybridization with it to identify conditionally essential genes, i.e. genes that are required for growth under one condition but not another.**
- 3. Use these technologies to assess the role and regulation of genes involved in the acclimation/adaptation to light and nutrient stresses.**

Ultimately, the results obtained in the course of this study will help to determine the physiological status of natural populations submitted to specific niches in the ocean. Understanding these processes will be of critical value to assess the effects of environmental changes in marine systems.