Cyanobacteria are the prokaryotes that grow by photosynthesis in a similar way to plants. These microorganisms are the oldest oxygenic phototrophs, converting solar energy and CO_2 into bioenergy and 50-65% of the molecular oxygen required to sustain aerobic life on Earth. They are also recognized for their sustainable production of biofuels and other valuable secondary metabolites, and for their ecological role as many species are important primary producers. Unfortunately, they are particularly vulnerable to the damaging effects of excess light or UV irradiation. In addition, like virtually all living species, cyanobacteria must adapt to limiting nutrient concentrations and abiotic stresses, such as high salinity. With global climate change and over-fertilization leading to high salinity and nitrate pollution of surface water sources, understanding cyanobacterial ecology is crucial for maintaining biodiversity, nutrient cycling, and overall ecosystem health. However, this requires an understanding of the molecular mechanisms governing their adaptation to environmental stresses.

Intriguingly, small regulatory RNAs (sRNAs) play a versatile role in bacteria, coordinating gene expression during various physiological processes, in particular stress adaptation. Although we have extensive knowledge about the importance of nitrogen fixation and photosynthetic protein modules, we know relatively little about how cyanobacteria cope with abiotic stress. To fill this gap, we plan to elucidate how different types of sRNAs precisely interact with their target transcripts to regulate protein levels and maintain cellular homeostasis under stress conditions.

Therefore, this project aims to investigate the role of sRNAs in regulating gene expression during stress adaptation in the highly recognized model cyanobacterium *Synechocystis sp.* PCC6803. Based on our preliminary data identifying several novel sRNAs, we propose the working hypothesis that in response to environmental stress, the cellular profiles of sRNAs change to allow selective degradation and accumulation of transcripts critical for cyanobacterial growth and survival.

Thus, we aim to address a fundamental question: to elucidate the role of specific sRNAs responsible for the adaptation to abiotic stress using a multidisciplinary approach. The results of this application in the long term, this could lead us to develop one day a feasible strategy of improving higher plants and crops to adapt to suboptimal growth conditions.