Physiological performance under high salinity conditions of *Nostoc commune* from hot and cold deserts

Roncero-Ramos B.¹, Savaglia V.¹, Wilmotte A.¹

¹ Department of Life Sciences, InBios-Center for Protein Engineering, University of Liège, Belgium

Cyanobacteria are phototrophic bacteria that grow in extreme environments, such as those in drylands or polar zones, where they are the first photosynthetic colonizers of soils and sediments. Strong resistance traits underpin their occurrence in these extreme and contrasted environments, for example, the production of pigments (such as the UV-screening scytonemin) or exopolysaccharides help them to withstand hostile conditions. A better understanding of the ecophysiological mechanisms developed to survive to different stresses will contribute to clarify how these processes work. In this study, we analyzed the ecophysiological response to an increasing salinity of two cyanobacterial strains identified as belonging to the same species, Nostoc commune (16S rRNA gene similarity > 99%), but isolated from two contrasted environments: a microbial mat in a lake (Larsemann Hills, Prydz Bay, East Antarctica) and a biological soil crust from a semiarid region in Southeastern Spain (a limestone quarry (Gádor)). After culturing them in BG11₀ medium with different salinities (from 0 M to 2.5 M NaCl) under a light intensity of 5 μ mol m⁻² s⁻¹, the pigment (chlorophyll, scytonemin and carotenoids) contents and the photosynthetic efficiency (F_v/F_m measured by Pulse-Amplified Modulation spectrophotometry) were determined after 1 hour, and 1, 7 and 43 days. Our results show that both strains were affected by salinity as the maximal chlorophyll and carotenoids yields were obtained after 43 days of cultivation without NaCl. The Antarctic strain could also grow in media with salinity concentrations up to 0.7 M NaCl, with an increase of physiological stress with salinity. In contrast, the strain from the hot desert could only grow till salinities of 0.05 M NaCl, with a similar increased stress. This work will contribute to a better understanding of the performance to salinity stress of related cyanobacterial strains growing in different extreme environments. However, further analyses relating these results to gene expression (RNASeq) would be desirable to obtain a more detailed understanding of these mechanisms.