

## **Title: Investigation of role and diversity of mineral-bioforming bacteria and their adaptation in evaporitic environments of Qatari Sabkha**

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January 01, 2023; Accepted: January 03, 2023; Published: March 27, 2023

The roles of extremophiles and of bacteria tolerating harsh conditions in ecosystems is still not well-known. Their contribution to the production of greenhouse gases, as well as to the major carbon, nitrogen and nitrate cycles is far from negligible. Often, the genome contains more than 90% of genes coding for proteins with unknown functions in extremophiles. Some tolerant bacteria are also abundant at harsh conditions. For what reasons? Their biological macromolecules known to be extracellular must necessarily adapt to the physico-chemical conditions, to the particular nutritional and energy resources of these extreme environments. These constraints can lead to the emergence of new metabolic pathways using substrates and cofactors different from those used by “conventional” organisms. Over the past 30 years, we have witnessed the discovery of an extraordinary diversity of microorganisms inhabiting environments previously thought to be hostile to life such as the evaporitic environments named Sabkhas. In all types of adaptations associated with microbial life in “extreme” conditions, changes in protein structures profoundly alter the biochemistry and physiology of biological systems.

In our research projects, halophilic bacteria (moderate and extreme) have been isolated from hypersaline evaporitic environments of Qatar Sabkhas. Their taxonomic biodiversity found in these environments is essentially linked to their characteristics: aerobic, halophilic and heterotrophic. We showed, using proteins profiles analyses, that they are endowed with metabolic and physiological activity involved in transformation and degradation of organic pollutants but in forming many types of minerals. They may exhibit the capability to induce and or mediate carbonate minerals formation including high magnesium carbonates considered as precursor of dolomite. The most representatives are essentially belonging phylogenetically to the genera, *Bacillus*, *Virgibacillus*, *Pseudomonas*, and *Halobacillus*. The ribotyping and MALDI-TOF/PCA analyses using their protein profiles used for the phylogenetic comparison, showed that many adaptation routes were implemented by these strains

### **Biography**

Prof Nabil Zouari is Full-Professor of Biotechnology and Environmental Microbiology at the Department of Biological and Environmental Sciences, College of Arts and Sciences, Qatar University. He obtained his PhD degree in Microbiology, Enzyme Engineering & Bioconversion from the University of Technology of Compiègne (UTC, France). He has 35 years of experience in Teaching and Research & Development in the fields of Environmental and applied Microbiology and transfer of technology in France, Tunisia and Qatar. Prof Nabil published more than 90 papers in international indexed journals.