



INSTITUTIONEN FÖR MARINA VETENSKAPER

## **From Sea to Society**

Climate Change, Microbial Community Interactions and Assessing  
Climate Risk on Society

**Gurpreet Kaur Kahlon**

Institutionen för marina vetenskaper  
Naturvetenskapliga fakulteten

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## *Abstract*

Unicellular organisms, microalgae and bacteria, less than one millimeter in size make the world go round. Phytoplankton and cyanobacteria, for example, plays an inevitable role contributing 50-85% to the world's oxygen via photosynthesis. Bacteria, one of the first life forms to appear on earth, are vital for nutrient cycling both in the terrestrial, limnetic and marine ecosystems. Both phytoplankton and marine bacteria in addition form an important foundation of marine food webs. The adversities of climate change loom large on the two, as impacts at the level of primary production will most likely have a bottom up effect across the different trophic levels. Warming of the earth system is proceeding at a rate that is unprecedented, yet its effects on the world's largest ecosystem, the marine pelagic realm, are largely unknown. Using experimental approaches including mesocosm settings and gene-expression analysis, this thesis aims to increase our understanding of climate-induced processes in a costal pelagic tropical ecosystem in southwest coastal Arabian Sea. The results show that sea surface warming and freshening is likely to cause an increase in the abundance of phytoplankton in winter season. While in the summer, freshening of sea surface water can be a leading cause for the increase in phytoplankton growth. The findings presented in this thesis also highlight the tight coupling between phytoplankton and bacterial community. Any impact of warming and freshening is subsequently propagated to bacteria as increased phytoplankton biomass supports increased biomass of bacteria. To understand the underlying bases of this phytoplankton-bacterial interrelationship, it is important to recognize the communication over species borders. We looked for signs of existing cross signalling between a predominant bacterial species, *Vibrio harveyi*, and a dominant diatom species, *Skeletonema marinoi*. In *V. harveyi*, quorum sensing (QS), cell-to-cell signalling among bacteria, indirectly regulates bacterial virulence gene expression. Previous studies have shown this communication being interrupted by inhibitory compounds produced by some species of macro- and microalgae. Our results indicate activation of QS in *V. harveyi* strains during the experiment period, but QS did not regulate the expression levels of virulence factors. This suggests that the QS activity of *V. harveyi* was not interrupted by the presence of *S. marinoi* strain, implying that this diatom-bacteria relationship may in this respect be considered a commensalistic relationship. In the face of climate change, our results make important predictions for the future scenarios suggesting faster growth and development of microbial blooms, both phytoplankton and bacteria including pathogenic bacteria and toxin-producing phytoplankton. These can accumulate in commercially important bivalves, subsequently passing to higher trophic levels. This may have considerable implications for seafood safety, putting human health at high risk. We propose an integrated science-social science framework for assessment of human vulnerability to climate change effects in marine ecosystems. This can help to weigh, more explicitly and systematically, human vulnerability influenced by complex and simultaneous environmental and socio-economic changes.

*Keywords:* Phytoplankton, Bacteria, Climate change, Quorum sensing, Microbial blooms, Vulnerability factors, Arabian Sea, Southwest India