

Macroalgal-bacterial interactions: Insights into the chemical ecology and developmental biology of the sea lettuce *Ulva* (Chlorophyta)

Thomas Wichard

Friedrich-Schiller-Universität Jena, Institute of Inorganic and Analytical Chemistry, Jena School for Microbial Communication, Lessingstr. 8, 07743 Jena, Germany
Thomas.Wichard@uni-jena.de

There is a growing interest in the occurrence and diversity of metabolites used as chemical mediators in cross-kingdom interactions within aquatic systems. Bacteria produce metabolites to protect and influence the growth and life cycle of their eukaryotic hosts. In turn, the host provides a nutrient-enriched environment for the bacteria. The cross-kingdom interactions between the marine green macroalga *Ulva mutabilis* (Chlorophyta) and its associated bacteria depend strongly on chemical stimuli. A pre-requisite for the investigation of these signal mediated interactions is the availability of axenic cultures. Under axenic conditions, *U. mutabilis*-gametes develop into callus-like colonies.

Interestingly, the combination of two bacteria, *Roseovarius* sp. and *Maribacter* sp., can induce the morphogenesis *via* diffusible compounds and replace the bacterial flora of *U. mutabilis* completely. Upon chemoattraction of bacteria leading to a biofilm, morphogenetic compounds stimulate cell division (*Roseovarius*-factor) and rhizoid formation (*Maribacter*-factor) in *Ulva*. The alga grows and is directly connected to the bacterial biofilm by the rhizoid formation. In turn, *Ulva* delivers a glycerol boundary layer as a carbon source for *Roseovarius* sp.

A combined approach in analytical chemistry and molecular biology was used to understand this tripartite community from chemical mediators to algal development and morphogenesis. As a result, the transformation of *Ulva* by vector plasmid integration into the genome was developed. The chromosomal *Ulva*-RbcS gene was used for designing a dominant selective marker cassette for shuttle vectors introduced efficiently in *Ulva* gametes for expression of, e.g. GFP. As the *Ulva* genome is now available, the approaches in cultivation, chemistry and genetics along with the short generation time make *U. mutabilis* well suited to model studies in chemical ecology and a robust model system for exploring the evolution of multicellularity.

References: Wichard and Beemelmanns (2018) Journal of Chemical Ecology 44:1008–1021 (review); Wichard et al. (2015) Frontiers in Plant Science 6:86 (review); Kessler et al. (2018) Molecular Ecology 27: 1808-1819; DeClerck et al. (2018) Current Biology 28: 2921-2933.

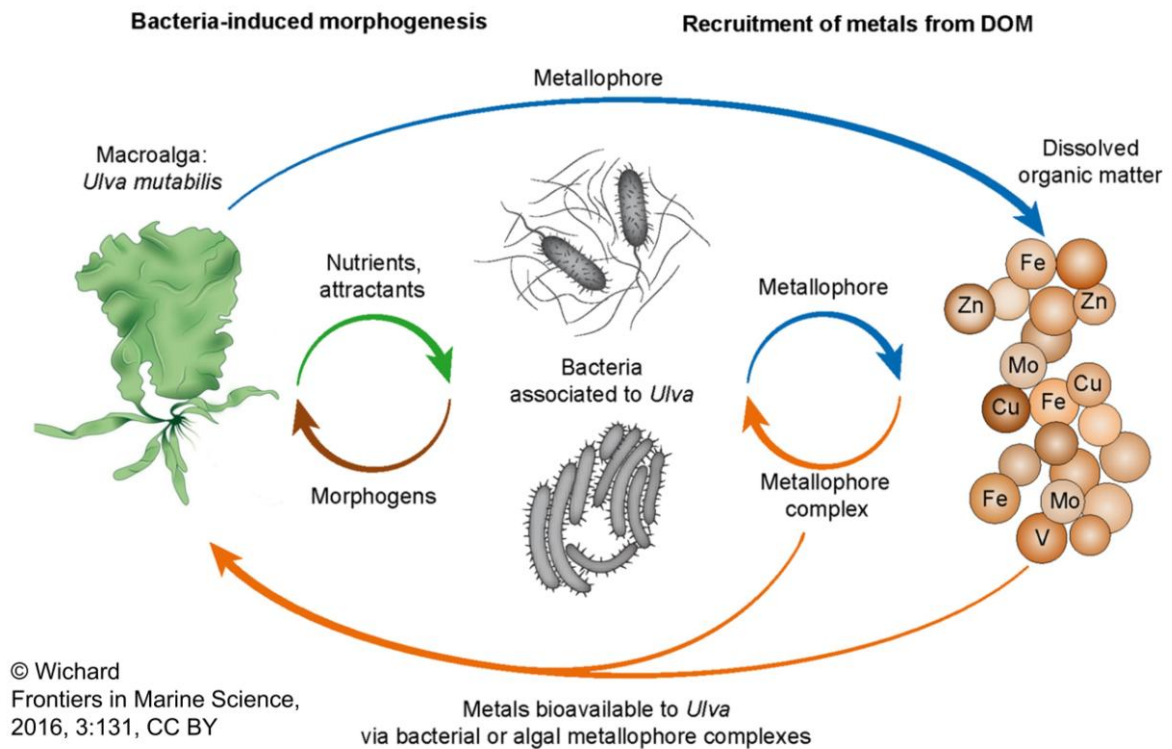


Figure: Mutualistic interactions are vital for *Ulva* and bacteria by releasing morphogens, nutrients, and attractants, and by controlling the metal acquisition by ligand exchange processes from particulate or dissolved metal-organic matter complexes within the chemosphere.