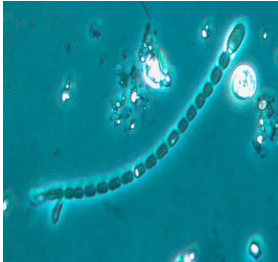




Exploratory project
2024–2025



Coordinators

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Keywords

Cyanobacteria, bacteria,
modelling, reconstruction
of metabolic pathways,
multi-omics approaches

Participating INRAE units

EABX
IEES
UNH

Partners

CNRS (France)
Inria (France)

Studying cyanobacteria–bacteria interactions in the phycosphere using in silico modelling and multi-omics in agrifood systems

Global change has led to a rise in cyanobacteria blooms, which come with serious health, environmental and economic consequences: degradation of ecosystem biodiversity; loss of aquaculture and fishing production; impacts on tourism with the closure of recreational sites; repercussions on plant, human and animal health (livestock deaths, contaminated vegetables, etc.) due to cyanotoxin poisoning; and significant economic costs for water treatment.

More specifically, blooms of the *Microcystis* genus have been described in the literature as some of the most detrimental. Reducing these blooms is therefore a major socioeconomic challenge.

Objectives

The consortium aims to gain a better understanding of how toxic cyanobacteria blooms form and persist by characterizing cross-feeding interactions (nutrient exchanges between microbial species) in the phycosphere between the major players in the world of plankton: cyanobacteria and heterotrophic bacteria. To do this, we propose an interdisciplinary approach combining meta-omics, mathematical modelling and environmental chemistry tools.

COMIC will leverage skills and knowledge from a range of complementary scientific disciplines to meet its objectives.

Partners

INRAE unit	Expertise	INRAE division
EABX	Environmental metabolomics; ecotoxicology	AQUA
IEES	Microbial ecology; cyanobacteria-heterotrophic bacterial interactions	ECODIV
UNH	Environmental metabolomics; microbial extract analysis; metagenomic data processing; biological networks	AlimH
Partner	Expertise	
CNRS (France)	Identification of new natural compounds and prediction of their functions; software for reconstructing metabolic pathways from the genome; mathematical modelling of biological networks at community level; cyanobacterial metabolism; metabolomics	
Inria (France)	Mathematical modelling of biological networks at the community level	