Access to the planktonic biodiversity of the northern Adriatic

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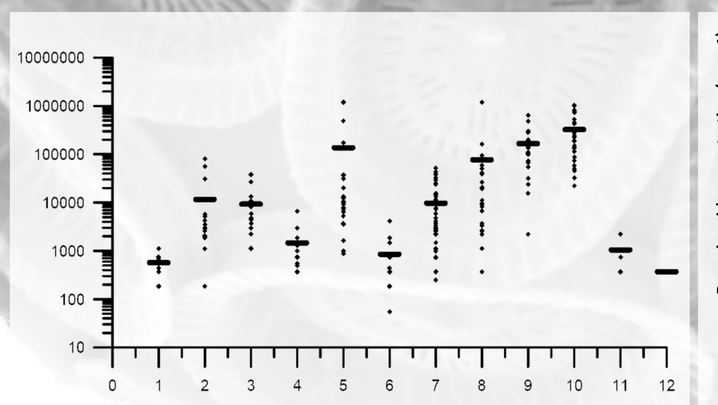
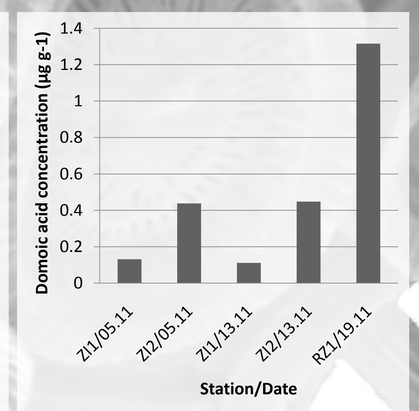
Abstract

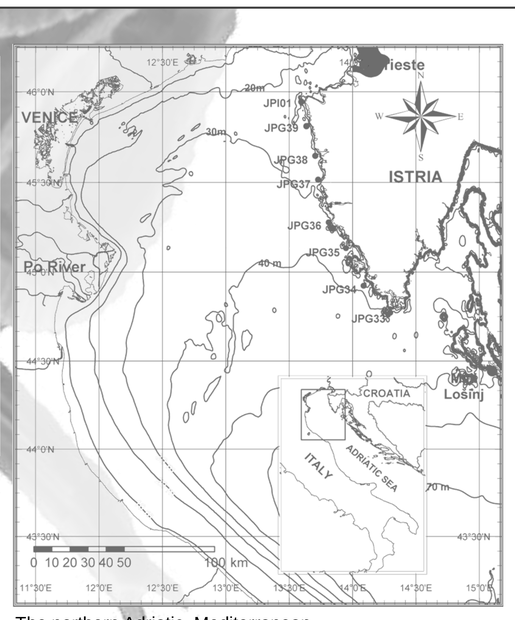
The northern Adriatic is the northernmost, shallow and enclosed part of the Adriatic (Mediterranean). It is characterized by complicated set of steep ecological gradients thus providing a large variety of ecological conditions. Due to its characteristics, the northern Adriatic is a natural experimental basin for a large variety of marine research topics (from climate change to the ecology of evolution). However, access to and detailed information about its biodiversity is still not organized at a desirable level. In a cooperation between the BGBM Berlin (Germany) and the CIM Rovinj (Croatia) we undertake first steps to institutionalize the access to data about the planktonic biodiversity as well as to the respective biodiversity resources. Efforts include the connection of local databases to the Global Biodiversity Information Infrastructure (GBIF), the connection of the phytoplankton cell culture at the CIM as well as the DNA-sample collection at the CIM to the DNA Bank Network. A formal investigation of the so far collected information about the northern Adriatics planktonic biodiversity aims at a taxonomically and systematically correct set of data. Tests of barcoding markers prepare for biodiversity analyses with next generation methods. This bilateral cooperation is supported by the German academic exchange service (DAAD) and the Croatian ministry for science, education and sports.



Temporal distribution of monthly mean of *Pseudo-nitzschia* spp. abundance in the northern Adriatic Sea.



Domoic acid (neurotoxin) concentrations produced by *Pseudo-nitzschia* sp. In the year 2011 in the northern Adriatic.

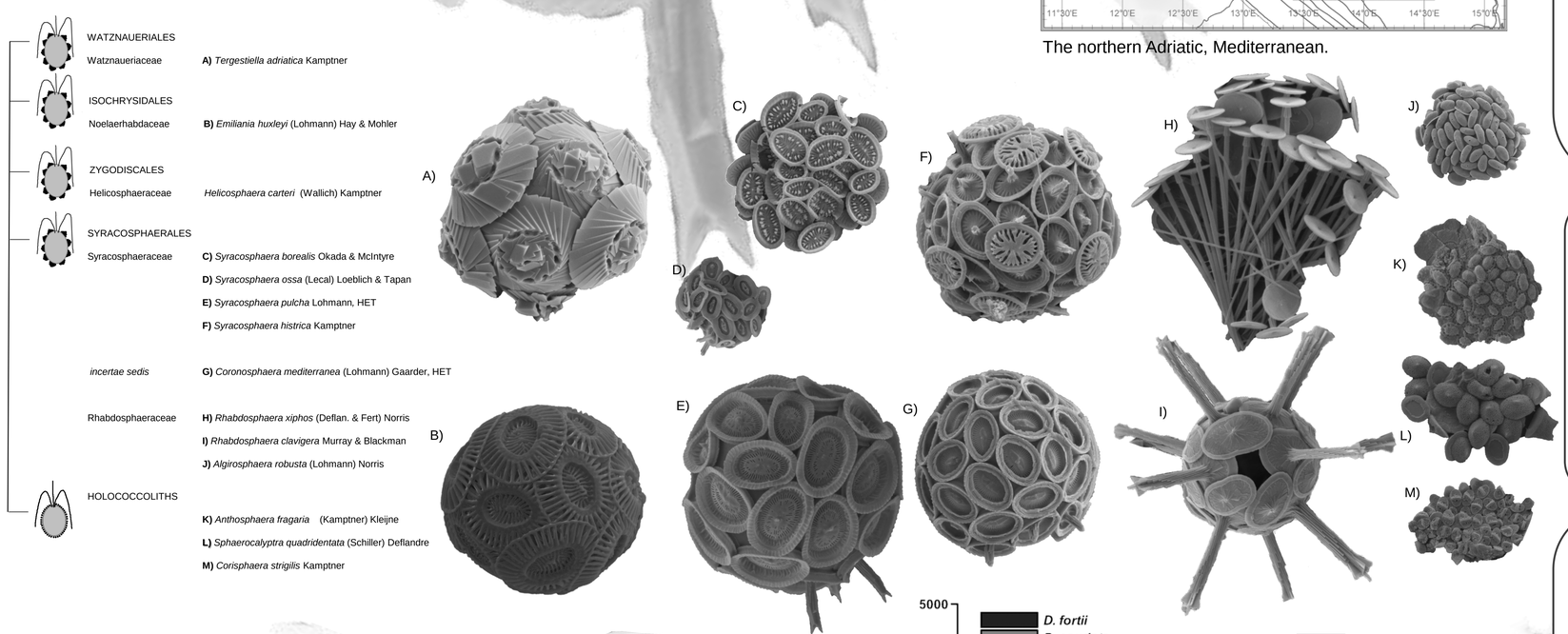


The northern Adriatic, Mediterranean.

Background

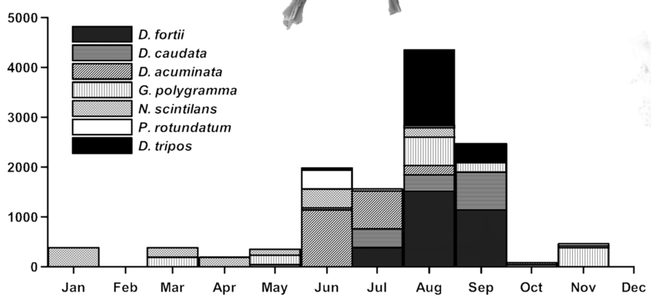
The northern Adriatic is an oceanographically well investigated area. Bulk parameters (*e.g.* concentrations of chlorophyll and pigments, lipid types, satellite imaging and remote sensing) are available in reasonable high spatio-temporal resolution. Light microscopic analysis from monitoring programs deliver a higher taxonomic resolution with identifications on group and species level. However, a closer look reveals that often the identification on species level is not possible (*e.g.* cryptic species) or not sufficient (strain or population related traits) to understand ecological phenomena and functions. We therefore aim at delivering tools to overcome those limits. Besides micromorphological approaches this also includes DNA based techniques, e.g. DNA barcoding using the protist PreBarcode 18SV4 (Pawlowski et al. 2012 – PlosBiol., Zimmermann et al. 2011 - ODE).

At the same time this approach should provide access to the extraordinary diversity concentrated in a relatively small marine basin, the northern Adriatic.



Focal topic: Coccolithophorids

Coccolithophorids play a major role in marine planktonic ecology and carbon fixation. Particular efforts (e.g. electron microscopy or molecular marker analysis) are necessary to identify and quantify coccolithophorid species. Again, identification on (at least) the species level is necessary to elucidate their ecological meaning.



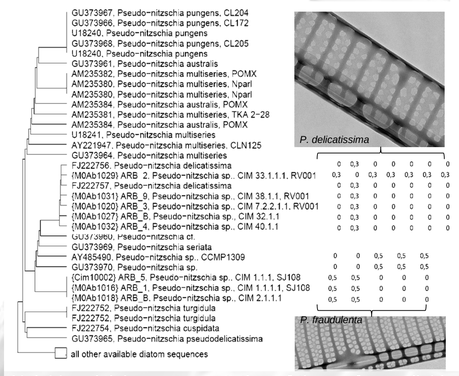
Maximal monthly abundances of toxic dinoflagellates in the year 2010 in the northern Adriatic.

Focal topic: toxic Dinoflagellates and Diatoms

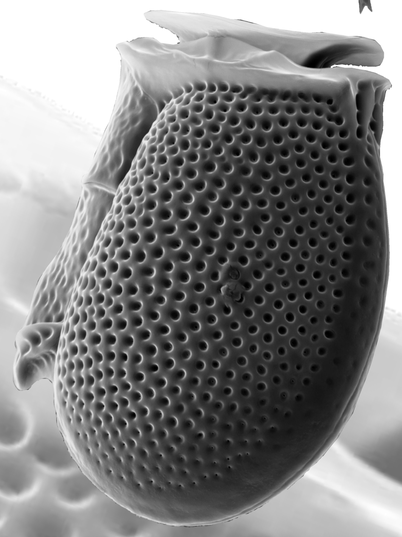
Harmful algae blooms often include the production of dangerous amounts of algal toxins. To understand the particular ecological circumstances that allow mass appearance of toxin producing species and to understand the particular adaptations of each toxic species/strain, a thorough understanding of the systematic background and an exact identification (species/strain level) is necessary.

In the case of the toxin producing diatom genus *Pseudo-nitzschia* H. Peragallo 1900 we experience a high level of cryptic species diversity and considerable phylogenetic uncertainty.

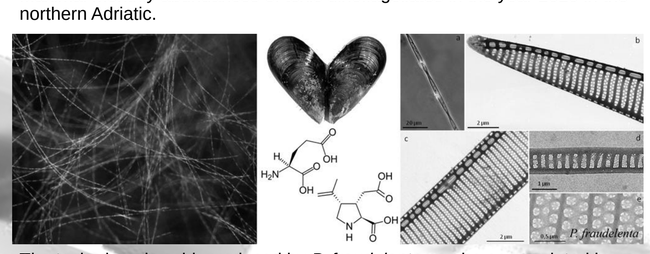
In the case of toxin producing dinoflagellates we face the peculiarity that already low abundances suffice for severe toxic effects (low detection limits are necessary) and again a considerable phylogenetic uncertainty with cryptic diversity. The identification of different species and strains is approached via the combination of morphological, chemical and molecular characterisation.



Neighbourjoining representation of the so far available *Pseudo-nitzschia* sequences (18S rRNA). Sequence differences are given within the *P. delicatissima* and the *P. fraudulenta* strains from the northern Adriatic. The cryptic diversity uncovered by molecular marker analysis helps explain the broad spectrum of environmental conditions leading to toxic bloom events.



Dinophysis fortii Pavillard 1923



The toxin domoic acid, produced by *P. fraudulenta* can be accumulated in filter feeders like the blue mussel.

Access to data and specimen

Live cell cultures and corresponding (sequence) information from the cell culture collection of the Center for Marine Research in Rovinj are made accessible through the DNA Bank Network. Information (identification and ecology) about the specimen and samples is made available through the Global Biodiversity Information Facility (GBIF). This approach is supported and facilitated by a bilateral project “Providing Access to the Phytoplankton Biodiversity of the Northern Adriatic Sea: Taxonomy, Systematics, Genetics, Ecology and Open Access Data Management” financed by the German academic exchange service (DAAD Project ID 54394574) and the Croatian Ministery for Science and Education.

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