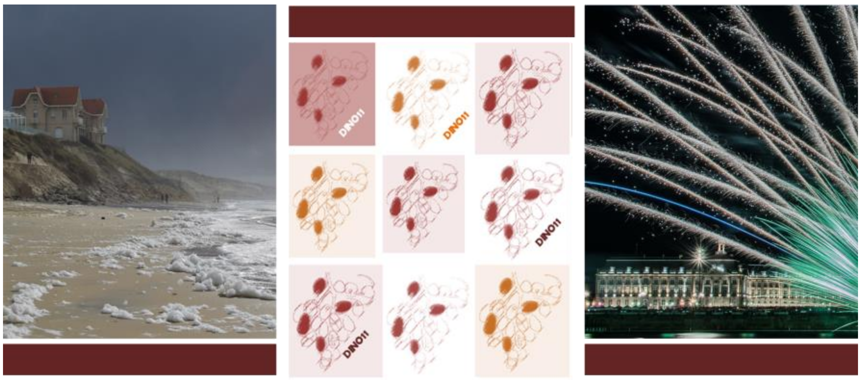

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Investigation of the metabolic pathways and interactions of DMSP and STX in *Alexandrium*

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Certain microalgae, such as the cosmopolitan *Alexandrium* genus, are able to produce metabolites that play a putative role in cell-to-cell signaling and defense mechanisms. At a larger scale, these molecules may also impact whole ecosystems and contribute to climate regulation. This is the case for dimethylsulphoniopropionate (DMSP) a molecule that influences climate via DMS emissions and saxitoxin (STX) that affects food safety. At the ecosystem level, both compounds may be part of the range of metabolites that structure relationships between marine organisms through chemical ecology for instance, in interactions of microalgae with their predators, viruses and parasites. Although DMSP and STX are very different chemically, these two relevant metabolites have methionine as a common precursor and unclear biosynthesis pathways. We present here the first results on our investigation of DMSP biosynthesis pathway in *A. minutum* and *A. catenella*. It includes search in an *A. minutum* transcriptomic database of transcripts corresponding to the diatom genes proposed for DMSP biosynthesis. To give a full picture, results also include search in *A. minutum* and *A. catenella* of the metabolic intermediates of DMSP biosynthesis proposed in algae. Therefore, new data lead to an update of the DMSP metabolic pathway in dinoflagellates, useful to pursue in investigating interactions with STX biosynthesis pathway.

Session 1.4: Toxic dinoflagellates: from cells to cysts. Poster presentation.

Molecular approaches for identification and quantification of harmful dinoflagellates

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In recent years, harmful algal blooms caused by dinoflagellates have become increasingly common in coastal waters throughout the world, causing negative impacts on human health, ecosystem quality and also affecting economic and commercial activities of the interested coastal areas. For the identification of potentially harmful microalgae, microscopy based methods are commonly used, but they are time consuming also requiring great taxonomic expertise. Thus, for the identification, counting and genetic characterization of these protists, more rapid, sensitive and specific molecular methods, such as real time PCR or microarray systems, have been developed and applied. Genus, species- specific primers and probes were designed on ribosomal DNA sequences (i.e. SSU, LSU and 5.8S genes, and ITS1 and ITS2 regions); they are suitable and highly informative molecular markers for studying the phylogeographic or phylogenetic relationships and the population genetic structure of the marine toxic dinoflagellates. The molecular methods have been applied to different kind of samples from cultured strains to field samples as surface seawater, macrophyte, sediment and aerosol samples in the Mediterranean Sea. These molecular systems proved to be effective tools for rapid, specific and sensitive detection and enumeration of potentially harmful microalgae, and thanks to their high throughput they can be applied in water monitoring programmes, to explore the community biodiversity and dynamics and to control and manage harmful blooms in marine coastal waters.