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ESTTAL

Expressed Sequence Tag (EST) Analysis of Toxic Algae

The Challenge

Harmful algal blooms (HABs) are caused by the proliferation of algae and are found in coastal waters throughout the world. Negative environmental effects include toxicity to human consumers of seafood, marine faunal morbidity or mortalities, habitat damage, disruption of marine food webs and economic losses to fishing, aquaculture, and tourism. Socio-economic factors and human health risk have led to comprehensive surveillance programmes for harmful microalgae and their toxins. Although structural identification of many of these groups of toxins has advanced, much less is known about their biosynthetic pathways and gene regulation.

The ESTTAL project proposed a limited genomic study of expressed sequence tags (ESTs) for toxigenic representatives of certain microalgal groups, including dinoflagellates, raphidophytes, cyanobacteria, prymnesiophytes and diatoms. Cultures were grown under various environmental conditions to investigate the effects of external factors on gene expression linked to toxicity and growth.

After cloning of cDNA of toxigenic strains the approach taken was to annotate ESTs and attempt identification of genes associated with toxin production, growth regulation, cell cycle, stress responses and induction of sexuality. DNA microarrays were developed for screening of toxigenic and non-toxigenic strains. In addition, the sequence data were analysed to identify other genes that may be involved in cell regulation or growth, cell cycle events, stress response and the induction of sexuality

Project Objective

The ESTTAL project aimed to provide new information on microalgal and cyanobacterial genomic sequences for a diversity of taxa and assisted in the diagnosis of genes related to toxin biosynthesis and the formation of toxic blooms. The project contributed to the understanding of genetic regulation of growth and algal bloom formation in response to environmental stimuli. This information can be used in the development of EU policy on HAB dynamics regarding human activities and the input of nutrients into coastal waters.

Construction of DNA microarrays to study gene expression in toxic algae under controlled physiological conditions

Key Points

- Development of a selected EST database for target toxic algal species for future genomic analysis
- Provision of comparative sequence data to examine the gene expression of particular metabolites, e.g. phycotoxins, stress proteins, and other bioactive compounds

EATiP Thematic Area of Relevance

TA1: Product Quality, Consumer Safety and Health

TA2: Technology and Systems

TA3: Managing the Biological Lifecycle

TA4: Sustainable Feed Production

TA5: Integration with the Environment

TA6: Knowledge Management

TA7: Aquatic Animal Health and Welfare

TA8: Socio-Economics and Management

Key Words

Harmful Algal Blooms, Expressed Sequence Tags, Genomics, toxin production genes, growth regulation genes

Project Information

Contract number:

511154

Contract type:

Specific Targeted Research Project

Duration:

45 months (01/12/2004 - 31/08/2008)

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- Contribution to the understanding of genetic regulation of biochemical pathways leading to synthesis of phycotoxins
- Contribution to the understanding of genetic regulation of growth and algal bloom formation in response to environmental stimuli
- Construction of DNA microarrays to study gene expression in toxic algae under controlled physiological conditions

Output Highlights

New information on toxic genes

The ESTTAL project provided new information on microalgal and cyanobacterial genomic sequences for a diversity of taxa and will assist in the diagnosis of genes related to toxin biosynthesis. It has produced a data-set that will allow a better understanding of formation of HABs and the molecular basis of toxin production. Knowing the sequences of toxin genes will allow for the recognition of these genes, or their transcripts, in the environment.

New understanding of bloom formation

The project generated a sequence data-set on genes related to toxin expression and the interactions of genetic and environmental factors (light, salinity, temperature, nutrients) influencing growth and hence bloom formation for a diversity of prokaryotic and eukaryotic algal species including the cyanobacteria, dinoflagellates, raphidophytes, prymnesiophytes, and diatoms.

Bloom prediction

Data gathered will assist in the diagnosis of genes related to toxin biosynthesis and the formation of toxic blooms, when interpreted with reference to the EST sequence data-base, the integration of genetic data with environmental forcing functions should contribute to a better understanding of the regulation of growth, leading to the phenomenon of bloom formation. Understanding the factors influencing toxicity will ultimately assist in prediction of the magnitude and environmental consequences of specific HABs and therefore constitutes an important element of an early warning system.

Standardisation of approach

The ESTTAL comparative approach to sequence data-base analysis will assist in the standardisation of methods and will assist in reducing operator-introduced variability in data sets.

The Full Report:

For a description of the research project, visit <http://genome.imb-jena.de/ESTTAL/cgi-bin/Index.pl>

Next Steps – Suggested Actions/Follow On



RTD

- The sequences of these genes are available to the scientific community and have the potential to assist marine biologists and genomics researchers from a variety of disciplines (including phylogeny, systematics, taxonomy, gene expression and biodiversity research). The sequence data will also add to the data-set generated by the EU Network of Excellence on Marine Genomics.



Networking

- Information gathered during the project can contribute to the formulation of EU policy regarding the potential effects on HAB dynamics and the input of anthropogenic nutrients into coastal waters..

Related Publications/Projects

GENBANK - Sequence data generated during ESTTAL will be provided to public scientific archives.