Marine Genomics 4 Users

THE USE OF GENOMICS FOR MARINE MONITORING: AN INTRODUCTION TO THE LATEST TOOLS AND TECHNIQUES

POLICY BRIEF

As part of the EU funded project "Marine Genomics for Users" (MG4U), a White Paper titled "Genomics in marine monitoring: New opportunities for assessing marine health status" has been published (Marine Pollution Bulletin, May 2013) that describes the potential application of Marine Genomic tools and techniques for use in marine monitoring.

This Policy Brief is intended to be a summarised version of the "White paper" for use as an information and discussion document specifically for policy makers.

The research leading to these results has received funding from the European Union's Seventh Framework Programme (FP7 /2007-2013) under grant agreement no 266055. This publication reflects the views only of the author, and the European Union cannot be held responsible for any use which maybe made of the information contained therein.

MARINE GENOMICS APPLICATIONS

BACKGROUND

One area of specialisation within Marine biology, the emerging field of marine biotechnology, offers great opportunity for marine biologists and a wide range of possible applications. Molecular biology is a related area of specialisation in this field. Researchers apply molecular approaches and techniques to many different organisms, from microscopic bacteria, plants and simple animals to marine mammals found in the various aquatic environments, from coastal ponds to the deep sea. For example, molecular biology can be used to identify the presence of a specific organism in a water sample. This is very useful when the organism in question is microscopic or of similar aspect to other organisms. The study of disease in organisms has also been aided by the use of molecular techniques. For example, researchers have developed specialised proteins (*antibodies*) that are specific to a particular disease agent – a *virus*, so that when the virus is present in the organism, detection and diagnosis are easier and faster. Likewise, new molecular techniques help scientists identify whether or not an animal has been exposed to pollutants and, in some cases, can determine the source of those pollutants. The field of molecular biology is growing and will continue to see significant advances.

THE MARINE CHALLENGE

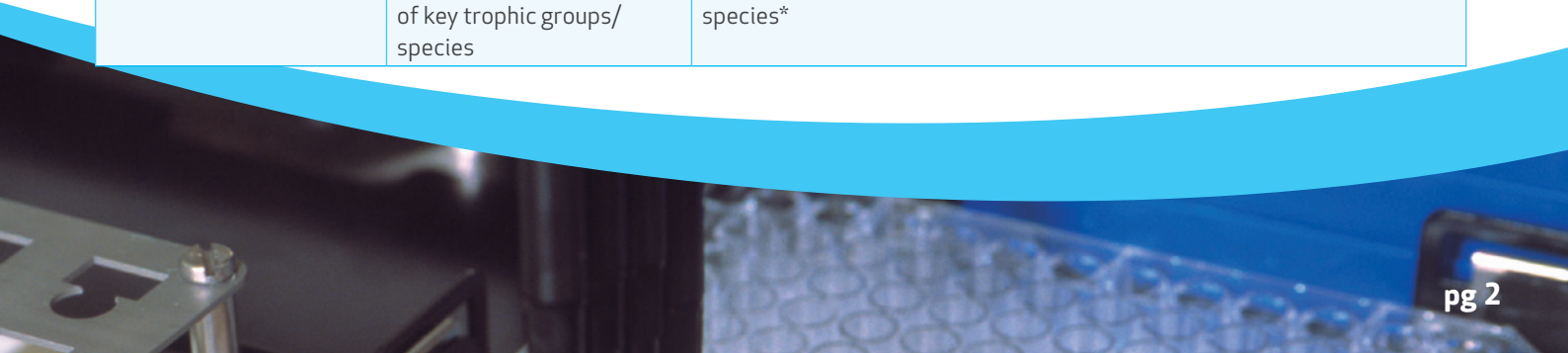
The interest in marine ecosystem protection and sustainable use of oceans has developed worldwide and the topic is now often part of legislation acts: in Canada, with their 'Oceans Act' (1997); and in the USA, with the 'National Ocean Policy' (2010). Europe adopetd the Marine Strategy Framework Directive (MSFD) in 2008. This policy focuses on the use of integrative monitoring tools for assessing the marine environmental status.

The EU MSFD is a good example of the policy approaches developed using current concepts of ecosystem-based management. Its aim is for all EU countries to achieve or maintain Good Environmental Status (GES) in their waters, by 2020. The environmental status is defined by 11 descriptors (e.g. alien species, fishing, eutrophication, seafloor integrity, etc.), and the maintenance of biodiversity is a cornerstone of GES.

The MSFD provides a framework for the exemplification of the application of genomic techniques in relation to marine environmental status assessment. To undertake such an assessment, the above-mentioned marine legislation requires adequate and rigorous monitoring at different spatial and temporal scales (sampling area and frequency). Despite the important costs that would be associated with failing to achieve the strategy's objectives, i.e. recovery and remediation policies and managerial actions, the current global economic crisis is leading many countries (and industries) to try and save on their environmental protection budgets. This only adds further motivation for adopting new, more cost-effective methods to monitor and assess marine waters, with the innovative application of the recent scientific advances.

Table 1: Qualitative descriptors and different criteria and indicators, to be used in environmental status assessment within the Marine Strategy Framework Directive, selected by the European Commission (2010). Asterisks show the indicators for which genomics could be used in monitoring and assessment.

DESCRIPTOR	CRITERIA	INDICATOR
1: Biological diversity	1.1 Species distribution	1.1.1 Distributional range*
		1.1.2 Distributional pattern within the latter*
		1.1.3 Area covered by the species (for sessile/benthic species)
	1.2 Population size	1.2.1 Population abundance and/or biomass
	1.3 Population condition	1.3.1 Population demographic characteristics
		1.3.2 Population genetic structure*
	1.4 Habitat distribution	1.4.1 Distributional range
		1.4.2 Distributional pattern
	1.5 Habitat extent	1.5.1 Habitat area
		1.5.2 Habitat volume, where relevant
	1.6 Habitat condition	1.6.1 Condition of the typical species* and communities
		1.6.2 Relative abundance and/or biomass, as appropriate
		1.6.3 Physical, hydrological and chemical conditions
	1.7 Ecosystem structure	1.7.1 Composition and relative proportions of ecosystem components (habitats, species)
2: Non-indigenous species	2.1 Abundance and state of non-indigenous species, in particular invasive species	2.1.1 Trends in abundance, temporal occurrence and spatial distribution of non-indigenous species*
	2.2 Environmental impact of invasive non-indigenous sp.	2.2.1 Ratio between invasive non-indigenous species and native species*
		2.2.2 Impacts of non-indigenous invasive species at the level of species, habitats and ecosystem*
3: Exploited fish and shellfish	3.1 Level of pressure of the fishing activity	3.1.1 Fishing mortality (F)
		3.1.2 Catch/biomass ratio
	3.2 Reproductive capacity of the stock	3.2.1 Spawning Stock Biomass (SSB)
		3.2.2 Biomass indices
	3.3 Population age and size distribution	3.3.1 Proportion of fish larger than the mean size of first sexual maturation
		3.3.2 Mean maximum length across all species found in research vessel surveys
		3.3.3 95 % percentile of the fish length distribution observed in research vessel surveys
		3.3.4 Size at first sexual maturation
4: Food webs	4.1 Productivity of key species or trophic groups	4.1.1 Performance of key predator species using their production per unit biomass
	4.2 Proportion of selected species at the top of food webs	4.2.1 Large fish (by weight)
	4.3 Abundance/ distribution of key trophic groups/ species	4.3.1 Abundance trends of functionally important selected groups/ species*



5: Human-induced eutrophication	5.1. Nutrients levels	5.1.1 Nutrients concentration in the water column
		5.1.2 Nutrient ratios (silica, nitrogen and phosphorus)
	5.2 Direct effects of nutrient enrichment	5.2.1 Chlorophyll concentration in the water column
		5.2.2. Water transparency related to increase in suspended algae
		5.2.3 Abundance of opportunistic macroalgae*
		5.2.4 Species shift in floristic composition such as diatom to flagellate ratio, benthic to pelagic shifts, as well as bloom events of nuisance/toxic algal blooms caused by human activities*
	5.3 Indirect effects of nutrient enrichment	5.3.1 Abundance of perennial seaweeds and seagrasses impacted by decrease in water transparency*
		5.3.2 Dissolved oxygen changes and size of the area concerned
6: Seafloor integrity	6.1 Physical damage, having regard to substrate characteristics	6.1.1 Type, abundance, biomass and areal extent of relevant biogenic substrate
		6.1.2 Extent of the seabed significantly affected by human activities for the different substrate types
	6.2 Condition of benthic community	6.2.1 Presence of particularly sensitive and/or tolerant species*
		6.2.2 Multi-metric indices assessing benthic community condition and functionality, such as species diversity and richness, proportion of opportunistic to sensitive species*
		6.2.3 Proportion of biomass or number of individuals in the macrobenthos above specified length/size
		6.2.4 Parameters describing the characteristics of the size spectrum of the benthic community
7: Hydrographical conditions	7.1 Spatial characterisation of permanent alterations	7.1.1 Extent of area affected by permanent alterations
	7.2 Impact of permanent hydrographical changes	7.2.1 Spatial extent of habitats affected by the permanent alteration
		7.2.2 Changes in habitats, in particular the functions provided due to altered hydrographical conditions
8: Contaminants	8.1 Concentration of contaminants	8.1.1 Concentration of the contaminants measured in matrices such as biota, sediment and water
	8.2 Effects of contaminants	8.2.1 Levels of pollution effects on the ecosystem components concerned, having regard to the selected biological processes and taxonomic groups where a cause/effect relationship has been established
		8.2.2 Occurrence, origin, extent of significant acute pollution events and their impact on biota physically affected by this pollution
9: Contaminants in fish and seafood	9.1 Levels, number and frequency of contaminants	9.1.1 Actual levels of contaminants that have been detected and number of contaminants which have exceeded maximum regulatory levels
		9.1.2 Frequency of regulatory levels being exceeded
10: Litter	10.1 Characteristics of litter in the marine and coastal environment	10.1.1 Trends in the amount of litter washed ashore and/or deposited on coastlines, including analysis of its composition, spatial distribution and source
		10.1.2 Trends in the amount of litter in the water column and deposited on the seafloor
		10.1.3 Trends in the amount, distribution and composition of micro-particles
	10.2 Impacts of litter on marine life	10.2.1 Trends in the amount and composition of litter ingested by marine animals
11: Energy and noise	11.1 Distribution in time and place of loud, low and mid frequency impulsive sounds	11.1.1 Proportion of days and their distribution within a calendar year over areas of a determined surface, as well as their spatial distribution, in which anthropogenic sound sources exceed levels that are likely to entail significant impact
	11.2 Continuous low frequency sound	11.2.1 Trends in the ambient noise level within the 1/3 octave bands 63 and 125 Hz (centre frequency) measured by observation stations and/or with the use of models

CURRENT BOTTLENECKS IN ASSESSING MARINE HEALTH

The assessment of the environmental status of coastal waters with traditional monitoring techniques requires long, labour intensive, costly sampling campaigns. Marine environmental monitoring is usually based on a few permanent/regular sampling sites). Observations are usually limited to specific groups of organisms (e.g. benthic macro-invertebrates, phytoplankton, or fish). Sometimes, the monitoring techniques also lack standardised protocols of analysis.

Ideally, an informed choice of what to monitor would be based on studies that include all taxa (including animals, plants, fungi, protists and bacteria) and life stages. In particular, microbial community interactions and their metabolic pathways are emerging as essential components of any comprehensive estimate of ecosystem function. Recently developed genomic technologies, such as DNA barcoding, metagenomics, transcriptomics etc., come up as an efficient and standardisable alternative. Currently, there are no genomic methods implemented for the assessment of MSFD indicators, and few genetic methods are considered for contribution to the MSFD. Yet, some of these indicators of biodiversity (e.g. species distribution, population genetic structure; see table 1 for a comprehensive list) could benefit from DNA-based techniques. All molecular approaches that could improve monitoring programmes are informed by the increasing knowledge of the variation found among whole genomes within and between species across the tree of life.

Shortcomings in current monitoring methods	Explanations for shortcomings
Maintaining a consistent and high quality standard of species-level identification	Monitoring programmes vary in their spatial, temporal and qualitative taxonomic coverage
Providing a good estimate based on all biodiversity in monitored marine waters	Biological monitoring relies on the identification of selected groups of species and the relative abundance of individuals belonging to the "vulnerable" or "disturbance tolerant" species because those are the species (and life stages) that are easy to count
Providing rapid, cost effective and scalable species identification for monitoring and traceability purposes	Species identification relies on the specialised knowledge of taxonomic experts, which for many species (in fact virtually all species if one considers the full range of taxa in a system) is time consuming, costly, unreliable, low throughput, and difficult to use for large scale monitoring programmes
Discovering species genetic diversity at the population level	The lack of precise population estimates makes it difficult to apply management and policy actions
Providing a comprehensive estimate of ecosystem function	Measurements of physical and chemical parameters alone is insufficient to give a good estimate of ecosystem function
Providing an estimate of trophic interactions in the ecosystem	Current methods to uncover the diversity of prey items are based on the morphological analysis of the gut contents of demersal fish, seabirds and benthic microfauna, which fails to facilitate the analysis of food web structure.

MARINE GENOMICS

Genomics, the science that uses nucleotide sequences (DNA or RNA) to analyse biological systems, represents perhaps the most likely source of innovation in marine monitoring techniques. There is great potential for the development of genomic techniques for in situ detection and monitoring of the biodiversity, abundance and activity of organisms; over the last decade, novel sequencing technologies have led to an enormous increase in the amount of genetic data available on organisms, communities and habitats.

Marine genomics is crucial for studying the marine environment, its organisms and the multitude of links between real-time evolutionary and ecological processes in the sea. It's important to provide both an introduction to these state-of-the-art approaches, as well as to link them to both fundamental scientific questions and relevant societal needs. Cutting-edge genomic approaches are now sufficiently mature to advance the knowledge based bio-economy in the marine sector.

Marine genomics knowledge is a vital part of "blue biotechnology", leading, for example, to applications in the management of the natural and cultured biological resources; and preserving marine environments with applications that could help detect biodiversity losses ("which," "when," and "where") - from genes to species, to habitats and ecosystems, and ultimately predict the compromisation of the ocean functions and services. As such, marine genomics has enormous potential to improve our lifestyles and prosperity.

MARINE GENOMIC TOOLS AND THEIR POTENTIAL APPLICATIONS

DNA BAR-CODING

Definition: Consists of assigning a specimen or sample (e.g. a piece of tissue or contents of a gut) to a particular species by sequencing a standardised short DNA fragment (the "DNA Barcode") and comparing it against a reference database.

ADVANTAGES

It is independent of the user's taxonomic expertise and makes it possible to assign species names on samples that are challenging or impossible to identify in any other way. This not only applies to individual organisms (or parts thereof) but also to environmental or bulk samples, from which the target gene barcode can be sequenced.

COST

The investment for building DNA barcode reference laboratories is significant as a result of the individual cost of sequencing remaining high.
However, the revolution in DNA sequencing technologies has decreased the cost of screening samples against a reference laboratory once built. Thus, after an initial high investment in characterising a biota of interest and creating a "genomic observatory", then biodiversity dynamics can be monitored at very low cost but at greater speed and accuracy than current methods.

CURRENT LIMITATIONS

In water quality sampling, for example testing for Marine Harmful Algae Blooms, time is the priority; however samples still have to be taken and brought back to a laboratory for testing. Quicker turnaround might require individually testing each site however this would require a larger cost in labour.

Potentially relevant MSFD Descriptors(s)

- 1. Biological Diversity (1.1.1, 1.1.2, 1.1.3, 1.6.1, 1.7.1)
- 2. Non- Indigenous Species (2.1.1)
- 4. Food Webs (4.3.1)
- 6. Seafloor integrity (6.2.1, 6.2.2)

DISADVANTAGES

- An essential prerequisite is the creation of a reference database consisting of a library of species names linked to the DNA barcodes. Building the reference laboratory requires an expert taxonomist to name a representative for each species and to sequence the specimen for the appropriate barcode gene designated by the International Consortium for the Barcode of Life (CBOL). Currently, the BOLD platform (**www.barcodinglife.com**) is one of the largest existing DNA barcode libraries containing over 2M sequences (Feb 2013) of which 130,000 are formally described animals, 42,000 are formally described plants and about 2,500 are formally described fungi and protists.
- This method is not yet quantitative.

POTENTIAL APPLICATIONS

Potential to contribute whenever species identification is required, such as indicators of biological diversity, non-indigenous species and food webs.

Molecular approaches can be used to identify species at all life cycle stages including highly digested tissue. Identifying species in food webs in one of the main limitations in trophic chain analyses e.g. mapping stomach contents of commercially important fish species is likely to be critical in the future management of fish stocks.

DNA Bar-coding data can be easily incorporated into population genetic and phylogenetic analyses, providing added value beyond the species name e.g. historical biogeography, demographic trends etc.

DNA sequences are "born digital" and are easily retained in public databases where they can be retrieved and reinterpreted as necessary. By contrast, traditional methods of species identification often rely on specialist knowledge. It can be hard to validate the decisions taken by the expert, even when detailed photographic and specimen records are kept.

MARINE GENOMIC TOOLS AND THEIR POTENTIAL APPLICATIONS

METAGENOMICS

Definition: Consists of assigning a specimen or sample (e.g. a piece of tissue or contents of a gut) to a particular species by sequencing a standardised short DNA fragment (the "DNA Barcode") and comparing it against a reference database.

ADVANTAGES

- Most often used to survey microbial species, the majority of which are not workable with the culturing techniques that would provide enough DNA for genomic sequencing of an individual isolate. Traditional methods would involve isolating and cloning DNA fragments from an environmental sample, however Next Generation Sequencing (NGS) techniques do not require cloning.
- Considerably faster than traditional methods: It is currently possible using the the Earth Microbiome Project (EMP) pipeline to process ~100/day environmental samples.
- Method achieves higher longitudinal, cross-sectional and taxonomic/functional resolution than previously.

COST

Difficult to compare to traditional methods. As Metagenomics is infinitely scalable, it can be both cheaper and more expensive.

CURRENT LIMITATIONS

- Some studies have reported that the abundance of taxa and their functional genes in a metagenomic library do vary depending on the DNA extraction protocol used to acquire the nucleic acid from the environmental sample.
- Metagenomic datasets are often only sequenced to a low depth compared with the quantity of DNA in a sample, which results in only the extremely dominant populations being observed.
- It is difficult to explain the function or taxonomy of a short sequence fragment resulting in a large portion of data lacking an appropriate annotation.

DISADVANTAGES

- Results can vary when different techniques for extraction and sequencing are used
- As for DNA Bar-coding, a prerequisite is the creation of a reference database consisting of a library of species names linked to the DNA barcodes.

POTENTIAL APPLICATIONS

Potential applications of Phylogenetic diversity (PD) based biodiversity analyses as for DNA barcodes also extend to Metagenomics. Many methods conventionally employed at the species level extend directly to PD analyses; these offer fresh prospects for the toolbox for marine monitoring, including assessments of marine health.

- Molecular approaches can be used to identify species at all life cycle stages including highly digested tissue. Identifying species in food webs in one of the main limitations in trophic chain analyses e.g. mapping stomach contents of commercially important fish species is likely to be critical in the future management of fish stocks.
- DNA Bar-coding data can be easily incorporated into population genetic and phylogenetic analyses, providing added value beyond the species name e.g. historical biogeography, demographic trends etc.
- DNA sequences are "born digital" and are easily retained in public databases where they can be retrieved and reinterpreted as necessary. By contrast, traditional methods of species identification often rely on specialist knowledge and can be hard to verify the decisions made even when detailed records are kept (Photographs & specimen).

Potentially relevant MSFD Descriptors(s)

- 6. Seafloor integrity (6.2.1, 6.2.2)

MARINE GENOMIC TOOLS AND THEIR POTENTIAL APPLICATIONS

QUANTITATIVE REAL TIME POLYMERASE CHAIN REACTION (QPCR)

Definition: DNA microarrays are coated solid surfaces onto which a large number of fluorescently labelled DNA probes can be spotted. Each probe is specific for a species, and when the probe hybridises with a sample, the sample/probe complex fluoresces in UV light.

ADVANTAGES

- Shorter turnaround time (24hr+ for cultivation method vs 2hr for qPCR)

COST

The investment for building DNA barcode reference laboratories is significant as a result of the individual cost of sequencing remaining high. However, the revolution in DNA sequencing technologies has decreased the cost of screening samples against a reference laboratory once built. Thus, after an initial high investment in characterising a biota of interest and creating a "genomic observatory", then biodiversity dynamics can be monitored at very low cost but at greater speed and accuracy than current methods.

CURRENT LIMITATIONS

In water quality sampling, for example testing for Marine Harmful Algae Blooms, time is the priority; however samples still have to be taken and brought back to a laboratory for testing. Quicker turnaround might require individually testing each site however this would require a larger cost in labour.

Potentially relevant MSFD Descriptors(s)

- 5. Human induced eutrophication (5.2.4)

DISADVANTAGES

- Primary limitations are cost and logistics (as quicker turnover needs timely transport of samples to laboratory)

POTENTIAL APPLICATIONS

- Water Quality monitoring – HABs, water borne pathogens etc.

MARINE GENOMIC TOOLS AND THEIR POTENTIAL APPLICATIONS

MICROARRAYS

Definition: DNA microarrays are coated solid surfaces onto which a large number of fluorescently labelled DNA probes can be spotted. Each probe is specific for a species, and when the probe hybridises with a sample, the sample/probe complex fluoresces in UV light.

ADVANTAGES

- An array can contain tens of thousands of probes therefore a microarray experiment can accomplish many genetic tests in parallel.
- In spotted DNA Microarrays, arrays may be easily customized for each experiment because researchers can choose the probes and printing locations on the arrays, synthesize the probes in their own lab (or collaborating facility), and spot the arrays themselves.
- Development of the Environmental Sample processor (ESP) for the autonomous detection of HAB species as well as their associated toxins using DNA probes.

DISADVANTAGES

- Dependant on good DNA extraction methodology
- Lack of standardisation in data makes exchange of results difficult
- Microarray data is found to be more useful when compared to other similar datasets- lack of one library of datasets

COST

Initial investment is large, both for an ESP and for the equipment needed to carry out the testing in a laboratory, as not only do you need the materials and facilities to develop the microarrays but you also need a specialised scanner to read the results. However, after the initial outlay, per sample cost compared with laboratory time may be less.

POTENTIAL APPLICATIONS

The rapid identification of HABs (Harmful Algae Bloom) forming algae and their associated toxins that can have serious health consequences.

CURRENT LIMITATIONS

- Statistical analysis of data can affect the results (Statistical challenges include taking into account effects of background noise and appropriate normalisation of the data)
- Accuracy and Precision as a result of interference between a probe within the Microarray and the genes it is designed to detect (false positives)

Potentially relevant MSFD Descriptors(s)

- 2. Non-indigenous species (2.1.1)
- 5. Human induced eutropication (5.2.3, 5.2.4)

MARINE GENOMIC TOOLS AND THEIR POTENTIAL APPLICATIONS

SNP (SHORT NUCLEOTIDE POLYMORPHISMS) BASED METHODS

Definition: Short Nucleotide Polymorphisms are DNA sequence variations occurring when a single DNA nucleotide in the genome (A,G,C,T) differs among individuals of the same species. For example the change of one nucleotide cytosine (C) to another nucleotide thymine (T) in a certain stretch of DNA would be a single SNP. Therefore SNPs can be used as biological markers to distinguish populations of individuals within a species.

ADVANTAGES

- Some SNPs can have very high information content for population structure analysis e.g. SNPs are the first marker that are capable of assigning fish back to population of origin at all stages of the food chain at relatively small geographic scales.
- A big advantage of SNP markers over size-based DNA methods (e.g microsatellites) is the digital nature of the outputs (presence or absence of a particular allele). This means extensive cross- calibration among labs is not necessary and results from published research can be easily compared.

COST

The cost of developing and genotyping large numbers of samples is still relatively high and likely to be beyond the means of many labs. However, sequencing costs are falling rapidly.

CURRENT LIMITATIONS

- Recent improvements in the speed, cost and accuracy of next generation sequencing and associated bioinformatic tools are revolutionising the discovery of single nucleotide polymorphisms (SNPs).

Potentially relevant MSFD Descriptors(s)

- 1 Biological Diversity (1.3.2) Population Genetic structure
- 3 Exploited Fish and Shellfish (3.1.1 Fishing Mortality)

DISADVANTAGES

- High cost as SNP technology is still in developmental and validation stages (e.g. Fishpoptrace project has successfully developed and tested SNPs for tracing fish populations of three species. Herring, Sole and Hake).

POTENTIAL APPLICATIONS

- Population genetics for use in Conservation management, product traceability and forensic genetic analysis etc.

MARINE GENOMIC TOOLS AND THEIR POTENTIAL APPLICATIONS

TRANSCRIPTOMICS

Definition: A Transcriptome is the set of all RNA molecules produced in one or a population of cells, here RNA refers to the second genetic carrier in organisms where DNA is the first. Transcriptomics refers to methods of analysis of gene expression changes of either an entire organism or parts of it (e.g. cells, tissues) under different conditions. The most common technologies utilised in trascriptomic techinques are Microarrays, qPCR and RNA sequencing.

ADVANTAGES

- Discovery of molecular biomarkers of exposure as early signs to predict the effects firstly at a physiological level and later at a population level
- Provide the mode of action of the chemicals or a stressor (e.g. the mechanisms of toxicity, mechanisms of adaptation to environmental change)

DISADVANTAGES

- Lack of standardisation of data for DNA microarray
- RNA extraction is the most important step as if not done correctly it will disrupt the entire chain of testing. Good technique is paramount.
- RNA can be quickly degraded and is unstable
- Need specialised scanner to analyse the results of the Microarray, which is costly and differs in outputs so no real standardisation of results.

COST

Costs have dropped recently, although the DNA microarray technique requires a dedicated instrument for scanning which is still costly. However, core facilities are available from several academic

POTENTIAL APPLICATIONS

- Environmental monitoring: Genomic technologies are increasingly used to evaluate the biological effects of various chemical pollutants on aquatic animals under either controlled conditions or in natural environments
- "Early warning system" for environmental monitoring, as it takes into account additional parameters, other than chemical monitoring alone, including temperature changes, nutrient depletion and pollutants as potential stressors on complex mixtures of organisms.

CURRENT LIMITATIONS

- There needs to be a reference library for comparison of samples and cross analysis of results
- Data standardisation needs to be resolved
- Research for method standardisation is expensive and often too routine and tedious

Potentially relevant MSFD Descriptors(s)

- 8. Contaminants (8.2.1) Levels of pollution effects on Ecosystem components, (8.2.2) Occurrence, origin, extents and impact on biota.

THE "MARINE GENOMICS FOR USERS" (MG4U) PROJECT

Marine genomics has enormous potential to improve our lifestyles and prosperity, and to assist with governance and sustainable management of the marine environment. Today, marine genomic knowledge is a vital part of "blue biotechnology", and is leading to applications in the management of natural and cultured resources, and preserving marine environments. However, many business leaders and legislators are not yet aware of how marine genomics hold great potential for problem solving and industrial commercial advantage. Valuable knowledge needs to be made accessible and disseminated in user-friendly contexts. In this context, the Marine Genomics for Users (MG4U) project was developed to facilitate knowledge transfer, technology transfer, and technology translation between high-throughput marine genomics and prospective users.

Funded by the EU's Seventh Framework Programme, the MG4U project ran from January 2011 to June 2013 and comprised of a consortium of seven partners led by Station Biologique de Roscoff, part of France's Centre National de la Recherche Scientifique (CNRS). The partnership brought together teams from Ireland, Germany, Spain, Portugal and Sweden.

The MG4U project focused on increasing Knowledge Transfer to Industry, Governance and the Scientific Community through training, as well as devising an overall awareness campaign on the potential of Marine Genomics. Using a varied strategy that included technical and informational workshops, conference and working groups' presentations, as well as developing promotional products for media, MG4U was able to highlight the unique selling points of Marine Genomics to a wide audience. These actions have lead to an uptake of marine genomic techniques, an up-skilled scientific base for public research organizations, durable relationships between scientists and industrial companies, and synergies with other marine genomic projects in Europe.

This policy brief was developed as part of the strategy for Knowledge Transfer to Governance, aiming to increase the resources available to legislators in a marine monitoring perspective.

For more information and to view the results and promotional materials of the MG4U project please visit the website:
www.mg4u.eu

For more information on the policy brief and the MG4U strategy on Knowledge Transfer to Governance, please contact
Prof John Benzie, University College Cork, Email: J.Benzie@ucc.ie
-or-
Cliona Ní Cheallacháin, AquaTT, Email: cliona@aquatt.ie