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SCIENCE DIRECT
Marine Environmental Research 62 (2006) S156–S186
MARINE ENVIRONMENTAL RESEARCH
www.elsevier.com/locate/marenvrev

Abstracts from Thirteenth International Symposium on Pollutant Responses in Marine Organisms (PRIMO 13) – Environmental Genomics and Proteomics

Incorporating proteomics into aquatic toxicology

T.M. Andacht[a], R.N. Winn[b]

[a]*Proteomics Resource Facility, Integrated Biotechnology Laboratories, USA*
[b]*Aquatic Biotechnology Environmental Laboratory, Daniel B. Warnell School of Forest Resources, University of Georgia, Athens, GA, USA*

Abstract

With a continual increase in the number of chemicals being introduced to the environment and the potential for adverse health risks associated with contaminant exposure, there is a growing need for tools to understand the cellular pathways altered in response to exposure. Proteomics provides an excellent tool to begin to explore the changes in protein expression in response to contaminant exposure. Technologies in comparative quantitation, such as DIGE and ICAT, are particularly well suited for studies in aquatic toxicology. However, despite these powerful technologies, several of the same issues plaguing the analysis of microarrays are encountered in proteomic studies in aquatic toxicology. Using several examples of fish comparative studies, we illustrate some of the challenges facing the incorporation of proteomics into aquatic research, including individual variation, normalization, tissue heterogeneity, and protein identification. The greatest obstacle in using proteomic approaches for aquatic toxicology is the lack of comprehensiveness of the gene databases for virtually all species. As these databases expand, protein identification will no longer be limiting. At that point, validation and functional studies will be the next challenge.

0141-1136/$ - see front matter © 2006 Published by Elsevier Ltd.
doi:10.1016/j.marenvres.2006.04.039

Redox proteomics in the mussel *Mytilus edulis*

David Sheehan[a,b], Brian McDonagh[a,b], Raymond Tyther[a]

[a]*Proteomics Research Group, Department of Biochemistry, University College Cork, Ireland (d.sheehan@ucc.ie)*
[b]*Environmental Research Institute, University College Cork, Ireland*

Abstract

Problem investigated: oxidative stress (OS) is a fundamental challenge to all biological systems. In the environmental context, pollutants such as polyaromatic hydrocarbons and metals can lead to OS by formation of reactive oxygen species. Proteomics provides a direct means for identifying effects on proteins as a consequence of OS. We are interested in applying selection and detection methodologies to bioindicator species such as clams and mussels.

Experimental design. Groups of *Mytilus edulis* (triplicate pools; $n = 5$) were sampled from a moderately polluted and control site in Cork Harbour, Ireland. Later, similar groups from the control site were sampled and held in tanks where they were exposed to 1mM H_2O_2 to directly generate OS.

Results: protein extracts of digestive gland and gill were separated by 2D SDS–PAGE. Immunoblotting detected carbonylation and glutathionylation in animals from the polluted site. Actin is glutathionylated. These effects were even more pronounced in animals experimentally exposed to OS. Immunoprecipitation was also used to select carbonylated proteins followed by silver staining and this gave generally similar patterns to immunoblots. Effects of OS on disulphide bridge patterns of proteins were investigated by first separating proteins in non-reducing gels followed by a second reducing dimension. The potential of our methodologies for applying redox proteomics to pollutant responses in marine organisms is discussed. (We are grateful to the Higher Education Authority of Ireland PRTLI programme for funding our work. B.M. is supported by an EMBARK studentship of the Irish Research Council for Science Engineering and Technology).

Proteome analysis of European Flounder: Methodological outline and analysis of effects of pollution

Adelina Rogowska-Wrzesinska[a], Stephen George[b], Vicky Sabine[b], Peter Mose-Larsen[a], Stephen J. Fey[a]

[a]*Centre for Proteome Analysis, University of Southern Denmark, Forskerparken 10C, 5320 Odense, Denmark*
[b]*Institute of Aquaculture, University of Stirling, FK9 4LA, Scotland, United Kingdom*

Abstract

Changes in protein expression analysed by 2D gel electrophoresis of solubilised liver proteins is potentially a very powerful tool in the determination of diagnostic toxicological responses to environmental pollutants. We are investigating responses of European Flounder both to a wide