

PROTEOMICS AS USEFUL TOOL FOR STUDING BIOMARKERS OF EARLY EXPOSURE TO POLYCHLORINATED BIPHENILS

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Introduction

Polychlorinated biphenyls (PCBs) are toxic persistent organic pollutants present in the hydrosphere. Mussels are used as sentinel organisms for the monitoring of marine pollution for their ability to bioaccumulate contaminants, their sessile nature, filter-feeding habits and widespread distribution. Alteration in protein expression is often indicative of toxic exposure or effect and changes in protein expression profiles derived from environmental stress may be used for the identification of novel biomarkers. Molecular biomarkers are among the most sensitive and earliest responses to pollutants. In this study, proteomics has been used in mussels as a preliminary screening of quantitative changes in protein expression caused by a mixture of PCBs, potentially useful as new biomarkers, following the identification of the proteins more drastically altered.

Methods

Mussels (*Mytilus galloprovincialis*) were exposed for three weeks to three NDL-PCB (138, 153, 180) under controlled conditions. The edible parts were taken, homogenized, lyophilized and then stored at -80 °C until analysis. Extracted proteins were quantified according to Bradford method and separated by two-dimensional electrophoresis (2-DE) in IPG strips (pH 3-10). The protein spots in gels were visualized by Coomassie Brilliant Blue staining. Gel images were obtained using a Image Scanner. Image analysis included spot detection, quantification and normalization, and matching. More than 500 spots were resolved and altered expression was qualitatively detected.

Results and Discussion

Our results showed a well conserved protein pattern regardless of the treatments, demonstrating that the exposition to low levels of PCB mixture did not impair the normal physiological function of the mussels. However, the levels of a restricted number of proteins were clearly and reproducibly affected by the treatment; therefore, these polypeptides were considered promising biomarker candidates. In conclusion, even if further studies are needed to validate these findings, our data demonstrated that proteomic approach represents a valuable tool for identifying biomarkers of exposure to environmental contaminants.

References

- Apraiz et al., Molecular and Cellular Proteomics, 2006, 4:1274-1284
- Dondero et al., Science of the Total Environment, 2010, 408:3775-3786
- Leroy et al., Ecotoxicology and Environmental Safety, 2010, 73:343-352
- Lopez et al., Marine Biotechnology, 2005, 7:396-404