# SPECTROSCOPIC ANALYSES AND GENOTOXICITY OF DIOXINS IN THE AQUATIC ENVIRONMENT OF ALEXANDRIA

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## Abstract

Dioxins have a global concerns of the bioaccumulation tendency and persistency. Twenty four samples of water, seabream Pagrus auratus and Seabass Dicentrarchus labrax samples were collected from Alexandria to evaluate the concentration of the 2,8-dichloro dibenzo-p-dioxin.Fourier Transform Infrared Spectrometer (FTIR) and HPLC with UV was applied. RT-PCR assay was conducted to verify the expression of some immune genes. The average detected concentrations ranged between 0.2 to 1.3  $\mu$ g/l. Immune genes expression revealed that MHC class 1 and C3 were highly upregulated in liver and muscles of seabass and seabream while T2BP was highly regulated in seabass liver and seabream muscle and also seabass muscle for transferrin. Application of HF/3-21G\* molecular model indicates that hydrated dioxin could interact with amino acid.

Keywords: Biotechnologies, Mediterranean Sea

### Introduction

Aquatic pollution is a serious problem due to its ubiquitous occurrence, recalcitrance properties, suspected carcinogenicity and mutagenicity to humans and biota. Moreover, water pollution with organic compounds is a hot topic of concern. Although some of such pollutants are naturally occurring, the majorities are anthropogenic and enter the environment through release of petroleum products or by combustion of organic matter. For millenniums, the Mediterranean Sea has been the scenery of human development, which has extensively influenced the coastal areas. Alexandria is an Egypt largest city on the Mediterranean coast, and is one of the most important industrial centers, comprised 100 large factories and about 260 smaller ones. Aquatic organism, such as fish, accumulates pollutants directly from contaminated water and indirectly via the food chain. Persistent organic pollutants can be detected in environment after being banned for generations (DDT banned in 1960s and still being detected).

#### Methodology

Several techniques including FTIR were used to study marine fish from the Mediterranean, then molecular modeling at HF/3-21G\* (Figure 1) was used to model the effect of dioxin upon protein. HPLC with UV was used to determine the concentration of dioxins while RT-PCR assay was conducted to verify the expression of some immune genes in the studied fish species (Figure 2).



Fig. 1. HF/3-21G\* optimized structure for the model molecule of dioxin- alanine which subjected to six water molecules.

#### **Results and discussion**

Elevated concentration of 2,8-dichloro dibenzo-p-dioxin were detected in summer and this may be attributed to the intensifying of maritime activities in

coastal area at this season. Pollution evoked an immune response in fish collected from Alexandria coastal water. The results verified by RT-PCR, revealed that MHC class 1 and C3 genes were highly upregulated in seabass and se bream muscle and liver, alsoT2BP was highly upregulated in liver of seabass and muscle of seabream. The molecular modelling suggests that a change in the protein structure may take place under the influence of the hydrated dioxin. Further studies are encouraged to identify gene expression biomarkers as indicator to specific pollutants.



Fig. 2. A) RT- PCR: M: Marker; 1,2: Seabass (muscle and liver) T2BP gene; 3, 4: Seabream (muscle and liver) T2BP gene; 5,6: Seabass (muscle and liver) Transferrin gene; 7,8 Seabream (muscle and liver) Transferrin gene; 9, 10 Seabass (muscle and liver) MHC class 1& 11, 12: Seabream (muscle and liver) MHC class 1.

Fig. 2 B) RT-PCR: B actin gene.

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