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ABSTRACTS BOOK

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Black Sea - Challenges Towards Good Environmental Status

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Back-to-back events

- Celebration of the International Black Sea Day 2013
- International Symposium "Protection and Sustainable Management of the Black Sea - 3rd Millennium Imperative" - 6th Edition



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Results of Hydrobionts Pollution Studies in the Zmiinyi Island Area of the Black Sea in 2011-2013

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Abstract

Pollution of marine hydrobionts is the problem being one of main topics of the Convention on the Protection of the Black Sea Against Pollution and the EU Marine Strategy Framework Directive.

The aim of our studies has been to investigate the current state of hydrobionts (fish and mussels) pollution with trace metals (TM), organochlorine pesticides (OCPs) and polychlorinated biphenyls (PCBs) in the Zmiinyi Island area, which according to our studies of water and bottom sediments pollution is the area with

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practically natural conditions. During 2011-2013 the Research Station of Odessa National I.I.Mechnikov University carried out fish and mussels sampling programme. Analysis of samples of hydrobionts tissues have been carried out in accordance with the national methods and the methods recommended by the ISO in the laboratory of the Ukrainian Scientific Centre of the Ecology of Sea. The data on hydrobionts pollution for 2011-2013 with 11 OCPs, 18 PCBs and TMs are being analyzed in details. The levels of pollution for fish species and for mussel species are presented in table 1.

Table 1. The limits and average values of concentrations [mkg/kg] of selected pollutants in fish (6 species) and in mussels (2 species) in the Zmiinyi Island coastal waters

waters				
Pollut	Concentration in Fish dry tissues		Concentration in	
ant			Mussels' dry tissues	
	Limits	Average	Limits	Average
As	1.18-19.3	5.15±2.87	0.38-11.3	6.81±3.36
Cd	0.03-0.17	0.07±0.02	0.42-1.98	1.84±0.79
Hg	0.24-0.62	0.41±0.06	0.037-0.60	0.68±0.11
Pb	0.69-3.42	1.33±0.42	0.89-5.56	9.73±5.80
Zn	36.4-103	71.0±13.3	21-149	73.7±39.3
Fe	47.3-112	73.3±10.8	129-878	384±251
Mn	0.3-37.8	12.0±5.7	6.69-43.3	46.5 ± 24.4
Sum of	68.3-201	168±24	9.56-25.8	21.4±4.4
PCB				
-HCH	< 0.05	< 0.05	0.05-0.35	0.20 ± 0.15
-HCH	0.78-5.99	3.26±0.73	0.05-14.0	7.03 ± 7.02
λ-HCH	0.05-0.29	0.15±0.04	0.11-0.55	0.33±0.22
DDE	0.12-2.09	1.00±0.38	0.44-0.65	0.54 ± 0.10
DDD	0.08-0.69	0.35±0.11	0.10-0.43	0.26±0.17
DDT	0.18-0.45	0.28±0.04	0.53-0.57	0.55 ± 0.02

Dependence of the TMs, PCBs and OCPs concentrations on fish and mollusk species is discussed. Coefficients of pollutants accumulation in fish and mollusk tissues have been calculated and are discussed using the data on the pollutants' concentration in water.

It is proposed to study the levels of TMs, OCPs and PCBs accumulation in hydrobionts in more details depending on the age of hydrobionts (fish and



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mollusks) and, first of all, on the peculiarities of their food chains, from which accumulation of toxicants in their tissues takes place.

The study has been carried out in framework of National research projects and as a contribution to the European FP7 project PERSEUS.

Composition of Microflora of the Upper Respiratory Tract of the Black Sea Bottlenose Dolphin (*Tursiops Truncatus*) in Captivity Condition

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Abstract

As a rule in the dolphinarium microbial pollution and species composition of microorganisms of the environment (water, air and other objects) are above and different than in natural areas of dwelling of wild cetaceans. Therefore even clinically healthy and adapted dolphins are exposed to risk of occurrence of infectious diseases. It is known that the specific composition of microbial associations in animal and human organisms is directly dependent on physiological state of macroorganism. So it is necessary to studying the consist of microflora of the upper respiratory tract of the Black Sea bottlenose dolphins containing in the captivity conditions for an estimation of their status of health. But now the species composition of normal microflora of the organisms of the different cetaceans is studied insufficiently. Therefore investigation of structure of microbial associations of upper respiratory tract of clinically healthy adapted animals containing in the