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THE STRUCTURAL DIFFERENCE OF BACTERIAL COMMUNITIES BETWEEN ANTHROPIC AND NATURAL LAKES

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Introduction

The hydrosphere represents about 71% of the total surface of the planet of which only 2.8% is represented by freshwater ecosystems. The ecosystem maintains a state of balance between the component populations, throughout its self-control function, maintaining the numerical variations of these populations within certain limits of sustainability. The exceeding of these limits could causes the balance disturbance by changing the structure and functioning of the ecosystem. The complex human activities influence the structure and functioning of ecosystems, transforming the environment and adapting it to its purposes. Microorganisms are present in all types of ecosystems, being endogenous, exogenous or transient due to contamination with various sources of pollution. Water is an essential natural factor of ecological balance increasingly exposed to microbial pollution. Indicators of fecal pollution are used to assess the degree of water contamination and to locate its origin. The continuous and uncontrolled usage of antibacterial agents that contributed to bacterial resistance determined/ caused pollution of aquatic ecosystems with antibiotic resistant microorganisms. The emergence of antibiotic resistant bacteria is predictable in any environment given that the use of antibacterial substances is constantly growing worldwide. Thus, antibiotic resistance induced in the aquatic environment can have an effect both on bacterial populations in the ecosystem and on human health. Aquatic environments are recognized as one of the reservoirs for the transmission and dissemination of antibiotic resistance. The main goal of this paper is to highlight the differences of bacterial communities from anthropogenic and natural aquatic ecosystems and to assess the potential impact they have on environment and human health.

Materials and methods

The study area focused on two lakes in Bucharest, Morii Lake (anthropic) and Snagov Lake (natural). Microbiological and molecular biology methods were applied for a bacterial communities' characterization. The fecal indicators were quantified by Most Probable Number method. The identification and characterization of bacterial populations in both aquatic ecosystems (Morii Lake and Snagov Lake) were performed by Omnilog (Biolog, USA) and by iSeq100 (Illumina, USA) gene sequencing techniques from bacterial aquatic ecosystem. Antibiotic susceptibility was tested following CLSI recommendation.

Results and conclusions

The results of quantitative analyzes (fig. 1) showed a higher density of total coliforms in Snagov Lake (345 CFU/100mL) compared to Morii Lake (214 CFU/100mL), but these results were opposite to fecal coliforms and *Escherichia coli* (*E. coli*) densities compared to the studied lentic ecosystems. The densities of fecal coliforms and *E. coli* were lower in case of natural lake than those detected in Morii Lake because Snagov Lake is very accessible for tourist activities compared to Morii Lake. High densities in fecal coliforms (44 CFU/100mL) and *E. coli* (29 CFU/100mL) in Morii Lake can be explained by the presence of uncontrolled pollution sources. In addition, the enterococci density (5 CFU/100mL for Snagov Lake and 27 CFU/100mL for Morii Lake) highlighted the anthropogenic characteristics of Morii Lake, emphasizing the original source of pollution from human activities.

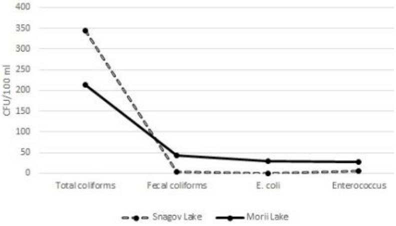
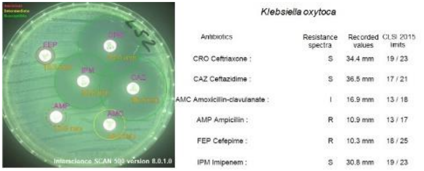


Figure 1. The density of total coliforms, fecal coliforms, *E. coli* and *Enterococcus* from surface water samples of Morii Lake and Snagov Lake.

Following bacterial identification with Omnilog system (Biolog, USA) and antibiotic susceptibility testing, several potentially pathogenic bacteria were identified among them *Klebsiella oxytoca*, identified from Snagov Lake, had a specific antibiotic resistant pattern (fig. 2).



Klebsiella oxytoca

Antibiotics	Resistance spectra	Recorded values	CLSI 2015 limits
CRO Ceftriaxone :	S	34.4 mm	19 / 23
CAZ Ceftazidime :	S	36.5 mm	17 / 21
AMC Amoxicilin-clavulanate :	I	16.9 mm	13 / 18
AMP Ampicilin :	R	10.9 mm	13 / 17
FEP Cefepime :	R	10.3 mm	18 / 25
IPM Imipenem :	S	30.8 mm	19 / 23

Figure 2. *Klebsiella oxytoca* from Snagov Lake that was resistant to Ampicillin (AMP) and Cefepime (FEP).

The bacterial DNA was extracted and quantified using nanodrop, the result indicating a low contamination, the A260 nm/A280 nm ratio being close to 1.8 for both lakes. The sequencing analysis of extracted bacterial DNA revealed the presence of several types of microorganisms (e.g. *Aeromonas salmonicida, Enterobacter sp., Klebsiella pneumoniae*), including those detected with the Omnilog system. The sequenced sequences were compared with NCBI GanBank for local similarity regions between nucleotide sequences.

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