

SANITARY-MICROBIOLOGICAL EXAMINATION OF YOUNG STURGEON IN THE VOLGA DELTA

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Abstract

The microflora of young sturgeons cultured at sturgeon farms located in the Volga Delta region originates to a great extent from that contaminating the fish feeds. It differs considerably from the microflora of young sturgeons in the wild. This suggests that microflora composition of the latter can serve as a reference when microbiological examinations of cultured sturgeons are carried out.

Introduction

The general growing interest to sturgeon aquaculture and its great importance, in particular for the Astrakhan Province, clearly demonstrate the need for regular microbiological examinations of these fish. The examinations are aimed at preventing negative impact of the environment on the health status of the fish as well as improving quality of young cultured sturgeons. It has been shown that development of aquaculture is often accompanied by technological stresses that can compromise fish resistance thus provoking outbreaks of bacterial diseases and resulting in fish losses (Borisenko, 1991; Kakhovsky, 1991). The goal of the present study was to carry out a comparative analysis of microbial flora of young sturgeons from the wild and those reared under aquacultural conditions. Two sturgeon farms were included in the study: Lebyazhy, with the traditional pond fish culture, and Ikryaninsky where an industrial technology of rearing fish in tanks has been used.

Materials and Methods

Collecting samples for the microbiological investigations was performed within spring-summer-autumn time of 1993-1996. Young fish (fry and fingerlings) were examined. In total one hundred samples from beluga (*Huso huso* L.), Russian sturgeon (*Acipenser gueldenstaedti* L.), starred sturgeon (*A. stellatus* P.), sterlet (*A. ruthenus* L.) and beluga x sterlet hybrid (besater) as well as thirty pond and tank water samples were taken at Ikryaninsky and Lebyazhy fish

farms. One hundred samples from the young wild starlet, caught in its native spawning grounds in the Volga river, and ninety water samples taken in the same areas served as controls. Samples of water, viscera (liver and intestinal contents) and muscles of the sturgeons were taken simultaneously and used for quantitative determination of the mesophilous aerobic and facultative anaerobic micro-organisms (MAFANM). The sam-

Table 1. Microflora of the river water and wild young sterlet (% prevalence)

Microflora	River water from spawning grounds	Wild fish
<i>Aerococcus</i>	ND*	0.9 ± 0.9**
<i>Aeromonas</i>	20.9 ± 4.1	12.9 ± 3.1
<i>Alcaligenes</i>	4.2 ± 2.0	ND
<i>Acinetobacter</i>	17.9 ± 3.9	4.3 ± 1.9
<i>Bacillus</i>	13.7 ± 3.5	7.8 ± 2.5
<i>Citrobacter</i>	5.3 ± 2.3	12.9 ± 3.1
<i>Edwardsiella</i>	ND	1.8 ± 1.2
<i>Escherichia</i>	ND	0.9 ± 0.9
<i>Flavobacterium</i>	8.4 ± 2.8	4.4 ± 1.9
<i>Klebsiella</i>	ND	0.9 ± 0.9
<i>Micrococcus</i>	3.2 ± 1.8	4.4 ± 1.9
<i>Moraxella</i>	5.3 ± 2.3	0.9 ± 0.9
<i>Plesiomonas</i>	2.1 ± 1.5	11.3 ± 2.9
<i>Proteus</i>	3.2 ± 1.8	7.8 ± 2.5
<i>Pseudomonas</i>	6.3 ± 2.5	1.8 ± 1.2
<i>Salmonella</i>	3.2 ± 1.8	7.8 ± 2.5
<i>Serratia</i>	ND	0.9 ± 0.9
<i>Shigella</i>	1.1 ± 1.0	0.9 ± 0.9
<i>Staphylococcus</i>	ND	0.9 ± 0.9
<i>Vibrio</i>	2.1 ± 1.5	2.6 ± 1.5
Fungi	ND	2.6 ± 1.5

* Not detected; **M ± std.

Table 2. Microflora of the water and reared sturgeons at the two fish farms employing different fish culture technologies (% prevalence)

Microflora	Farm inlet water	Farmed fish	
		Lebyazhy fm	Ikryaninsky fm
<i>Aerococcus</i>	ND*	ND	2.9 ± 1.9**
<i>Aeromonas</i>	14.8 ± 6.1	25.0 ± 2.4	6.8 ± 2.9
<i>Acinetobacter</i>	16.7 ± 6.5	8.6 ± 2.7	13.0 ± 4.1
<i>Bacillus</i>	10.8 ± 5.5	26.0 ± 2.7	25.3 ± 4.2
<i>Citrobacter</i>	8.9 ± 4.9	10.0 ± 2.4	2.7 ± 1.9
<i>Edwardsiella</i>	3.0 ± 2.9	ND	2.8 ± 1.9
<i>Escherichia</i>	ND	ND	1.5 ± 1.4
<i>Micrococcus</i>	3.0 ± 2.9	9.0 ± 1.3	8.9 ± 2.9
<i>Plesiomonas</i>	8.9 ± 4.9	8.6 ± 1.9	ND
<i>Salmonella</i>	6.0 ± 4.0	ND	4.2 ± 2.3
<i>Staphylococcus</i>	6.0 ± 4.0	ND	14.2 ± 1.3
<i>Vibrio</i>	ND	5.1 ± 1.3	1.4 ± 1.3
Fungi	3.0 ± 2.9	5.0 ± 1.9	9.7 ± 3.5

* Not detected

ples were treated by using standard bacteriological methods.

Results and Discussion

The number of MAFANM in the Volga river water close to the fish farm areas and that in spawning grounds varied within 1.75×10^2 - 3.1×10^4 CFU/ml with *Aeromonas*, *Acinetobacter* and *Bacillus* as the predominant genera (Tables 1 & 2). The data showed that there was no principal differences in sanitary-hygienic quality between river water that feeds the fish farms and that the wild sturgeons inhabit during their fresh water life time.

At the same time at Ikryaninsky fish farm the pond water samples had higher mean microbial counts than those from tanks supplied with flowing river water: 8.13×10^4 and 9.75×10^5 CFU/ml, respectively. As a consequence, the mean number of MAFANM in the liver of pond reared Russian sturgeon and starred sturgeon was higher compared to that of the fish maintained in tanks: 1.54×10^3 and 7.5×10^1 CFU/g, respectively. Meanwhile the wild fingerling sterlet had generally no bacteria in its liver. Intestinal

bacteria counts at the fish farm varied from 1.5×10^5 to 2.3×10^7 CFU/g.

At Lebyazhy fish farm, where pond culture and natural feeds have been traditionally used, the MAFANM numbered from 1.75×10^2 - 3.36×10^3 CFU/ml water. The mean intestinal bacteria counts of the farmed fish were 1.4×10^2 CFU/g in beluga, and 1.5×10^6 and 2.9×10^6 CFU/g in Russian sturgeon and starred sturgeon, respectively, while it ranged from 2.75×10^4 to 4.93×10^5 CFU/g in the wild starlet. Microbial spectrum of the farmed fish was close to that of wild fish, in which bacteria of the genera *Aeromonas*, *Citrobacter* and *Plesiomonas* had been dominating (Table 1). On the contrary, the microflora of the sturgeons reared on artificial feeds at Ikryaninsky

fish farm (Table 2) was somewhat different and qualitatively resembled that of the feeds (Lartseva & Rogatkina, 1996). In comparison with the wild sturgeon significant increase in Gram-positive bacilli and micrococci, Gram-negative acinetobacteria and malds was found in the farmed sturgeons (Tables 1 & 2).

The prevalence of bacteria possessing proteolytic (gelatinase) activity was higher among the bacterial strains isolated from farmed sturgeons compared to that from wild fish (55.6% and 48.3%, respectively), as was the prevalence of DNAase-positive aeromonads isolated (42.9% and 36.0%, respectively).

Thus rearing sturgeons under aquacultural conditions leads to establishment of a specific fish microflora that is represented to a great extent by one contaminating the fish feeds and differs substantially from that of wild sturgeons. Considerable microbial contamination of all the components of fish farm biocoenosis as well as increased prevalence of pathogenic bacteria found there may be

one of the causes of pathological conditions in reared sturgeons.

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