Occurrence of Mycobacterium spp. in ornamental fish

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INTRODUCTION

Fish mycobacteriosis is caused by several species of bacteria from the genus Mycobacterium. Mycobacterial infections are found in both freshwater and marine fish worldwide [1]. The most important species causing fish mycobacterioses are M. chelonae, M. fortuitum, and M. marinum. Mycobacteria infecting fish also include zoonotic pathogens. M. marinum is the cause of most cases of fish-related mycobacterial infection in humans. The disease occurs more frequently in workers in the fishing industry, people whose hobbies involve water activities, and aquarists. The aim of the present study was to examine the occurrence of different species of mycobacteria in freshwater ornamental fish.

Materials and method. The occurrence of Mycobacterium spp. in freshwater ornamental fish was studied from January 2015 – December 2016. Material isolated from skin scrapings, contents of the digestive tracts, and internal organs of ornamental fish was stained with Ziehl-Neelsen (ZN) and inoculated on Lowenstein-Jensen medium. All isolates found positive by ZN were identified by amplification of the gene encoding the Hsp65 protein. A total of 408 samples obtained from 136 ornamental fish from 36 species were tested.

Results. Using the culture method Mycobacterium was isolated from 69 fish (50.1%) and 99 samples (24.3%). Sequence analysis of gene fragments coding for the Hsp65 protein of 99 isolates revealed occurrence of 13 species of mycobacteria: M. abscessus, M. chelonae, M. fortuitum, M. gordonae, M. marinum, M. mucogenicum, M. neoaurum, M. peregrinum, M. salmoniphilum, M. saopaulense, M. senegalense, M. septicum, and M. szulgai.

Conclusions. The obtained results indicate a significant role of ornamental fish as a source of mycobacteria which are potentially dangerous, especially to humans.

Key words
Mycobacterium spp., ornamental fish, prevalence, public health
interspecies variability, compared to some other conserved genes such as 16S rRNA or rpoB [20, 21].

The zoonotic potential and the great importance of mycobacteriosis for fish breeders highlight the need to characterize the diversity of mycobacteria in ornamental fish.

**OBJECTIVE**

The aim of the presented study was to examine the occurrence of different species of mycobacteria in diseased freshwater ornamental fish in Poland.

**MATERIALS AND METHOD**

From January 2015 – December 2016, 136 diseased ornamental fish sent from private aquaria and pet shops to the laboratory of the Department of Fish Diseases and Biology, Faculty of Veterinary Medicine, University of Life Sciences in Lublin, Poland, were examined for mycobacteria. Fish were euthanized using an overdose of ethyl 3-aminobenzoate methanesulfonate (Sigma Aldrich, USA). Skin, gut content, and visceral organs (spleen, liver, and kidney) were taken from each fish. If sampling the gut content was not possible due to their small size, entire guts were subjected to the cultivation protocol. Before decontamination, smears of homogenized biological material were prepared, stained with Ziehl-Neelsen (ZN) and observed under 100x (oil immersion) objective lens for the detection of AFB. A negative report was not given until at least 100 fields had been examined. For mycobacterial culture, the samples were mixed with an equal volume of a 5% oxalic acid solution and incubated for 15 min. Afterwards, the samples were centrifuged at 3,000 g for 15 min. The pellets were washed twice in sterile phosphate buffered saline and inoculated onto one egg Lowenstein-Jensen (LJ) media at 25°C and 37°C. The slants were checked daily for 2 months. Clearly visible colonies were examined according to their morphology and confirmed by microscopic examination after ZN staining of smears prepared from the colonies. AFB positive colonies were identified by the amplification of a 439 bp mycobacterial DNA fragment of the hsp65 gene using primers Tb11 (5’-ACCAACGATGGTGTGTCAT-3’) and Tb12 (5’-CTTGTGAAACCGATACCCCT-3’) [21]. PCR reactions were performed in a thermal cycler (MJ-Mini, Bio-Rad, USA) with the amplification profile: initial denaturation at 94°C for 10 min, followed by 45 cycles at 94°C for 1 min, 60°C for 1 min, 72°C for 1 min, and a final extension at 72°C for 5 min. The PCR products were analysed by 1 % agarose gel electrophoresis. DNA fragments of expected length were purified using Gel-Out Extraction Kit (A&A Biotechnology Gdynia, Poland), according to the manufacturer’s instructions, and subjected to direct sequencing at a DNA sequencing core facility (Genomed S.A., Warsaw, Poland). DNA sequences were aligned with the available hsp65 gene sequences from the National Centre for Biotechnology Information Gene Bank for Mycobacterium spp. using the MEGA6 software.

**RESULTS**

During the study, a total of 136 fish were examined. AFB ZN-stained specimens provided positive microscopic results in 15.44% (n = 21) of the examined fish. Culture methods provided positive results in 69 examined fish (50.74%) and in 99 of the total 408 examined samples (24.26%). All isolates were identified using sequencing of the hsp65 gene. The identity of mycobacterial isolates according to fish species are shown in Table 1. Carassius auratus, Danio rerio, Poecilia reticulata, Xiphophorus maculates, Paracheirodon innesi, Pterophyllum scalare, and Poecilia sphenops were the most commonly sampled fish. M. marinum, M. gordonae, M. peregrinum, and M. chelonae were the most frequently identified mycobacteria in the above-mentioned fish. M. marinum was detected in all of the most commonly sampled fish species with the exception of C. auratus and X. maculates. Granulomatous lesions suggestive of mycobacteriosis were observed in 5.15% (n = 7) of the fish. Mycobacteria were most frequently isolated from the skin scrapings and contents of digestive tracts, but less frequently from the internal organs (data not shown). A total of 99 mycobacterial isolates were obtained (Tab. 1). The majority of isolates were represented by M. marinum (33.33%), M. chelonae (16.16%), M. gordonae (15.15%), M. peregrinum (12.12%), and M. fortuitum (10.10%). Other isolates were identified as M. senegalense (4.04%), M. septicum (2.02%), M. neoaurum (2.02%), M. abscessus (1.01%), M. mucogenicum (1.01%), M. salmoniphilum (1.01%), M. saapulense (1.01%), and M. szulgai (1.01%). All the sequences obtained from the hsp65 gene were submitted to the GenBank database under the accession numbers listed in Table 2.

**DISCUSSION**

Numerous studies have shown that aquaculture organisms are a source of human bacterial infections [15, 16, 17, 22]. Of the bacterial pathogens present in fish and causing human infection, bacteria from the Mycobacterium genus are of great importance. A previous study revealed the occurrence of mycobacterial infections in 4 species of ornamental fish [23]. Mycobacterial infections in freshwater African catfish (Clarias gariepinus) were described by Antychowicz et al. [24]. Besides these reports, little is known about mycobacterial infections in fish in Poland.

In the presented study, AFB were detected by microscopy in 15.44% of the fish and mycobacteria were isolated from 50.74%. Similar results were obtain in Italy by Zanoni et al. [12], who detected AFB in 21.70% of fish and isolated mycobacteria from 35.9% of fish. In the Czech Republic, Lescenko et al. [5] detected AFB in 45.70% of fish and isolated mycobacteria from 70.60% of fish. In another study carried out in the Czech Republic by Beran et al. [3], AFB were detected in 14.30% of fish and mycobacteria were isolated from 42.90% of fish. These researchers also isolated mycobacteria from 75.40% of environmental samples taken from aquariums. In Sweden, Hongso et al. [25] detected AFB in 23% of fish and isolated mycobacteria from 89% of fish. In Slovenia, Pate et al. [9] detected AFB by microscopy in 37.10% of fish and isolated mycobacteria from 82.90% of fish. In India, Shukla et al. [18] isolated mycobacteria from 25% of examined aquarium fish. One cause of these differences in the NTM smear positivity rates and bacteriology results is the different numbers of mycobacteria in the samples. Other studies support the concept that specimens with low colony counts of mycobacteria are less likely to be detected by smear microscopy [26]. The discrepancy in positive microscopy
results and bacteriology results could also relate in part to the differences in acid-alcohol-fastness, which tends to be a stronger attribute in slow-growing mycobacteria [27].

All 13 species of mycobacteria isolated in the present study were previously isolated from ornamental fish. In the Czech Republic, studies on the occurrence of mycobacteria in aquarium fish were conducted by Lescenko et al. [5], who isolated M. fortuitum, M. flavescens, M. cheloneae, M. gordonae, M. terrae, M. triviale, M. diernhoferi, M. celatum, M. kansasi, and M. intracellulare. The most frequently isolated mycobacteria were M. fortuitum,
### Table 2. Mycobacterium strains identified by sequencing of hsp65 PCR products.

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<th>Source Species</th>
<th>Strain</th>
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M. flavescentis, M. chelonae. However, they did not isolate 
M. marinum, i.e. a species that was most frequently identified 
in the presented study. However, in studies carried out in 
Sweden by Hongso et al. [25], the most frequently isolated 
species was Mycobacterium marinum, followed by M. chelonae 
and M. gordoneae. In Italy, Zanoni et al. [12] isolated 
M. fortuitum, M. peregrinum, M. chelonae, M. abscessus, 
M. marinum, M. gordoneae, M. nonchromogenum, and 
M. interjectum. The most frequently isolated mycobacteria 
were M. fortuitum, M. peregrinum, and M. chelonae. In 
India, Shukla et al. [18] isolated M. abscessus, M. gordoneae, 
M. fortuitum, M. conceptionense, M. parascrofulaceum, and 
M. senegalense. The most frequently isolated mycobacteria 
were M. abscessus and M. gordoneae.

The difference in the prevalence of mycobacteria among 
different countries could relate to the endemic occurrence of 
certain species of mycobacteria in water-supply systems. For 
example, the Czech Republic is a country with an endemic 
incidence of M. kansasii in water [3]. The variation in 
prevalence may also depend on the fish supplier. Smith et al. 
[28] suggest that cleaning regimes, filtration, or handling 
procedures influence the diversity of bacteria within the 
tanks. The differences in the mycobacterial isolation rate 
may also depend on the diversity of fish species from which 
samples were taken. Numerous species of ornamental fish 
have been reported with mycobacterial infections; however, 
some species appear to be more susceptible and therefore 
demonstrate a higher incidence of infections [12].

The present study has shown that aquarium fish are a 
source of mycobacteria, which are potentially pathogenic 
for both fish and humans. It is noteworthy that M. marinum, 
i.e. the most frequently isolated species in this work, causes 
most cases of fish-related mycobacterial infection in humans.

Conflicts of interest
The authors declare that they have no competing interests.

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The authors declare that they have no competing interests.

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