

Multiple antibiotic resistant *Streptococcus agalactiae* and *Streptococcus iniae* in Nile tilapia aquaculture

Noura Kelany, Hosnia Abdel-Mohsein*, Saber Kotb, Abd El-Moez Ismail

Department of Animal, Poultry Hygiene and Environmental Sanitation, Faculty of Veterinary Medicine, Assiut University, 71526 Egypt.

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*Correspondence:

Corresponding author: Hosnia Abdel-Mohsein
E-mail address: hosnia18@aun.edu.eg

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ABSTRACT

Streptococcosis is a zoonotic bacterial disease in tilapia and other fresh that creates economic losses, caused mainly by *Streptococcus agalactiae* and *Streptococcus iniae*. The hazard of the disease is that it may present apparently healthy as well as its presence in culture water. So, this work aimed to detect streptococci in Nile tilapia farms located in Assiut and Minia Governorates, Egypt. *Streptococcus agalactiae* (42 isolates) and *Streptococcus iniae* (59 isolates) were identified. Two *Streptococcus agalactiae* isolates were molecularly confirmed and exhibited resistance to most antibiotics and a multiple antibiotic resistant index of 0.9-1. The identified isolates could not form biofilm. Identification of these hemolytic, resistant *Streptococcus* poses a potential hazard for human health; hence, alternative antimicrobials should be searched against infections caused by these bacteria.

Introduction

Fish offers the most promising source of safe, highly nutritious protein food (Rasco *et al.*, 2015). Nile tilapia (*Oreochromis niloticus*) is among the most important farmed aquatic species in the world, cultured in more than 170 countries worldwide (Cai *et al.*, 2019; FAO, 2020). Interestingly, the world production of farmed tilapia reached 6.03 million tons in 2018, which further consolidated tilapia as the second-most important farmed finfish group (Miao and Wang, 2020). Egypt is the topmost tilapia producer in Africa with more than 1,000,000 tons produced in 2018 (FAO, 2020), representing a cornerstone of tilapia fish farming (Ali *et al.*, 2020b). Tilapia have many characteristics that make them an ideal candidate for aquaculture, such as their herbivorous feeding nature, fast growth, tolerance to a wide range of environmental conditions and ability to reproduce in a short generation time (El-Sayed, 2006). However the culture of tilapia under intensive systems can pose a stressful conditions (Van Doan *et al.*, 2019). These stressors unfavorably alter the fish immune system, making it vulnerable to infection (Portz *et al.*, 2006).

Streptococcus infection represents the most important threat to tilapia culture in Egypt, causing several outbreaks with devastating mortalities mainly in summer season (Alazab *et al.* 2022). In Egypt, *Streptococcus agalactiae* and *Streptococcus iniae* have been considered the two primary species causing streptococcosis in tilapia culture resulting in significant economic losses in the aquaculture industry (Younes *et al.*, 2019; Ghetas *et al.*, 2021). Globally, streptococcosis has become one of the most violent aquatic diseases, resulting in massive mortality of up to 50% and economic loss yearly as high as \$150 million (Jansen *et al.*, 2019; Niu *et al.*, 2020). *Streptococcus* adherence, colonization, and invasion are relat-

ed to their virulence factors, as surface pili and proteins (Kaminska *et al.*, 2020). These virulence factors contribute to *Streptococcus* biofilm formation (Konto-Ghiorgi *et al.*, 2009). Bacterial biofilms facilitate bacterial persistence under environmental stresses and provide protection against antibiotics (Kaur *et al.*, 2009; Rosini and Margarit, 2015).

Moreover, *Streptococcus iniae* and *Streptococcus agalactiae* are human pathogens (Erfanmanesh *et al.*, 2012; Zhang *et al.*, 2017). Zoonotic Streptococcosis infections occur due to direct contact with a diseased or dead fish and indirect contact with contaminated water resulting in the development of cellulite, endocarditis, meningitis, severe systemic infections, and rarely death in human (Koh *et al.*, 2009; Ziarati *et al.*, 2022). Additionally, fish consumption has been associated with an increased risk of *Streptococcus agalactiae* colonization in humans (Foxman *et al.*, 2007). Therefore, fish farmers are forced to use antibiotics to avoid the threat of infection, which may pose a risk to the aquatic environment and consumer health (Rico *et al.*, 2014). Misuse of antibiotics not only induces bacterial resistance but also plays a role in their biofilm formation capabilities (Kaplan, 2011).

Due to insufficient diagnostic facilities at the fish farms, the majority of causative agents responsible for diseases remained uncharacterized, leading to an inappropriate treatment process that further increases fish mortality (Akter *et al.*, 2021). Due to *Streptococcus* phenotypic diversity, it is not possible to be identified accurately, so it is essential to search for accurate diagnostic methods to apply the effective treatment (Franco-Duarte *et al.*, 2019). Polymerase chain reaction is a highly specific molecular tool for *Streptococcus* identification (Abdelsalam *et al.*, 2017; Deng *et al.*, 2019). So, this study aimed to isolate and identify *Streptococcus* species from tilapia fish and their aquaculture water of tilapia cultured

ponds in Assiut and Minia Governorates. Additionally, to evaluate their antibiotic susceptibility and biofilm-producing abilities.

Materials and methods

Ethical approval

The examined tilapia fish in the current research were caught, transported, and examined with permission (Number: 06/2023/0114) of the ethical committee of the Faculty of Veterinary Medicine, Assiut University, Assiut, Egypt.

Study area

Fish and water samples were collected during the period from December 2021 to June 2022 in routine farm fishing. The investigation was carried out in three fish farms through four visits, two farms in Assiut (A, B) and one in Minia (C), Egypt.

Water and tilapia samples

A total of seventy water samples in sterile falcon tubes and seventy-nine apparently healthy tilapia fish with water in sterile containers were transported in an ice box to the Animal and Poultry Hygiene and Environmental Sanitation Department laboratory, Faculty of Veterinary medicine, Assiut University, Egypt.

Streptococcus isolation

In the laboratory, total and standard lengths, and weights were measured for each fish. Tilapia bodies were cleaned from dirt with sterile distilled water, and their scales were removed. The fish skin was disinfected by alcohol (70%), then their bellies were aseptically opened with sterile scissors. Swabs were collected aseptically from the liver, kidney, intestine, spleen, and gills of each fish. A sterile loop was inserted through the sterilized area, and then the inoculum was transported into trypticase soya enrichment broth (Biomark Laboratories, India). The inoculated tubes were incubated at 37°C with 5% CO₂ for 24 hours. Then inoculums from the enriched broth were streaked into *Streptococcus* selective media (Biolife Laboratories, Italiana) supplemented with 5ml/L sheep blood. For each sample, a maximum of four colonies, which presumptively appeared pen-headed, white opaque in color, circular, with entire raised edges, and glistening appearance were picked up and inoculated in trypticase soya agar slants for identification. Water samples were examined according to Standard Methods for the examination of water and wastewater examination (APHA, 2017), where one ml from each sample was transferred aseptically to a sterile trypticase soya broth tube, then incubated at 37°C with 5% CO₂ for 24 hours.

Streptococcus biochemical identification

Presumptive identification was performed according to Buller (2004), using conventional biochemical characters including catalase negative, Gram positive, urease negative, citrate negative, urease production, and hemolytic activity in sheep blood agar. Further identification of the isolates was performed according to the methods described in Bergey's Manual® of Systematic Bacteriology (Vos et al., 2011). Identified isolates were kept at -20°C in trypticase soya broth with 25 % glycerol for further molecular identification.

Molecular identification of *Streptococcus* species

The species diversity of *Streptococcus* fish pathogens highlights the troubles of confirmed identification of *Streptococcus* based only on phe-

notypic traits, so it is important to molecularly identify these pathogens (Baeck et al., 2006). After biochemical identification, twenty-three *Streptococcus agalactiae*, and thirteen *Streptococcus iniae* isolates were selected for molecular identification.

DNA extraction

Genomic DNA of the isolates was extracted using the boiling method as described by Queipo-Ortuño et al. (2008). One µL from the extracted DNA was used for estimating the purity and concentration using the GeneQuant®1300 Spectrophotometer (Bioscience, Sweden). The A260/A280 ratio was calculated and ratios between 1.8 and 2.0 were accepted for DNA purity.

PCR conditions and amplification

PCR reactions were carried targeting the intergenic space of *Streptococcus agalactiae* using 16-23S intergenic space primer STRA-AgI: 5'AAG-GAAACCTGCCATTG-3', STRA AgII:5'TTAACCTAGTTTCTTAAAACTAGAA-3' (Phuektes et al., 2001). Lactate oxidase (lctO) gene of *Streptococcus iniae* was investigated using lactate oxidase (lctO) gene with the following sequence; LOX-1:(5'AAGGGGAAATCGCAAGTGCC-3', LOX-2: 5'ATATCT-GATTGGGCCGTCTAA-3' according to Mata et al. (2004). Amplification of each DNA was performed in a reaction mixture containing 5 µL of Willowfort Master Mix, 1 µL (10 µM) of each forward, and reverse primer, 3 µL of DNA template, and DNase-free water up to a total volume of 20 µL. The amplifications were carried out in a Veriti thermocycler (Applied Biosystem) with the following conditions: primary denaturation at 95°C for 5 minutes, followed by 40 cycles at 95°C for 1 minute, annealing temperature at 58°C for 30 seconds, extension at 72°C for 45 seconds and final extension at 72°C for 10 minutes for the 16-23S intergenic spacer region. While for the lactate oxidase (lctO) gene, the reaction was carried out with initial denaturation at 95°C for 5 minutes, followed by 35 cycles at 95°C for 1 minute, varying annealing temperatures at 50, 52, 56, 58, and 61°C for 60 seconds, extension at 72°C for 2 minutes and final extension 72°C for 10 minutes.

The amplified PCR products of both bacterial isolates were separated by electrophoresis on a 1% agarose gel. The gel was placed in a UV band illuminator and photographed. For evaluation of PCR products, the band appeared at 270 bp for the 16-23S intergenic spacer region primer, and 870 bp for lactate oxidase primer.

Antibiotic sensitivity testing

The confirmed two isolates were evaluated for their antibiotic sensitivity for the following antibiotics: chloramphenicol (30 mcg), streptomycin-S (10 mcg), doxycycline-D (30 mcg), colistin-CT (10 mcg), trimethoprim/sulfamethoxazole-SXT (1.25/23.75mcg), norfloxacin-NOR (10mcg), ciprofloxacin-C (30 mcg), amoxicillin-AX (25 mcg), and novobiocin-NV (30 mcg). The sensitivity test was carried out according to Verma et al. (2023) with modifications. Briefly, homogenous bacterial suspensions of 0.5 McFarland turbidity standards were prepared from fresh bacterial cultures incubated for 18 hours. Each bacterial suspension was spread on Mueller-Hinton agar with 5% sheep blood using a sterile cotton swap. After dryness, specific antibiotic discs were placed on the lawn using sterile forceps then the plates were incubated overnight at 37°C. The developed zone of inhibition was manually measured and the results were interpreted as susceptible, intermediate or resistant according to the interpretative criteria following the guidelines of the Clinical and Laboratory Standards Institute (CLSI) (CLSI, 2013; 2017; EUCAST, 2023). The multiple antibiotic index (MAR index) was calculated according to Krumperman (1983) to determine the dissemination and prevalence of bacterial resistance in the isolated strains (Kinge et al., 2010).

Biofilm evaluation assays

Biofilm evaluation assays were performed as described by Silvestre et al. (2020), with modifications. Briefly, bacterial suspension was prepared in trypticase soya broth from overnight cultures in blood agar. Biofilm experiments were performed in 96-well flat-bottom polystyrene cell culture plates using trypticase soya broth with or without 1% glucose. Each strain was inoculated in triplicates where 180 µl of sterile broth was added to the wells and then 20 µl of the bacterial suspension was added. Two hundred microliter of broth-only (with or without glucose) were used as blank. The microplates were incubated at 37°C under 5% CO2 for 48 hours. After incubation, the well content was removed, and each well was vigorously washed thrice with sterile distilled water. The attached bacteria were fixed with 200 µl methanol for 15 minutes then washed three times with distilled water and stained for 15 minutes with 0.2% crystal violet. The stained wells were washed three times with distilled water to remove excess dye and allowed to dry at room temperature. The plate was inspected for the development of biofilms on the bottom and walls of the wells.

Statistical analysis

The result was represented as a percentage using Excel (Microsoft

Office 2013). The obtained data were subjected to statistical analysis using the SPSS software, version 22. The data weren't normally distributed and weren't homogenous.

Results

The tested fish lengths and weights are presented in Table 1.

Streptococcus species on *Streptococcus* selective media supplemented with blood appeared as small pinpoint colonies with a smooth, white regular edge surrounded by a beta-hemolytic zone. The bacterial isolates were biochemically identified, and only Gram-positive cocci, non-motile, catalase-negative, and hemolytic colonies were further differentiated into *Streptococcus agalactiae* and *Streptococcus iniae* based on their variable reactions in different reactions like mannitol fermentation, hippurate hydrolysis, and esculin hydrolysis. Of the 79 tilapia, 70 isolates (69.3%) were identified as *Streptococcus* species, and from the 70 water samples 31 isolates (30.69%) were identified as *Streptococcus* species. In tilapia, the highest percentage of isolates were identified from the intestine (27.14%), then the kidney (22.85%), followed by the gills (21.42%), then the liver (20%), and finally, the spleen (8.57%) as shown in Table 2.

According to Table 3, *Streptococcus agalactiae* accounts for 41.6% of all *Streptococcus* isolates. The gut had the largest amount of *Streptococcus agalactiae* isolates (29.6%), followed by the gills (25.9%), the liver (22.2%),

Table 1. Values of tilapia fish total and standard lengths and weights.

Visits	Total length/cm			Standard length/cm			Weights/g		
	Mean±SD	Min	Max	Mean±SD	Min	Max	Mean±SD	Min	Max
V I	21.2±2.3	18.5	27.5	17.4±1.9	15.0	23.0	190.4±65.5	122.0	435.0
V II	20.9±3.2	17.0	30.0	17.5±2.9	13.0	25.5	158.9±46.6	98.0	285.0
V III	25.1±0.7	24.0	26.0	20.8±0.3	20.5	21.0	251.2±14.3	231.0	275.0
V IV	22.5±1.0	20.5	24.0	18.3±1.0	17.0	20.0	187.4±21.4	145.0	230.0

Table 2. Prevalence of biochemically positive *Streptococcus* species in Nile tilapia aquaculture.

Visits	<i>Streptococcus</i> species														Total isolates			
	Tested	In Nile tilapia fish ^a												In aquaculture water		No.	% ^c	
		liver		Kidney		Intestine		Spleen		Gills		Total fish isolates		Tested	Isolates			
		No.	%	No.	%	No.	%	No.	%	No.	%	No.	%		No.			% ^b
I	25	0	0	4	5.71	2	2.85	0	0	6	8.57	12	17.14	10	10	32.25	22	21.78
II	14	5	7.1	2	2.85	2	2.85	3	4.28	5	7.14	17	24.28	20	5	16.12	22	21.78
III	20	0	0	2	2.85	3	4.28	0	0	2	2.85	7	10	20	7	22.58	14	13.86
IV	20	9	12.9	8	11.42	12	17.14	3	4.28	2	2.85	34	48.57	20	9	29.03	43	42.57
Total	79	14	20	16	22.85	19	27.14	6	8.57	15	21.42	70	69.3	70	31	30.69	101	

a. Data presented as percentage to the total number of isolates of tilapia (70). b. Data presented as percentage to the total number of isolates of water (31). c. Data presented as percentage to the total number of isolates (101).

Table 3. Prevalence of biochemically positive *Streptococcus agalactiae* in Nile tilapia aquaculture.

Visits	<i>Streptococcus agalactiae</i>														Total isolates		
	liver	Nile tilapia fish ^a												Aquaculture water		No.	% ^c
		Kidney		Intestine		Spleen		Gills		Total fish isolates		No.	% ^b				
		No.	%	No.	%	No.	%	No.	%	No.	%						
I	0	0	0	0	1	3.7	0	0	2	7.4	3	11.1	6	40	9	21.42	
II	3	11.1	0	0	1	3.7	1	3.7	3	11.1	8	29.6	1	6.7	9	21.42	
III	0	0	0	0	2	7.4	0	0	1	3.7	3	11.1	2	13.3	5	11.9	
IV	3	11.1	3	11.1	4	14.8	2	7.4	1	3.7	13	48.1	6	40	19	45.23	
Total	6	22.2	3	11.1	8	29.6	3	11.1	7	25.9	27		15		42		

a. Data presented as percentage to the total number of isolates of tilapia (27). b. Data presented as percentage to the total number of isolates of water (15). c. Data presented as percentage to the total number of isolates (42).

and the kidney and spleen (11.1%). Additionally, *Streptococcus agalactiae* was recovered from the aquaculture water of the three ponds; six isolates were found in visits I and IV, two isolates in visit III, and one isolate in visit II. *Streptococcus iniae* could be isolated from tilapia aquaculture and represented 58.41% of the total *Streptococcus* species isolates. The total *Streptococcus iniae* isolated was 59 isolates: 15 from the water and 43 from the fish as shown in Table 4. In tilapia fish, the kidney isolates showed the highest percentage, followed by the intestine, and finally the spleen.

The suspected *Streptococcus* isolates were subjected to molecular identification (PCR) using species-specific 16-23S intergenic space primer to identify *Streptococcus agalactiae* and lactate oxidase (*lctO*) gene primer for *Streptococcus iniae*. PCR reaction for *Streptococcus agalactiae* identification was performed for twenty-three suspected isolates at an annealing temperature 58°C and only two isolates were identified as positive *Streptococcus agalactiae* at base pair 270: one isolate from the liver in visit I and the other from the kidney in visit III. The identified two isolates represent 8% (2/23) of the tested isolates. Also, thirteen biochemically identified *Streptococcus iniae* isolates were tested the using lactate oxidase (*lctO*) gene. Although wide range of annealing temperatures (50, 52, 56, 58, 61°C) were applied during the PCR reaction, no isolate was

confirmed as *Streptococcus iniae*.

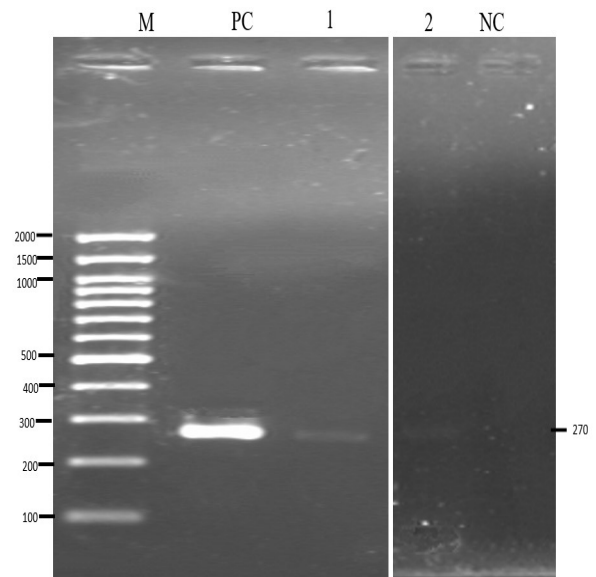


Fig. 1. Gel electrophoresis of *Streptococcus agalactiae*; Lane M: 100 bp DNA marker, Lane (PC): positive control, lane (1-2): positive isolates 270 bp, NC: negative control.

Table 4. Prevalence of positive biochemically positive *Streptococcus iniae* in tilapia aquaculture.

Visits	<i>Streptococcus iniae</i>												Aquaculture water		Total isolates	
	Nile tilapia fish ^a															
	Liver		Kidney		Intestine		Spleen		Gills		Total		No.	% ^b	No.	% ^c
I	0	0	4	9.3	1	2.3	0	0	4	9.3	9	20.9	4	25	13	22
II	2	4.6	2	4.6	1	2.3	2	4.6	2	4.6	9	20.9	4	25	13	22
III	0	0	2	4.6	1	2.3	0	0	1	2.3	4	9.3	5	31.3	9	15.3
IV	6	14	5	11.6	8	28.6	1	2.3	1	2.3	21	48.8	3	18.7	24	40.7
Total	8	18.6	13	30.23	11	25.58	3	6.9	8	18.6	43		16		59	

a. Data presented as percentage to the total number of isolates of tilapia (43). b. Data presented as percentage to the total number of isolates of water (16). c. Data presented as percentage to the total number of isolates (59).

Table 5. Antibiotic resistance of the isolated *Streptococcus agalactiae* (2 isolates).

Mode of action	Class	Antibiotic	Sensitive		Intermediate		Resistant	
			No.	%	No.	%	No.	%
Cell wall inhibitors	B- lactams	Amoxicillin-AX	1	50%	-	-	1	50%
Cell membrane disruptors	Colistin	Colistin-CT	-	-	-	-	2	100%
	Chloramphenicol	Chloramphenicol-C	-	-	-	-	2	100%
Protein synthesis inhibitors	Tetracycline	Doxycycline-D	-	-	1	50%	1	50%
	Aminoglycoside	Streptomycin-S	-	-	-	-	2	100%
Nucleic acid synthesis disruptors	Aminocoumarine	Novobiocin-NV	-	-	-	-	2	100%
	Floroquinoline	Norfloxacin-NOR	-	-	-	-	2	100%
		Ciprofloxacin-CIP	-	-	-	-	2	100%
	Sulfonamides	Trimethoprim/Sulphamethoxazole (SXT)	-	-	-	-	2	100%

Table 6. Percentage of resistance and multiple antibiotic index.

Isolate code	Isolate origin	AX	CT	C	D	S	NV	NOR	CIP	SXT	Multiple antibiotic index ^a
1	liver	s	r	r	r	r	r	r	r	r	0.9
2	kidney	r	r	r	i	r	r	r	r	r	1
Number of resistant isolates		1	2	2	1	2	2	2	2	2	
Percentage of resistance		50%	100%	100%	50%	100%	100%	100%	100%	100%	

a. calculated through dividing the number of antibiotics the isolate is resistant against by the number of the tested antibiotics. AX (Amoxicillin), CT (Colistin), C (Chloramphenicol), D (doxycycline), S (Streptomycin), NV (Novobiocin), NOR (norfloxacin), CIP (Ciprofloxacin), and SXT (trimethoprim/sulfamethoxazole).

In this study, the two confirmed *Streptococcus agalactiae* isolates were tested for their antibiotic susceptibility. Each was exposed to nine antibiotics in a disk diffusion test. The developed zones of inhibition were measured. Both tested isolates exhibited complete resistance (100%) to colistin, chloramphenicol, streptomycin, novobiocin, norfloxacin, ciprofloxacin, and trimethoprim/sulphamethoxazole. Moreover, one isolate was resistant to amoxicillin and doxycycline. On the other hand, the other isolate was susceptible to amoxicillin and moderately resistant to doxycycline. The two strains exhibited a multiple antibiotic resistance index of 0.9-1.

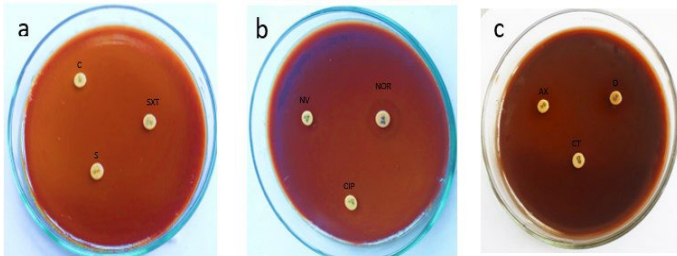


Fig. 2. *Streptococcus agalactiae* sensitivity zone for antibiotic. (a); C (Chloramphenicol), SXT (trimethoprim/sulfamethoxazole), and S (Streptomycin), (b); NV (Novobiocin), NOR (norfloxacin), and CIP (Ciprofloxacin), and (c); AX (Amoxicillin), CT (Colistin), and D (doxycycline).

The biofilm formation ability of the resistant isolates was assessed quantitatively using the crystal violet polystyrene microtiter plate method. After 48 hours incubation period, the two strains failed to form biofilm.

Discussion

Streptococcal infections in fish, in particular those produced by the pathogens *Streptococcus iniae*, and *Streptococcus agalactiae* have increased markedly with the intensification of aquaculture practices (Amal and Zamri-Saad, 2011). A diversity of fish species are susceptible to *Streptococcus* infection and *Streptococcus* species have been identified worldwide from different freshwater fish as Amur sturgeon in China (Yang and Li, 2009), red garra in Ireland (Ruane et al., 2013), catfish in China (Tavares et al., 2018), Siberian sturgeon in China (Deng et al., 2017), freshwater seabass in Thailand (Piamsomboon et al., 2020), Adriatic sturgeon in Northern Italy (Colussi et al., 2022), and *Streptococcus* species were detected in different marine fish around the world (Nho et al., 2009; Pourgholam et al., 2011; Erfanmanesh et al., 2012; Tsai et al., 2015). Streptococcosis of fish should be regarded as a significant non-apparent hazard because of the subclinical form caused by *Streptococcus iniae* and *Streptococcus agalactiae* (Sun et al., 2016; Rahmatullah et al., 2017).

Noticeably, with the expanding industry of tilapia aquaculture in Egypt, Streptococcosis has become an important and significant problem. Streptococcosis frequently occurred in the ponds in northern Egypt such as Kafr El-Sheikh, Port Said, Dakahlia, and Damietta Governorates mainly during the summer seasons (Saleh et al., 2017; Eissa et al., 2021; Alazab et al., 2022). There are many reasons that make Egyptian tilapia susceptible to Streptococcosis. The first, is that tilapia aquaculture is mainly distributed in northern Governorates, because of the availability of water there as well as the suitable temperature for the growth of tilapia is 28–32°C (El-Sayed, 2006). The second, is that tilapia is susceptible to *Streptococcus* during the hot season of each year because the water temperature is usually rise which may increase the tilapia's susceptibility (Saleh et al., 2017; Eissa et al., 2021). The third is the management system as with the high-density, and low quality feed the fish culture would be at the risk of Streptococcosis. Different *Streptococcus* species have been found to be the causative agent of Streptococcal infection, mainly *Streptococcus agalactiae* and *Streptococcus iniae* (Amal and Zamri-Saad, 2011).

One hundred and one *Streptococcus* species isolates from tilapia aquaculture could be identified: seventy from tilapia and thirty-one from the aquaculture water. In tilapia, the highest percentage of isolates were identified from the intestine, followed by the kidney. This result was similar to that obtained by Ali et al. (2020a) and close to that recorded by Auzureen et al. (2016) who identified 144 *Streptococcus* species isolates from hybrid red tilapia in local wet markets. This recorded result was lower than that reported by Abdelsalam et al. (2017) who isolated nine isolates from moribund red tilapia. Furthermore, Chitambo et al. (2023)

recorded one *Streptococcus* species isolated from healthy Nile tilapia.

Thirty-one isolates of the *Streptococcus* species were obtained from the water, accounting for 30.96% of all isolates. This result was similar to that reported by Ali et al. (2020a) who found isolates of 20 different *Streptococcus* species in tilapia farming water..

Twenty-seven *Streptococcus agalactiae* isolates were detected in tilapia fish this result was higher than that recorded by Abbas et al. (2022) who identified fourteen bacterial isolates from naturally infected Nile tilapia as *Streptococcus agalactiae*, but lower than that recorded by Sudprasert et al. (2021) who reported fifty-nine isolates from Nile tilapia. Also, one hundred and forty-six isolates were confirmed to be *Streptococcus agalactiae* according to the biochemical profiles by Sun et al. (2016) from healthy tilapia fish. Furthermore, among the *Streptococcus agalactiae* isolates found in the aquaculture water of the three ponds, fifteen isolates were found in this investigation, accounting for 35.7% of all isolates. This percentage is comparably higher than that reported by Ali et al. (2020a), who identified three *Streptococcus agalactiae* isolates. While, Reyes et al. (2018) obtained 250-270 CFU/mL of *Streptococcus agalactiae* count in tilapia pond water in Lubao, Pampanga, Philippines. Forty-three *Streptococcus iniae* isolates were identified from tilapia fish in Assiut and Minia Governorates and this was nearly similar to the recovered forty-seven isolates by Saleh et al. (2017) from mortality suffering Nile tilapia. Younes et al. (2019) identified fourteen isolates from diseased Nile tilapia. Also, in our study, sixteen *Streptococcus iniae* isolates were identified from the water. Compared to our results, Hardi et al. (2018) identified two *Streptococcus iniae* isolates from tilapia culture water and fish feces.

Two *Streptococcus agalactiae* isolates (8%) were molecularly confirmed: one isolate from the tilapia liver and the other from the kidney. The water isolates tested for molecular identification failed to give the required band (270bp). Alazab et al., (2022) molecularly confirmed 21 *Streptococcus agalactiae* isolates with 23.6% (21/89) of the suspected isolates from tilapia as follows: 10 (47.6%) from the liver; 6 (28.57%) from the kidney; 2 (9.5%) from each eye and gill samples; 1(4.85) from spleen samples using specific primers targeting the *Streptococcus agalactiae*-specific *dltS* gene. Also, Auzureen et al., (2016) confirmed eight *Streptococcus agalactiae* isolates using PCR with a band size 220 bp. While, Abbas et al., (2022) confirmed a higher number representing (100%) of the studied *Streptococcus agalactiae* isolates in tilapia fish using 16sRNA universal primer. The lactate oxidase gene (*lctO*) has been stated to be able to detect *Streptococcus iniae* with superior specificity than the 16S rRNA gene (Mata et al., 2004), so this species-specific *lox*- primer was used in the molecular identification of thirteen *Streptococcus iniae* isolates. Despite of its high specificity (Mata et al., 2004), no isolate achieved the band 870bp. Similar to our result, Oviedo-Bolaños et al. (2021) couldn't identify *Streptococcus iniae* using the same primer in infected tilapia in Costa Rica. In contrast to our data, Legario et al. (2020) succeeded in identifying seven *Streptococcus iniae* isolates from tilapia aquaculture using the same *lctO* gene primer of *Streptococcus iniae*. In a follow-up investigation, Younes et al. (2019) used a species-specific 16S RNA primer to confirm that the isolates of *Streptococcus iniae* recovered from cultured Nile tilapia produced the desired 300 bp band in every test; additionally, Saleh et al. (2017) verified that three of the four isolates were in fact *Streptococcus iniae* at 300 base pair. Using a 16S-RNA primer, El Tawab et al. (2022) were also successful in validating 15 *Streptococcus iniae* out of 30 *Streptococcus* isolates. The gene encoding lactate oxidase is very unusual among *Streptococcus* species and related genes, indicating its specificity to *Streptococcus iniae* (Al-Harbi, 2011). The difficulty in *Streptococcus iniae* identification may be related to the lack of a serological identification system because *Streptococcus iniae* is non-Lancefield grouped (Pretto Giordano and Scarpassa, 2015). Also, the struggle of *Streptococcus iniae* accurate identification can be linked to its phenotypic diversity and the unavailability of commercial identification systems includes (Mata et al., 2004). Moreover, there is a close homology (98%) in 16S rRNA gene between *Streptococcus iniae* and *Streptococcus parauberis* (Täpp et al., 2003).

The extensive misuse of antibiotics has resulted in the emergence of antibiotic resistance in terrestrial and aquatic bacterial species, which is an international issue (Rico et al., 2014). Recently, the occurrence of antibiotic resistance among bacterial isolates has highlighted the importance of continuous monitoring of antibiotic resistance patterns. The tested two *Streptococcus agalactiae* isolates were highly resistant to all tested antibiotics except that one isolate was inhibited by amoxicillin and the other was slightly inhibited by doxycycline. Aleru-Obogai et al. (2022) found that all tested *Streptococcus agalactiae* isolated from cage-cultured red hybrid tilapia were susceptible to all antibiotics used. While, *Streptococcus agalactiae* strains isolated by Alazab et al. (2022) exhibited 95% resistance against ampicillin and erythromycin, followed by trimethoprim-sulfamethoxazole and cefotaxime (76% each), ceftriaxone (72%), tetracycline (66%), gentamicin (62%), penicillin (57%), and finally, 43% against ciprofloxacin. In the current study, the two strains tested were resistant to at least eight antibiotics tested, indicating the presence of multi-antibiotic

resistance profile with a multiple antibiotic resistance index of 0.9-1. Multiple antibiotic resistance in bacteria happens by acquiring and accumulating resistant plasmids, integrons or transposons of multiple genes that each encode resistance to a specific agent and/or by the activity of efflux pumps. *Streptococcus agalactiae* resistance to macrolide (norfloxacin, ciprofloxacin) has been stated to be mainly caused by efflux pumps encoded by the *mefA/E* genes (Verma et al., 2023). The resistance of *Streptococcus agalactiae* versus beta-lactams including amoxicillin has been reported to be due to mutations in penicillin-binding proteins, which affect the binding capacity of penicillin (Metcalf et al., 2017). While doxycycline resistance of *Streptococcus agalactiae* is due to the presence of *tetM* and *tetO* genes or drug efflux mediated by efflux pumps or target protection mediated by ribosomal protection proteins (Liu et al., 2023). The cell wall of the Gram-positive *Streptococcus* species is intrinsically less permeable to aminoglycosides; therefore, *Streptococcus agalactiae* is resistant to aminoglycosides at low concentrations, also ribosomal mutations contribute to its resistance to aminoglycosides (streptomycin) (Liu et al., 2023; Zakerifar et al., 2023).

Streptococcus species are ubiquitous in culture water and can also be isolated from healthy fish and apparently healthy fish, moreover, *Streptococcus* infection occurs in certain instances as stress conditions (Sun et al., 2016; Kannika et al., 2017). *Streptococcus* infection from the natural route of infection through direct contact can be systemically disseminated, affecting mainly the brain, kidney, and intestine and causing cell death (Iregui et al., 2016; Liu et al., 2016). The same in human *Streptococcus* bacteria present commensally in the gastrointestinal and genital tract of healthy women as part of the normal flora (Wernecke et al., 2009; Zakerifar et al., 2023). The bacteria can climb up through the birth canal and reach the newborn resulting in sepsis and meningitis in 1% of infants while 10% die and a significant percent of survived infants suffer from multiple nervous problems (Horváth-Puhó et al., 2021). Unfortunately, fishermen, farm workers, seafood handlers, as well as fish consumers are at risk of *Streptococcus* infection through contact with infected fish or contaminated water. The routine action in case of infection, is that antibiotics are used. However, every time these antibiotics are applied, antibiotic resistance develops. So, great attention should be paid to search for antibiotic alternatives.

Biofilms are aggregates of microbial communities in which bacteria adhere, cluster to a surface, and are surrounded by an extracellular matrix of carbohydrates or exopolysaccharides (Silvestre et al., 2020). This matrix protects from host immune defenses and antibiotics (Vestby et al., 2020). Therefore, biofilm formation by *Streptococcus agalactiae* can enhance its pathogenicity. Several studies investigated *Streptococcus* biofilm assembly in vitro (Dilrukshi et al., 2021; Verma et al., 2023). The biofilm formation for the two identified isolates was carried out according to Silvestre et al., (2020), however the two isolates could not form biofilm. The inability of the tested *Streptococcus agalactiae* to form biofilm may be related to the conflicting data regarding their biofilm-forming capacity, the glucose concentration, or the pH value (Kaur et al., 2009; Silvestre et al., 2020). Although higher biofilm production was described, under acidic pH conditions (Ho et al., 2013; D'Urzo et al., 2014), their inability to form biofilm at low pH values has also been reported (Dilrukshi et al., 2021). Glucose also seems to be important for the biofilm production by *Streptococcus agalactiae* (Silvestre et al., 2020), however in the absence of glucose, the biofilms of *Streptococcus* are formed (Kaur et al., 2009). Furthermore, several studies showed a greater ability of *Streptococcus agalactiae* to produce biofilm with a longer incubation time (48 hours) (Silvestre et al., 2020), but the biofilms were formed after 24 hours of incubation and lower (Parker et al., 2016; Verma et al., 2023). Also, there was a correlation between *Streptococcus agalactiae* biofilm formation and their virulence (Verma et al., 2023), but biofilm-forming strains were identified in asymptomatic carriers (Kaur et al., 2009; Parker et al., 2016). This may explain the inability of our isolates to assemble in biofilms, so further studies are required to find the optimum conditions for *Streptococcus agalactiae* biofilm formation.

Conclusion

Streptococcus bacteria is an opportunistic ubiquitous bacterial pathogen. Two *Streptococcus* isolates could be identified in healthy Nile tilapia. The identified isolates exhibited resistance to most of the tested antibiotics. Due to the outbreaks caused by *Streptococcus* every year around the world and Egypt, there is a critical need to search for and develop of new antimicrobials against these bacteria.

Conflict of interest

The authors declare that they have no conflict of interest.

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