ANTIMICROBIAL RESISTANCE PROFILES OF *Streptococcus agalactiae* SEROTYPE Ia FROM TILAPIA IN VIETNAM (2024–2025)

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01 Introduction

Streptococcus agalactiae is a major bacterial pathogen causing streptococcosis in farmed tilapia in Vietnam and other Asian countries. Disease outbreaks result in substantial mortality and economic losses, while antimicrobial treatment may contribute to development of antimicrobial resistance (AMR).

This study investigated:

- Occurrence of *S. agalactiae* outbreaks,
- Serotype distribution,
- Clinical characteristics, and
- Antimicrobial resistance profiles

Among diseased tilapia cultured in ponds and cages in Northern and Central Vietnam during 2024–2025.

02 Methods

2.1 Sample collection

A total of 229 diseased tilapia were collected from 26 farms in Bac Ninh, Hanoi, Hai Phong, Ninh Binh, and Nghe An provinces during 2024–2025.

2.2 Bacterial isolation and identification

Bacteria isolated from liver, spleen, and kidney were identified by culture characteristics, biochemical testing, nested PCR, and 16S rRNA gene sequencing.

2.3 Serotyping detection

Molecular serotypes were determined by multiplex PCR targeting capsular polysaccharide (cps) genes.

2.4 Antimicrobial *susceptibility testing*

Susceptibility to 14 commonly used antimicrobials was determined by disk diffusion method according to CLSI guidelines.

03 Results

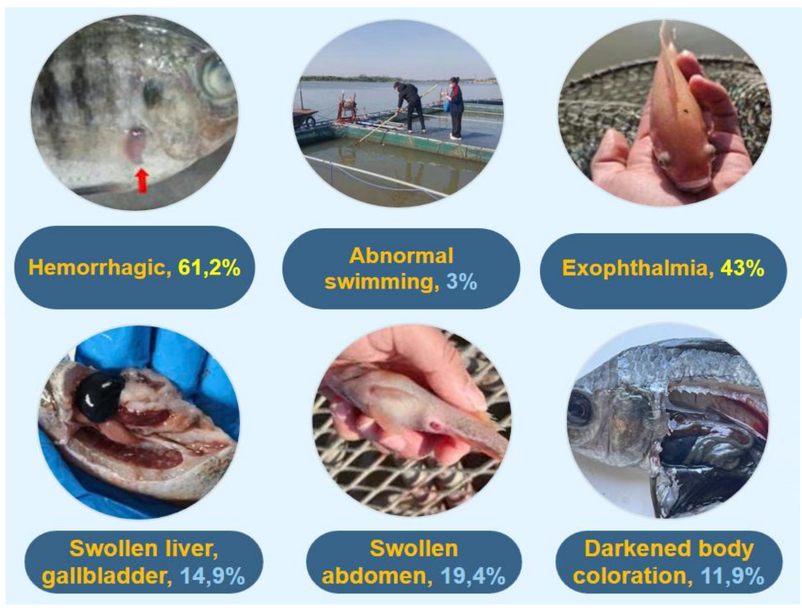
3.1 Outbreak disease and isolate *S. agalactiae* distribution

Table 1. The isolates *S. agalactiae* from tilapia in Vietnam (2020-2025)

Year	No. of farms	No. of samples	No. of isolates	Regions	% total isolates (%)
2024	9	38	2	North	5,3
2025	17	191	65	North, Centre	34,0
Total/ Ave.	**26**	**229**	**67**		**29,3**

A total of 67 *S. agalactiae* isolates were obtained from diseased tilapia originating from 26 farms. Most outbreaks occurred in fish weighing 300–600 g.

3.2 Clinical characteristics



3.3 Serotype distribution

All isolates were identified as serotype Ia (100%); a uniform serotype distribution across regions.

3.4 *Antibiotic resistance profiles*

Table 2. Multi-drug resistance (MDR) phenotype of the *S. agalactiae* isolates in infected tilapia

Resistance phenotype	No. of resistance isolates (%)
NEO	1 (1.5)
KAN+NEO	22 (32.4)
OXA+KAN+NEO	1 (1.5)
KAN+NEO+TET	9 (13.2)
OXA+KAN+NEO+SXT	1 (1.5)
OXA+AMP+KAN+NEO	1 (1.5)
KAN+NEO+TET+OXY	9 (13.2)
KAN+NEO+TET+SXT	1 (1.5)
OXA+VAN+KAN+NEO+SXT	2 (2.9)
KAN+NEO+TET+DOX+OXY	17 (25.0)
KAN+NEO+TET+DOX+OXY+SXT	1 (1.5)
OXA+AMP+VAN+KAN+TET+DOX+OXY	1 (1.5)
OXA+KAN+NEO+ERY+TET+OXY+SXT	1 (1.5)
OXA+AMX+VAN+KAN+NEO+ERY+TET+DOX+OXY+SXT	1 (1.5)

- High resistance: kanamycin and neomycin (99%)
- Moderate resistance: tetracycline (58%) oxytetracycline (43%), and doxycycline (28%).
- Resistance to other tested antibiotics was below 12%.
- All isolates were MDR, exhibiting resistance to 2–10 antibiotics and forming 13 distinct resistance phenotypes.
- MDR patterns were most frequently observed in Bac Ninh and Ninh Binh provinces.

04 Discussion

- Swidespread circulation of serotype Ia;
- Concerns regarding multidrug resistance;
- Implications for treatment efficacy and antimicrobial stewardship.

05 Conclusion

These findings demonstrate widespread multidrug-resistant *S. agalactiae* serotype Ia circulating in Vietnamese tilapia farms and indicate reduced effectiveness of several commonly used antibiotics; need for improved disease prevention and prudent antimicrobial use.

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