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Genetic Diversity, Virulence Genes, and Antimicrobial Resistance of *Streptococcus dysgalactiae* Isolates from Different Aquatic Animal Sources

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Short running title

Genetic diversity and virulence properties of *S. dysgalactiae*

ABSTRACT

Lancefield group C *Streptococcus dysgalactiae* represents an etiological agent causing high mortality in many farmed fish species worldwide. Despite its pathogenic importance, limited epidemiological knowledge related to this pathogen is available. In the present study, 79 *S. dysgalactiae* isolates from diseased aquatic animals in Taiwan (n = 67) and Japan (n = 12) were characterized using pulsed-field gel electrophoresis (PFGE). The distribution of isolate virulence factors and antimicrobial susceptibility were also investigated. PFGE with SmaI and ApaI digestions displayed 19 and 20 different pulsotypes respectively, reflecting a genetic diversity among isolates from different sources. All examined strains harbored the virulence-associated genes *sagA*, *NAPlr*, and α-*enolase*, whereas 76/79 (96.2%) and 77/79 (97.5%) harbored *spegg* and *sof*, respectively. PCR analysis of the most common tetracycline and macrolide resistance genes demonstrated that isolates carried *tet*(M) (14/79, 17.7%), *tet*(S) (12/79, 15.2%), *erm*(B) (5/79, 6.3%), and *mef*(A) and *msr*(D) (3/79, 3.8%). Isolates harboring one or more resistance genes showed resistance to drugs by the disk diffusion method. Together, our data indicates that *S. dysgalactiae* isolates in Taiwan and Japan