

Genetic diversity and geographical distribution of atypical *Aeromonas salmonicida* in farmed Atlantic salmon (*Salmo salar*) from Chile.

Panel/Poster

Genética molecular

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Introduction

Bacteria of the genus *Aeromonas* are Gram-negative, facultative anaerobic bacilli widely distributed in aquatic environments (Ajmi et al., 2025; Majeed et al., 2023). Among them, *Aeromonas salmonicida* is recognized as the etiological agent of furunculosis, a systemic disease that primarily affects salmonids (Godoy et al., 2024). This species exhibits marked phenotypic and genotypic variability, leading to its classification into typical and atypical strains based on pigment production on solid media, and into mesophilic or psychrophilic strains according to thermal tolerance. In Chile, furunculosis was first diagnosed in 1995 in Atlantic salmon (*Salmo salar*), rapidly spreading through freshwater and estuarine systems. The inclusion of *A. salmonicida* antigens in multivalent vaccines from 2002 successfully controlled the disease, limiting outbreaks to freshwater hatcheries. However, since 2022, new clinical cases associated with atypical strains have been reported. The objective of

this study was to determine the genetic variability of atypical *A. salmonicida* isolates obtained from recent outbreaks in farmed Atlantic salmon in Chile.

Methodology

Pathological, histological, and epidemiological data from 41 clinical outbreaks recorded between 2022 and 2025 were analyzed. Strains were characterized through whole-genome sequencing (WGS). Whole-genome single nucleotide polymorphisms (wg-SNPs) were identified using Snippy and evaluated with ModelTest-NG to select the optimal nucleotide substitution model. Phylogenetic trees were constructed using the Maximum Likelihood method in IQ-TREE. Recombination events were corrected with ClonalFrame/ClonalFrameML, and clonal relationships were visualized in iTOL. Core genome analysis was performed with Panaroo, complemented by Average Nucleotide Identity (FastANI) and pairwise SNP distance matrices. Additionally, an MLST analysis based on seven conserved genes (*atpD*, *dnaJ*, *dnaX*, *gyrA*, *gyrB*, *recD*, and *rpoD*) was conducted, aligned with MAFFT, and inferred with IQ-TREE using ultrafast bootstrap.

Results and Conclusion

Chilean isolates exhibited high genomic similarity (ANI 97–99%), with notable variation in virulence and antimicrobial resistance genes. These findings reveal substantial genetic diversity, phenotypic plasticity, and adaptive potential among atypical *A. salmonicida* strains, suggesting recent evolutionary processes driven by environmental conditions and antimicrobial pressure in local aquaculture.

Palabras Clave

(1) Epidemiología molecular, (2) salmón, (3) Furunculosis atípica, (4) *Aeromonas salmonicida* atípicas.

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