

Genetic diversity and geographical distribution of Piscine orthoreovirus (PRV) variants in salmonid farming in Chile

Panel/Poster

Microbiología y salud animal

Marcos Godoy^{1, 2}, Molly Kibenge³, Fred Kibenge³, Diego Caro², Karina Kusch², Juan Pablo Pontigo¹, Eduardo Lazo², Rudy Suarez^{2, 4}.

(1) Universidad San Sebastián, Veterinaria, lago Panguipulli 1390, Puerto Montt, Chile.

(2) Centro de Investigaciones Biológicas Aplicadas (CIBA), Lago Panguipulli 1390, Puerto Montt, Chile.

(3) University of Prince Edward Island, Department of Pathology and Microbiology, Atlantic Veterinary College (AVC), 550 University Ave, Charlottetown, Canadá.

(4) Universidad Católica del Norte, Departamento de Acuicultura, Facultad de Ciencias del Mar, Larrondo 1281, Coquimbo, Chile.

marcos.godoy@uss.cl

Background

Piscine orthoreovirus (PRV) is a member of the family *Spinareoviridae*, genus *Orthoreovirus*, that infects salmon and trout worldwide. This virus is the etiological agent of heart and skeletal muscle inflammation (HSMI), an inflammatory condition mainly affecting the heart and skeletal musculature of salmonids. The aim of this study was to genetically characterize PRV strains obtained from clinical and subclinical cases in Atlantic salmon (*Salmo salar*) and coho salmon (*Oncorhynchus kisutch*) in Chile, to determine their geographic distribution and explore possible associations with clinical and epidemiological data.

Methods

Samples of heart, spleen, kidney, and liver were collected from fish showing clinical and subclinical signs, corresponding to 26 cases diagnosed between 2018 and 2023. PRV detection was performed by RT-qPCR. Viral RNA was extracted using the E.Z.N.A.® Total RNA Kit I (Omega Bio-tek, Inc., Norcross, GA, USA). The S1 and M2 genome segments were sequenced following the method described by Kibenge et al.

(2013). Reference sequences were obtained from the NCBI GenBank database, and phylogenetic analyses were conducted according to the procedures described by Kibenge et al. (2023), Godoy et al. (2021), and Vatne et al. (2021).

Results

Sequence analyses revealed the presence of different PRV genotypes in farmed Atlantic and coho salmon in Chile. The study defined the genetic and phylogenetic distribution of national strains and their relationship with isolates of European and American origin. No consistent association was found between the detected genotypes and the clinical status of the fish, although clustering patterns indicated considerable genetic variability among circulating strains.

Conclusion

These findings confirm the circulation of multiple PRV genotypes in farmed Atlantic and coho salmon in Chile, demonstrating viral genetic diversity. The lack of a clear link between genotype and clinical presentation suggests that other epidemiological and host-related factors may influence disease manifestation.

Palabras Clave

(1) Acuicultura, (2) salmónes, (3) virus, (4) HSMI, (5) PRV.

Financiamiento:

Spatial and functional genomics of PRV induced myocarditis in salmonids - Fondecyt de Iniciación en Investigación 2025 - N° 11251070

Virus endémicos en cultivo de salmónidos en Chile, CIBA_V_2025 - Centro de Investigaciones Biológicas Aplicadas (CIBA)

Agradecimientos:

Fondecyt de Iniciación en Investigación 2025 - N° 11251070.

Centro de Investigaciones Biológicas Aplicadas (CIBA).

Empresas productoras de salmónidos.