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February 16-19, 2026
Paris Las Vegas
Las Vegas, Nevada USA

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GENOMIC INSIGHTS INTO RESISTANCE TO PROLIFERATIVE KIDNEY DISEASE IN RAINBOW TROUT: THE RESILTROUT PROJECT

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Aquaculture is one of the fastest-growing food production sectors, playing a central role in the global economy. However, climate change is increasingly altering the quantity, quality, and seasonality of water resources, leading to significant shifts in aquatic ecosystems. These changes can induce physiological stress in fish, reducing their immune system and increasing susceptibility to infectious and parasitic diseases, which represent major constraints to aquaculture productivity and sustainability. Among these, Proliferative Kidney Disease (PKD), caused by *Tetracapsuloides bryosalmonae*, is one of the most serious parasitic diseases affecting salmonid aquaculture in Europe and North America. The disease causes high mortality rates in *Oncorhynchus mykiss* and is temperature-dependent, with outbreaks more frequent in farms using surface water. To date, no effective treatment or vaccine exists.

Within the RESILTROUT project, a Genome-Wide Association Study (GWAS) based on single nucleotide polymorphism (SNP) analysis was applied to identify genetic markers associated with resilience to PKD. During the first year, methodologies for phenotyping (using ddPCR for PKD detection) and genomic DNA extraction were optimized. Trout lines were exposed to natural PKD outbreaks, and symptomatology, mortality, and tissue samples were recorded. In the second year, both dead and surviving fish, as well as broodstock populations, were genotyped using the Axiom Trout 57K SNP array, followed by bioinformatic analysis for GWAS. A total of 1,000 rainbow trout from an autochthonous genetic line were naturally exposed in three raceway sectors. Dead fish were collected in spring–summer 2024, and survivors in winter 2024. PKD diagnosis was confirmed via end-point PCR and quantified by ddPCR, revealing infestation levels ranging from very low to very high, with most samples showing moderate to high pathogen loads. Sectoral prevalence ranged from 4% to 73%, with variable pathology and bacterial coinfections. GWAS included 200 PKD-positive cases and 200 controls, revealing two significant SNPs on chromosome 8 (73.22 Mbp and 38.44 Mbp). Functional annotation and pathway analyses are currently in progress. These results will inform selective breeding programs starting in late 2025.