# Abstract book of « Fish Physiology in support of Sustainable Aquaculture » Conference

The comprehensive understanding of fish physiology is essential for the advancement of a sustainable aquaculture. This discipline analyses the fundamental biological functions of farmed species, encompassing the respiratory, digestive, immune and reproductive systems, in addition to physiological responses to environmental stress.

Studying physiological parameters such as temperature tolerance, optimal salinity and dissolved oxygen requirements, helps to optimise rearing conditions, thereby reducing morbidity, mortality and economic losses. Moreover, the extensive knowledge of energy and nutrient metabolism is instrumental in formulating more efficient diets, adapted to the developmental stages of fish, while concurrently limiting nitrogen and phosphorus discharges into aquatic ecosystems.

Physiology also plays a pivotal role in the health management of fish farms. The analysis of immune mechanisms has enabled the development of prophylactic strategies as alternatives to antibiotic treatments, such as the use of probiotics, targeted vaccination or the genetic selection of individuals with better resistance to pathogens.

In the context of reproduction, the regulation of hormonal cycles and the factors that trigger reproduction in captivity is imperative to ensure the controlled production of fry, thereby minimising the need for fish to be captured from the wild and contributing to the preservation of biodiversity.

Finally, the assessment of physiological responses to stress, induced in particular by handling, rearing density or transport, can enhance animal welfare with direct impacts on growth, product quality and the sustainability of aquaculture systems.

In summary, integrating scientific knowledge/findings (pertaining to) on fish physiology into aquaculture practices can be regarded as a strategic lever for resolving the tensions between husbandry performance, environmental sustainability and animal ethics in contemporary aquaculture.

During this international conference “Fish Physiology in Support to a Sustainable Aquaculture” we will emphasise recent achievements as well as constraints of research conducted in the domain of fish physiology. The overarching goal is to enhance the conditions for aquaculture farming and to ensure the sustainable development of aquaculture. A significant number of the world's leading scientific experts will convene in Namur, Belgium, to share their knowledge and latest discoveries in the field, which has been steadily growing for several decades.

# T00-Fish Physiology in Support of Sustainable Aquaculture – introductory lecture

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Fish physiology investigates the integrated functioning of fish from molecular to behavioural levels, within the constraints of aquatic environments. It explains how fish maintain homeostasis—covering respiration, osmoregulation, metabolism, immunity, growth and reproduction—despite variability in temperature, salinity, oxygen and food availability. Importantly, there is no single “fish physiology”, as major groups exhibit distinct adaptive strategies. This diversity complicates the definition of optimal aquaculture conditions, particularly as most farmed species are teleosts with species-specific requirements. Over the past five decades, advances in fish physiology have been central to the development of sustainable aquaculture. Understanding physiological responses has enabled optimisation of environmental conditions, reducing mortality and improving growth performance. In parallel, progress in nutritional physiology has led to the formulation of efficient, stage-specific diets, improving feed conversion and reducing nitrogen and phosphorus emissions. The transition from fishmeal-based feeds to plant, microbial and novel protein sources reflects both physiological insights and sustainability constraints. Reproductive physiology has profoundly transformed aquaculture by enabling controlled breeding. Improved knowledge of environmental and hormonal regulation of gametogenesis has allowed year-round production and the use of hormonal induction protocols when necessary. Broodstock management, including nutrition and stress control, has enhanced gamete quality, while cryopreservation of sperm has facilitated genetic management. Techniques such as sex control and triploidy have further improved production efficiency and biosafety. Research in immunology, particularly since the 1990s, has led to major breakthroughs in disease control. The identification of innate and adaptive immune mechanisms has supported the development of vaccines and immunostimulants, drastically reducing antibiotic use. Emerging approaches now integrate microbiota interactions and molecular tools. The study of stress physiology and welfare has also become a key component of aquaculture. Biomarkers such as cortisol have enabled the quantification of stress responses, highlighting the detrimental effects of chronic stress on growth and immunity. This has driven improvements in farming practices and the development of welfare indicators combining physiological, behavioural and performance data. Future research will focus on integrative and predictive approaches, combining omics technologies, microbiome studies and artificial intelligence. These advances aim to enhance resilience, optimise resource use and support precision aquaculture, ultimately reducing environmental impacts while improving fish welfare and production efficiency.

# T01-Fish reproduction in mediterranean aquaculture and its control

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Development of aquaculture production for any species requires absolute control of reproductive function and the production of large numbers of good quality fertilized eggs for larval rearing. Reproduction of almost all fish species in aquaculture exhibit some form of dysfunction, ranging from (a) lack or incomplete gametogenesis (vitellogenesis and spermatogenesis), (b) failure of oocyte maturation and ovulation at the end of vitellogenesis, (c) reduced sperm volume and/or quality, and (d) failure of spawning after ovulation and spermiation.

In Mediterranean aquaculture, the major species of interest include the gilthead seabream (*Sparus aurata*), European seabass (*Dicentrarchus labrax*), meagre (*Argyrosomus regius*), Senegalese sole (*Solea senegalensis*), Japanese red seabream (*Pagrus major*), renamed as “short-finned porgy” for the European market, and recently greater amberjack (*Seriola dumerili*). All species have asynchronous ovarian development and produce small pelagic eggs.

Gilthead seabream spawn daily for 3-6 months and can be maintained throughout the year under constant temperatures (18-20°C), responding to photoperiod alone in maintaining their annual reproductive cyclicity. Similarly, meagre may maintain vitellogenesis and spermiation for many months past their natural season (April-June) by maintaining the water temperature constant at 19-20°C, but a winter drop in water temperature is necessary to restart the next gametogenic cycle. European seabass, on the other hand, require more strict thermal cycles for proper reproduction. Senegalese sole presents a very serious reproductive dysfunction, since hatchery-produced male breeders produce very small volumes of sperm and fail to express breeding behavior and spawning. As a result, the industry still relies on the use of wild-caught, captivity-acclimated breeders, while artificial insemination protocols have recently been implemented with some success.

Meagre and greater amberjack also do not spawn readily when maintained in tanks, but hormonal therapies using gonadotropin releasing hormone agonists (GnRHa) in the form of liquid injections of long-release implants, have been developed to induce tank spawning of eggs for commercial hatcheries. Similar hormonal methods have been used to control oocyte maturation, ovulation and spermiation in all Mediterranean species, in order to implement selective breeding programmes, especially those using in vitro fertilization.

A major issue in the reproduction of fish in aquaculture is the limited parental contribution of males during a particular day’s spawning. This results in only a limited number of families being produced and a gradual reduction in the genetic variability of the stock of each hatchery, as not all of the males contribute equally to the produced offspring. The small number of families produced is very important and is limiting the implementation of breeding selection programmes based on mass spawning protocols and communal rearing of the eggs and larvae.

The use of GnRHa-based hormonal therapies may be used to increase parentage contribution of a given stock by (a) synchronizing the maturation and spawning of more females at a given time and (b) increasing the number of males that contribute to the fertilization of larger numbers of eggs.

# T02-Transcriptomic Insights into the Onset and Maturation of the Circadian Clock in Eurasian Perch

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The circadian clock coordinates multiple aspects of physiology (Frøland Steindal and Whitmore, 2019), yet its developmental onset in fish remains poorly understood. Using high-resolution temporal sampling, we demonstrated that core circadian clock genes in Eurasian perch begin to oscillate at 3 days post-hatching (DPH) and exhibit robust rhythmicity by 28 DPH under a controlled photoperiod (14L:10D). These two developmental stages were therefore selected for transcriptomic profiling using 24-hour round-the-clock sampling to capture diel gene expression dynamics and identify molecular pathways involved in the emergence and consolidation of circadian regulation. Rhythmically expressed genes were identified using MetaCycle, clustered with TCseq, and further compared through Venn diagram and gene ontology analyses. This approach revealed both shared and stage-specific rhythmic transcripts, including several genes not previously described as circadian biomarkers in fish. Among these were, for example, *ciart* and *cipc*, which are known components of the negative regulatory arm of the circadian clock in other vertebrates but have not yet been characterized in fish. To further investigate candidate genes associated with early circadian development, we implemented two complementary validation strategies. First, a cross-species approach targeted genes previously reported in mammals or other model organisms but not in fish, including *ciart* and *cipc*, to assess their evolutionary conservation and functional relevance in teleost circadian systems. Second, we selected a set of ten putative novel circadian rhythm-associated genes identified from our transcriptomic dataset, representing candidates with no prior links to circadian regulation. Collectively, these findings expand current knowledge of the genetic architecture underlying early circadian development and lay the groundwork for further mechanistic exploration.

**References**

I. A. Frøland Steindal, D. Whitmore. Biology 8, 17 (2019).

# T03-Integrated proteomic and transcriptomic analysis reveals mechanism of *in vivo* post-ovulatory egg ageing in pikeperch

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Egg quality unpredictability remains a major bottleneck for reproductive efficiency in aquaculture. This study investigated the molecular mechanisms underlying in vivo post-ovulatory ageing, defined as prolonged retention of eggs within the ovaries after ovulation, in pikeperch (*Sander lucioperca*). Eggs were collected at 1 and 5 h post-ovulation (hPO) and analyzed using integrated proteomic and transcriptomic approaches to elucidate the underlying biological processes and identify early molecular markers of egg quality deterioration. Although eggs retained normal morphology up to 5 hPO, fertilization and hatching success were significantly reduced ($p < 0.01$). Quantitative TMT-LC–MS/MS proteomics identified four early ageing-responsive proteins (Gins4, Atrx, DnaJB14, Mrpl10; FDR < 0.05) linked to DNA replication, chromatin organization, protein folding, and mitochondrial function. Among the 202 post-ovulatory ageing-related altered transcript abundance between the two time points, 82 DETs were down-regulated while 120 were upregulated at 5 hPO. Gene ontology analysis revealed that post-ovulatory ageing influenced significant biological processes linked to cellular component organization and RNA metabolism, underscoring their importance in cellular functions and developmental processes of eggs. Several hub genes (*ago2, ep300, kmt2c*) were identified as potential key regulators of egg competence, and *ivns1abp* and *setdb1*emerged as promising candidate conserved markers of egg quality across species In summary, our results indicate that optimal egg collection time should not exceed 4 hPO to ensure high fertilization and hatching success. Early *in vivo* ageing alters the transcriptome but not proteome of pikeperch eggs. Contrary to the remarkably stable pikeperch egg proteome, the transcriptome is highly sensitive, revealing the molecular mechanisms underlying *in vivo* post-ovulatory ageing. The identified potential conserved candidates represent promising targets for the development of molecular assays capable of detecting subtle declines in egg quality before visible deterioration occurs.

# T04-Non-genetic inheritance factors as key drivers shaping progeny phenotype and intergenerational adaptability to aquaculture conditions

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Inheritance in fish is not limited to DNA sequence. During reproduction, parents transmit a broad spectrum of non-genetic information through gametes, including maternal mRNAs, proteins, lipids, metabolites, small non-coding RNAs, hormones, and epigenetic marks (Adrian-Kalchhauser *et al*. 2020). These factors can modulate early development, stress responsiveness, immune competence, metabolism, behavior, and ultimately the capacity of progeny to cope with aquaculture conditions. In externally fertilizing fish, where the egg and sperm represent the only direct parental contribution to the embryo, non-genetic inheritance may be particularly important as a mechanism linking parental environment, gamete quality, and offspring phenotype.

Current evidence indicates that maternal effects are often dominant during early development, largely through the molecular and nutritional cargo of the egg. However, paternal effects mediated by sperm-borne RNAs and epigenetic marks are increasingly recognized as important modulators of embryonic gene expression and offspring performance. Studies in commercially relevant species show that domestication, broodstock nutrition, thermal history, stress, gamete handling, and post-ovulatory aging can all reshape gamete molecular profiles and influence developmental trajectories. Our recent work in percid fishes further supports this concept, showing that both maternal and paternal contributions can affect offspring transcriptomes and phenotypes under controlled rearing conditions (Debernardis *et al*. 2026, Panda *et al*. 2026).

Understanding non-genetic inheritance offers a new perspective for fish biology. It may help explain variation in egg quality, larval robustness, adaptation to captivity, and broodstock-dependent differences that are not fully captured by classical genetics. In the longer term, integrating molecular indicators of gamete quality, parental conditioning, and epigenetic memory into breeding and husbandry programs may provide new tools to improve offspring performance, resilience, and sustainability of aquaculture production. This emerging field therefore represents both a fundamental biological challenge and a practical opportunity for next-generation aquaculture.

## References

I. Adrian-Kalchhauser *et al*. Trends Ecol Evol. 35, 1078-1089 (2020).
R. Debernardis *et al*. BMC Biol (in press) (2026).
A. Panda *et al*. BMC Genomics, 27:311 (2026).

# T05-Optimizing short-term storage of common carp sperm: impacts on motility, hatchability, and offspring epigenetics

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This study investigated the effects of short-term storage of common carp (*Cyprinus carpio* L.) sperm on fertilization and offspring performance. Carp sperm is routinely contaminated with urine. Storage of sperm without an extender results in a significant reduction in sperm motility and fertility within 24 hours, and sperm become immotile after 3 days of storage. In this study, sperm from mature males was collected, diluted 1:1 with carp extender (Cheng et al. 2025), and stored under aerobic conditions at 0–2 °C for up to 30 days, with or without antibiotics (Ma et al., unpublished). Prior to fertilization, samples were warmed to 20 °C for 2 hours (Zhang et al., 2023). Proper dilution, storage, and warming significantly improved fertilization success and hatchability (Zhang et al., 2023). Prolonged *in vitro* storage for 14 days significantly reduced sperm motility and fertilizing ability, which coincided with changes in DNA methylation patterns. Integrated analyses of offspring DNA methylomes, comparative transcriptomics, and cardiac performance measurements revealed storage-induced alterations in genes associated with nervous system development, myocardial morphogenesis, and cellular responses to stimuli (Cheng et al., 2025). The use of antibiotics did not result in detectable changes in global DNA methylation, either at the whole-genome or chromosome level, although effects on some specific genes were observed (Ma et al., unpublished). Overall, these findings provide practical guidance for optimizing sperm handling in carp aquaculture. Minimizing sperm storage duration is recommended when stored sperm is used in carp genetic programs. Flow cytometry was successfully used to separate viable and motile sperm from dead sperm in stored samples. Short-term *in vitro* storage of carp sperm was found to promote DNA methylation in genes associated with sperm motility (Ma et al., unpublished). Finally, the results of sperm separation also highlight a general concern associated with the ICSI technique, in which natural conception is bypassed by the manual injection of a single sperm into the egg, regardless of sperm quality. The inadvertent use of dead or dying sperm may contribute to epigenetic alterations and subsequent developmental defects.

## Funding information

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## References

Cheng Y. et al., BMC Biol. 23, 264, 2025
Zhang S. et al., Aquaculture, 565, 739126, 2023

# T06-Post-thaw storage of sperm as a tool towards revealing paternal-effect genes in Eurasian perch, *Perca fluviatilis*

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The influence of paternity on progeny quality, particularly during early developmental stages, has long been underappreciated. However, altered sperm phenotypes are increasingly recognized as effective tools for identifying paternal-effect-genes (PEGs), whose expression in the progeny is influenced by genetic or non-genetic factors carried by the sperm (Panda et al., 2024). We investigated the impact of post-thaw sperm storage (PTS) as a stressor to verify its effect on larval performance and to reveal PEGs in Eurasian perch (*Perca fluviatilis*) progeny. *In vitro* fertilizations were performed using cryopreserved sperm that was either used immediately after thawing (0 min; CON) or after 30 min of post-thaw storage at 4°C. Despite a marked decline in sperm motility during PTS, fertilization success remained unaffected, allowing the use of PTS to study its effect on progeny phenotype. Notably, larvae from the PTS group exhibited significantly higher mortality starting from 9 days post-hatch, indicating strong paternal influences on early larval viability. Transcriptomic profiling of larvae at the mouth-opening stage, identified 41 differentially expressed genes (DEGs), many linked to immune regulatory pathways. This suggests that paternal inputs may shape larval immune function, potentially contributing to observed mortality differences. Among the DEGs, several genes, *mfap4*, *gimap*, *hlag*, *pigr*, *neo1* and *pde6g*, emerged as strong candidate PEGs. Along with the transcriptomic data we also show the interplay between paternal effects and maternal modulation of gene expression which highlights the inherent complexity of parental contributions to developmental regulation. We show that even a brief, 30-minute PTS not only reduces sperm motility but also imprints lasting effects on progeny performance and survival. By selectively shaping the pool of functional sperm, PTS acts as an additional layer of selection, enriching for cells with specific traits and offering a powerful, controlled system for studying non-genetic inheritance factors and identifying PEGs in fish. Transcriptomic analysis uncovered a deeper dimension to this process, revealing that maternal identity can amplify or buffer paternal contributions which serves as evidence of a complex parental interplay that influences early development.

## References

Panda *et al.*, Sci. Rep. **14:6396**, 1 (2024).

# T07-The pikeperch (*Sander lucioperca*) mRNAome: from multi-tissue atlas to reproductive axis specificity

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Despite the growing importance of pikeperch (Sander lucioperca) in European recirculating aquaculture systems (RAS), limited genomic resources hinder the development of physiologically relevant reproductive biomarkers. To address this, we characterized the adult pikeperch mRNA transcriptome, establishing a high-resolution, tissue-specific expression atlas focusing on the reproductive axis (brain, pituitary, gonads, liver). RNA was extracted from 13 adult tissues using sex-balanced sequencing pools (three males/females for somatic tissues; six males/females for gonads). Mapping to the reference genome identified 32,987 mRNAs, with 26,166 demonstrating robust expression (>1 TPM). Principal Component Analysis and hierarchical clustering of the top 500 mRNAs confirmed massive global variance primarily driven by tissue origin. Applying a stringent tissue-specificity threshold (Tau ≥ 0.9) to the reproductive axis revealed distinct transcriptional specializations: the brain exhibited the most specific transcripts (2,315), followed by female gonads (1,419), male gonads (762), liver (539), and pituitary (418). Functional enrichment (ShinyGO) confirmed these cohorts govern distinct, organ-appropriate roles. Brain and pituitary markers were enriched for central regulatory networks, specifically anterograde trans-synaptic signaling (FDR < 3.1E-21) and dopaminergic transmission (FDR < 5.2E-04). Liver transcripts were dominated by aromatic amino acid catabolism (FDR < 2.8E-08) and coagulation processes (FDR < 5.9E-11). Gonadal profiles highlighted gametogenesis, including female mitotic/DNA replication cycles and male meiotic/synaptonemal complex assembly. Analysis of the highest-expressing specific mRNAs confirmed extreme expression of hepatic apolipoproteins (apoa1b, apoc1, apoa2) and fgb, brain epd and tfa, and pituitary reproductive hormones (gh1, smtla, cga, prl, lhb). Gonadal profiles featured specialized recognition transcripts: galactose-specific lectin nattectin-like (LOC116034121) in females and myelin-associated glycoprotein-like (LOC116049328) in males. This first comprehensive, tissue-resolved transcriptomic atlas of the pikeperch reproductive axis identifies a suite of highly specific candidate molecular markers, offering a foundation to develop biomarker-based tools for monitoring reproductive status in aquaculture.

# T08-Integrative egg quality assessment in European plaice (*Pleuronectes platessa*): linking morphological and molecular markers

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Egg quality is a critical determinant of reproductive success in aquaculture, yet the molecular mechanisms underlying its decline in captive-reared broodstock remain poorly understood. Using an integrative approach combining morphological and molecular markers, we assessed egg quality in wild-captured and farmed European plaice (*Pleuronectes platessa*), an emerging aquaculture species, to investigate how captive rearing affects reproductive output. Egg quality was assessed using fertilization rate and embryonic survival prior to hatching (16 days post-fertilisation). Seven candidate genes previously identified as candidate egg quality markers in Atlantic halibut (Yilmaz et al., 2022), with developmental, cellular, and mitochondrial functions (*ghitm, cyc1, atp5f1b, sod1, ppid, uqcrb, uqcrfs1b*), were used to assess their cross-species transferability and the influence of captive rearing on egg quality-associated gene expression in European plaice.

Farmed fish showed markedly lower embryonic survival compared to wild-captured individuals (median 27% vs 69%, $p<0.0001$, rank-biserial $r=0.766$), despite comparable fertilization rates (median 79% vs 84%, $p=0.314$), indicating that captive rearing specifically compromises embryonic developmental competence rather than the fertilization process itself. Good quality (GQ) eggs showed significantly higher fertilization rates than poor quality (BQ) eggs (91% vs 77%, $p=0.0003$, rank-biserial $r=0.517$), and embryonic survival (70% vs 24%, $p=0$, rank-biserial $r=1.0$) was completely separated between quality groups, validating the quality classification. Fertilization rate and embryonic survival were moderately but significantly correlated (Spearman $\rho=0.572$, $p<0.0001$), suggesting they capture partially independent dimensions of egg quality. Six of the seven candidate markers were significantly differentially expressed between GQ and BQ eggs, consistent with previous findings in Atlantic halibut, and the same six genes differed significantly between wild and farmed broodstock, with farmed eggs mirroring the BQ transcriptional profile; *uqcrb* alone showed no significant quality effect. These six markers were significantly negatively correlated with both fertilization rate and embryonic survival, with survival showing consistently stronger associations (rho range: -0.309 to -0.587) than fertilization (rho range: -0.253 to -0.410), highlighting their utility as predictive markers of embryonic developmental competence. Together, these findings suggest that mitochondrial dysfunction and oxidative stress are conserved mechanisms underlying poor egg quality across flatfish species, provide novel molecular insights into how domestication compromises reproductive success in plaice, and establish a transferable marker panel with practical utility for egg quality assessment in flatfish aquaculture.

**References**

O. Yilmaz et al., BMC Genomics 23(1), 635 (2022).

# T09-Why do larvae hatch when they do? An extended analysis and first physical modelling approaches.

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Hatching, the moment an individual leaves its egg envelope, is considered by many specialists as a key moment in a fish life cycle and a clear boundary between the embryonic and larval period. It occurs at different developmental moments in different species (Lecointre et al., 2020). For instance, the mouth and jaws are not formed at hatching for certain species, while for others, the alimentary tract is nearly functional; the same being true for eyes, fins or fin rays among others. Therefore, no "developmental milestones" are reached prior to hatching, nor embryos are "fully developed for survival outside the egg capsule" (Teletchea and Lecointre, 2026). In conclusion, individuals do not hatch when there are "ready" but rather when a signal triggers or forces them to do so.

In 2024, Teletchea and Pauly proposed that larvae hatch when they do to avoid asphyxia, i.e., when the diffusion of oxygen through the egg envelope is no longer sufficient to cope with the physiological needs of the developing embryos. In proof-of-concept study tested the hypothesis that fish larvae hatch when a specific ratio between egg surface area (ESA) and larval surface area (LSA) is reached, irrespective of egg diameter and abiotic factors. A mean ratio of 1: 1.52 (CI=1.39–1.63) was established between the ESA of 33 species of teleosts, with diameters ranging from 0.63 to 5.7 mm, and the LSA of their newly hatch larvae. Beyond this ratio, the oxygen supply through the egg surface cannot cope with the oxygen requirements of the embryo, i.e., larvae must hatch or die due to asphyxia.

Here, we first tested this hypothesis with a larger dataset (ca. 100 species, with a wider range of egg diameters), then we developed a physical framework which accounts for the growth of embryos and oxygen diffusion to determine how asphyxia evolves during embryogenesis. These new results will be presented and discussed at the congress.

## References

Lecointre G, Schnell N, Teletchea F. Sci. Rep. **10**, Article number: 19732 (2020)
Teletchea F, Lecointre G. What is a mature larva? Cybium **50**, 5 (2026)
Teletchea F, Pauly D. Environ. Biol. Fishes **107**, 583 (2024)

# T10-Essential Fatty Acids in Aquaculture Hatcheries: Implications for Reproduction, Larval Development, and Sustainable Omega-3 Production

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Successful control of spawning and the development of selective breeding programs have significantly advanced aquaculture production. However, the effectiveness of these strategies depends heavily on broodstock nutrition, which remains a critical determinant of reproductive performance, egg quality, larval viability, and overall production success. Among dietary nutrients, essential fatty acids (EFAs), particularly the long-chain polyunsaturated fatty acids (LCPUFAs) docosahexaenoic acid (DHA), eicosapentaenoic acid (EPA), and arachidonic acid (ARA), play a central role during fish reproduction and early larval development.

Lipids in broodstock and larvae serve multiple physiological functions, including providing metabolic energy, forming structural components of cellular membrane phospholipids, and acting as precursors of bioactive molecules. DHA is especially important as a structural component of cell membranes, supporting membrane integrity and facilitating key cellular processes, while ARA serves as a major precursor for eicosanoids involved in physiological regulation. Together, DHA, EPA, and ARA influence membrane structure and function, promote growth and larval development, improve survival rates, regulate immune responses, modulate gene expression, enhance stress resistance, and support the development and function of neural, sensory, and skeletal tissues. Research has further demonstrated that adequate EFA nutrition can improve behavioral and physiological performance, including enhanced neuronal activity and increased burst swimming capacity in fish larvae.

Beyond their importance in fish health, omega-3 fatty acids are essential nutrients for human nutrition. Aquaculture has become a major contributor to global omega-3 production, increasing the supply of long-chain omega-3 fatty acids from aquatic products by approximately 70%. Despite this contribution, a substantial annual deficit of nearly 500,000 tons of these nutrients remains worldwide. At the same time, the continued expansion of aquaculture may be constrained by the requirement for dietary omega-3 fatty acids in farmed fish feeds.

To overcome these challenges, several innovative strategies have emerged. These include the production of omega-3 fatty acids from microalgae and other microorganisms, the recovery of valuable lipids from fisheries and aquaculture byproducts within circular economy frameworks, selective breeding for fish with enhanced endogenous omega-3 biosynthetic capacity, and nutritional programming approaches designed to increase the synthesis of long-chain omega-3 fatty acids. Collectively, these advances offer promising pathways to improve broodstock performance, enhance aquaculture sustainability, and contribute to meeting the growing global demand for omega-3 fatty acids.

# T11-Growth and physiological responses of rainbow trout (*Oncorhynchus mykiss*) to dietary replacement of soy protein concentrate with brewer's spent grain protein isolate

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Brewer's spent grain (BSG) is the major by-product of the brewing industry, and its valorization as a protein isolate (PI) for aquafeeds can reduce reliance on soy proteins and contribute to sustainability (Karlsen & Skov, 2022). To investigate the potential of BSG PI, a 60-day feeding trial was conducted in rainbow trout (Initial body weight: 62.5 ± 0.2 g) by replacing graded levels of soy protein concentrate (SPC) (0, 15, 25, 50 and 100%) with BSG PI in the diet. All diets were formulated to be isonitrogenous (47%) and isolipidic (24%). Fish were randomly distributed into 25 tanks (n = 5) at a density of 40 fish/tank. At the end of the trial, growth performance and feed utilization were significantly affected only at 100% replacement. Orthogonal polynomial contrasts indicated a negative linear trend for weight gain and a positive linear trend for feed conversion ratio with increasing replacement level (Figure 1). Viscerosomatic index increased at 50% and 100% replacement, while hepatosomatic index increased only at 100%; perivisceral fat index remained unaffected. Among digestive enzymes, amylase activity increased at 100%, showing positive linear trend. Whereas no differences were observed in liver oxidative stress markers and hematological parameters. Among serum biochemical parameters, only AST differed significantly, being higher at 25% replacement compared to 15% and 50%. Overall, growth and physiological parameters were relatively unaffected up to 50% replacement (70 g SPC/kg of diet), highlighting the potential of BSG PI as a sustainable alternative to soy protein in rainbow trout diets.

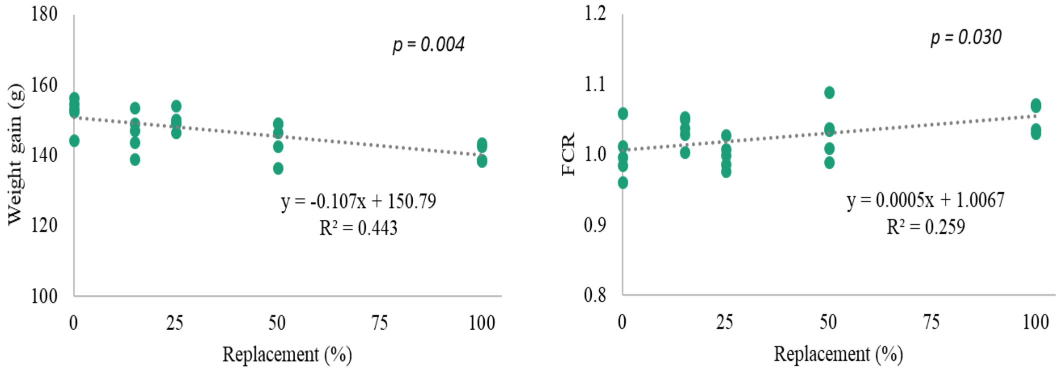

Figure 1. Mean individual weight gain and feed conversion ratio (FCR) of rainbow trout fed diets with graded replacement levels of soy protein concentrate by brewer's spent grain protein isolate

## References

F. Karlsen *et al.*, J. Clean. Prod. **357**, 131986 (2022).

# T12-Feeding Regime Effects on Growth Performance and Feed Utilization in in Grow-Out Stage Pangasius Catfish *(Pangasianodon hypophthalmus)*

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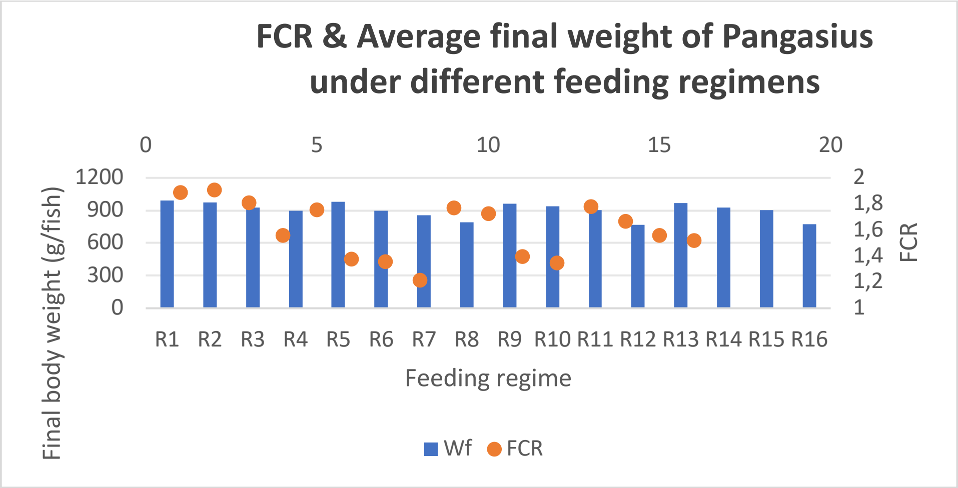
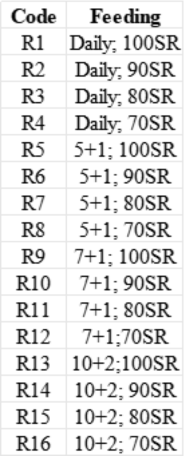
Vietnam is currently the largest global producer of pangasius, contributing significantly to international fish supply chains. Live feed regime improves growth performance and survival rate for early life sages of Pangasius ( Vu, N.U & Huynh T.G., 2020)**.** This study investigated the effects of feeding–fasting regimes and ration levels on survival rate, growth performance, and feed utilization efficiency of pangasius catfish (*Pangasianodon hypophthalmus*). Four experimental feeding–fasting regimes included: continuous feeding (daily feeding), feeding for 5 consecutive days followed by 1 day of fasting (5+1), feeding for 7 consecutive days followed by 1 day of fasting (7+1), and feeding for 10 consecutive days followed by 2 days of fasting (10+2). Within each feeding regime, ration levels were tested at 100% of satiation requirement (100% SR), 90% SR, 80% SR, and 70% SR. Fish with an initial body weight of 20±0,1 g per individual were cultured in 48 hapas of 6 m² at a stocking density of 50 fish/m² over a period of 6 months.





| Code | Feeding |
|---|---|
| R1 | Daily; 100SR |
| R2 | Daily; 90SR |
| R3 | Daily; 80SR |
| R4 | Daily; 70SR |
| R5 | 5+1; 100SR |
| R6 | 5+1; 90SR |
| R7 | 5+1; 80SR |
| R8 | 5+1; 70SR |
| R9 | 7+1; 100SR |
| R10 | 7+1; 90SR |
| R11 | 7+1; 80SR |
| R12 | 7+1;70SR |
| R13 | 10+2;100SR |
| R14 | 10+2; 90SR |
| R15 | 10+2; 80SR |
| R16 | 10+2; 70SR |

The results indicated that neither feeding regime nor ration level significantly affected survival rate; however, both factors had pronounced effects on growth performance and feed utilization. Fish fed to apparent satiation (100% SR) exhibited higher feed conversion ratios (FCR), whereas reducing the ration level improved FCR but resulted in slower growth rates.

In commercial pangasius farming, the optimal harvest size is around 900 g fish$^{-1}$. The feeding regime of 7 days feeding followed by 1 day fasting (7+1), combined with a ration level of 80% of satiation requirement (R11), yielded the most favorable results, with a low FCR (1.4) and an average harvest weight of approximately 900g fish$^{-1}$. Further studies are needed on the physiological capacity of striped catfish to adapt to intermittent feeding regimes and moderate feed restriction.

## References

Ut V.N. *et al.*, Fishes 2020, 5, 20; doi:10.3390/fishes5030020

# T13-Growth and Physiological Responses of Rainbow Trout (*Oncorhynchus mykiss*) to Alternative Feed Ingredients Derived from *Agaricus bisporus* and *Pleurotus ostreatus* Stem By-Products

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The diversification of aquafeed formulations by incorporating novel ingredients with reduced environmental impact and improved compatibility with circular economy approaches is among the strategies for the sustainable development of aquaculture. In this context, the valorization of mushroom industry by-products, estimated at 60 Mt annually worldwide and often discarded through composting, landfilling, or incineration, represents a promising strategy. This study evaluated mushroom stem meals derived from *Agaricus bisporus* (AB) and *Pleurotus ostreatus* (PO) by-products, as lower-impact alternatives to soybean meal (SBM) in rainbow trout (BWi: 22.1 ± 0.3 g) diets. Five isoproteic (47%) and isolipidic (23%) diets were tested: a control diet (CTRL), containing 12% SBM and four diets replacing 25%–50% of SBM with AB or PO meals (AB25, AB50, PO25, PO50). Fish fed AB diets, particularly AB25 showed growth performance, feed intake, and nutrient retention comparable to the CTRL group ($p > 0.05$), whereas PO diets reduced growth and increased feed conversion ratio ($p < 0.05$) (Figure 1). Histological analysis revealed normal gut morphology in fish fed the AB diets, while PO-fed fish exhibited villus shortening, lamina propria expansion, and leukocyte infiltration, indicating impaired gut integrity. Gene expression analyses supported these findings in which AB diets induced minimal transcriptional changes, consistent with maintained gut homeostasis, whereas PO diets resulted in downregulation of genes involved in immune function (*cathepsin s*, *cd4*, *cd8*, *tnf-α*, *myd88*, *mhc ii*, *il-10*), stress response (*hsp70*, *hsp27*), apoptosis (*caspase-3*, *tgf-β*), and barrier integrity/permeability (*aqp7*, *muc2*), alongside upregulation of nutrient transporters (*glut2*, *pept1a*, *cd36*) and oxidative stress markers (*cat*), indicative of impaired immune competence and compensatory physiological responses. Overall, AB by-products, particularly at 25% SBM replacement maintained growth, gut health and physiological balance, while PO inclusion impaired growth, gut integrity and immune competence. These results demonstrate differential effects of mushroom by-products, identifying AB as a viable alternative to SBM in rainbow trout diets.

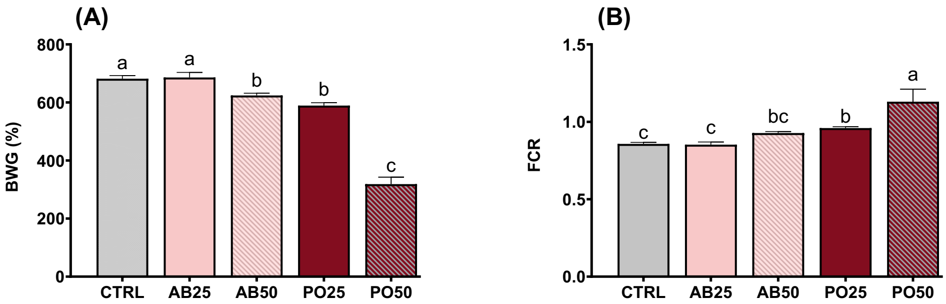

Figure 1. (A) Growth (% body weight gain, BWG) and (B) feed conversion ratio (FCR) in rainbow trout fed experimental diets replacing SBM with mushroom stem meals from AB and PO for 60 days.

# T14-Prospects of using live feed substitutes in early larval fish nutrition: Current status and remaining challenges

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The replacement of live feeds with formulated inert micro-diets or live-feed substitutes during the earliest larval stages of fishes remains a central objective of nutrition research in aquaculture. Across diverse taxa, complete replacement from first feeding has proven challenging and full replacement is not universally achieved[1] Early digestive capacity and ontogeny constrain the timing and effectiveness of substitution strategies. If the micro-diet is not aligned with larval digestive maturity early weaning can depress growth; alter digestive enzyme ontogeny with long term physiological consequences. Outcomes and performance gains are dependent on species, species ontogeny, diet design, co-feeding strategies, and rearing conditions and live-feed substitutes in early larval fish nutrition show substantial promise to reduce dependence on live prey[2], yet robust, species-specific protocols are essential. The most successful implementations share core elements: (a) staged co-feeding to ease physiological transitions, (b) microdiet designs that closely simulate the peptide/protein and lipid profiles of live prey, (c) incorporation of essential lipids (DHA/EPA/ARA), phospholipids, and carefully matched phospholipid levels, and (d) manufacturing precision to yield palatable, stable, and digestible microparticles. In the presentation I will synthesize evidence on the prospects and limitations of live-feed substitutes for early larval nutrition, emphasizing physiological constraints; mechanisms, technological approaches, and practical implications, with references to cited literature and own experimental studies. Future research should advance: (a) standardized digestion-and-absorption markers to compare across species and diets, (b) systematic exploration of peptide-size distributions and their interaction with larval proteolytic ontogeny, (c) refinement of lipid profiles with emphasis on DHA/EPA/ARA and their ratios, and (d) scaling pilot inert-diet weaning protocols under commercial hatchery constraints to assess economic viability.

## References

[1] Hamre, K., *et* al. (2013). Fish larval nutrition and feed formulation: knowledge gaps and bottlenecks for advances in larval rearing. *Reviews in Aquaculture*, *5*(s1). https://doi.org/10.1111/j.1753-5131.2012.01086.x

[2] Pedro, J., *et al* (2025). Early nutrition impacts on growth, skeletal anomalies and organ ontogeny in larval Atlantic Cod (*Gadus morhua*)," Animals, 2025, doi: 10.3390/ani15202985

# T15-Impact of growth trajectory on muscle cellularity in juvenile rainbow trout (*Oncorhynchus mykiss*)

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Post-larval muscle growth in rainbow trout (*Oncorhynchus mykiss*) involves hyperplasia (the formation of new muscle fibers) and hypertrophy (an increase in the fiber size of existing fibers). These mechanisms depend on the recruitment and activation of muscle stem cells (MuSCs), located beneath the muscle fiber basal lamina, which proliferate and differentiate to increase muscle mass. Although it is well known that periods of growth arrest strongly alter muscle cellularity, it remains unknown whether transient changes in growth rate have lasting effects on muscle cellularity.

To address this question, four groups of juvenile rainbow trout (initial weight: 8.3 ± 1.7 g) were subjected to contrasting feeding regimes for 6 months: (i) continuous growth (CG, 80% of an ad libitum ration), (ii) early high growth (EG, ad libitum ration followed by 20%), (iii) late high growth (LG, 20% followed by an ad libitum ration), and (iv) discontinuous growth (DG, ad libitum ration with one week of fasting every four weeks). Finally, all groups were then fed a similar ration (80% of an ad libitum ration) for 3 weeks to standardize growth. At the end of the experiment, the four groups reached a similar average weight (280 g ± 56 g for all groups combined), corresponding to the pan-size commercial stage, thereby enabling an unbiased comparison independent of body mass.

Histological analysis of muscle tissue showed that the LG group had a markedly slower increase in total fiber number compared to the CG group (26 171 vs. 40 307 at week 7; $p < 0.001$). The EG and DG groups had total fiber numbers similar to the CG group. Over the same period, the mean fiber size of the EG and DG groups were similar to that of the CG group (44.5 ± 2.1 µm and 42.9 ± 1.8 µm respectively vs. 45.4 ± 3.9 µm; $p>0.05$), while the LG group displayed smaller muscle fibers than the CG group (38.1 ± 1.9 µm vs. 45.4 ± 3.9 µm; $p < 0.001$).

At the end of the experiment, no significant differences in total muscle fiber number were observed among the groups. However, the DG group exhibited a lower mean fiber size than the CG group (50.4 ± 3.6 µm vs. 54.7 ± 2.9 µm; $p < 0.05$). The EG and LG groups did not differ from the CG group in terms of mean fiber size (52.5 ± 3.8 µm and 53.5 ± 3.3 µm, respectively; $p>0.05$). Nevertheless, analysis of fiber size distribution revealed a significant increase in the proportion of small fibers (<20 µm) in the EG group compared with the CG group.

Overall, these results suggest that post-larval growth trajectory leaves a lasting imprint on fiber size distribution but not on the total number of fibers, which appears to be more dependent on fish weight.

# T16- Skeletal Deformities in Fish: The Holy Grail of the Aquaculture Industry

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Skeletal deformities represent one of the widespread biological challenges in intensive fish farming, affecting a wide range of cultured species and production systems. These abnormalities, which include vertebral deformities and curvatures, craniofacial malformations, and fin anomalies, can significantly compromise fish growth performance, feed utilization, survival, and fish welfare, while they can also affect product quality, ultimately leading to substantial economic losses for the aquaculture industry and undermining the public perception and overall image of the sector.

The etiology of skeletal deformities is multifactorial, reflecting complex interactions between genetic, nutritional, environmental, and management factors. Genetic predisposition and inbreeding may increase susceptibility, while nutritional imbalances, particularly deficiencies or excesses of minerals, vitamins, and essential fatty acids among other nutrients, have been closely linked to abnormal skeletogenesis during early developmental stages (Boglione et al., 2013). In parallel, suboptimal rearing conditions such as excessive stocking density, inappropriate water temperature, poor water quality, and mechanical stress can disrupt normal skeletal development and exacerbate deformity prevalence. Emerging evidence also highlights the role of early ontogenetic windows, where disturbances during embryonic and larval stages have long-lasting effects on skeletal integrity.

Beyond their biological causes, skeletal deformities raise increasing concerns regarding animal welfare and sustainability. Deformed fish often exhibit impaired swimming ability, altered feeding behavior, and increased susceptibility to secondary stressors. From an industry perspective, deformities increase hatchery production costs, decrease feed efficiency, reduce fillet yield, processing efficiency, and market acceptance (Chandra et al., 2024).

This presentation synthesizes current knowledge on the main causes and consequences of skeletal deformities in farmed fish, emphasizing the need for integrated preventive strategies. Improved broodstock management, optimized nutrition, and refined rearing practices are discussed as key approaches to reduce deformity incidence and promote both ethical and sustainable aquaculture production goals.

## References

C. Boglione *et al*., Skeletal anomalies in reared E uropean fish larvae and juveniles. Part 2: main typologies, occurrences and causative factors. Rev. Aquac. **5**, S121-S167 (2013).

G. Chandra *et al*., Deformities in fish: A barrier for responsible aquaculture and sustainable fisheries. Rev. Aquac. **16**, 872-891 (2024).

# T17-Effects of dietary protein sources and pigment supplementation on growth performance and fillet quality in Rainbow Trout

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Two feeding trials were conducted to evaluate the effects of dietary composition on growth performance and fillet quality in rainbow trout (Oncorhynchus mykiss). In the first trial, different compositions of dietary protein sources were tested to assess their impact on biomass gain. The results demonstrated significant differences among protein compositions, indicating that both protein origin and dosage play an important role in optimizing production efficiency.

In the second trial, pigment-containing supplements, including astaxanthin, were evaluated for their effects on fillet coloration and color stability over time. Fillet color was measured following the feeding period, as well as during subsequent depuration period to assess pigment retention and color degradation. The trial revealed clear effects of dietary pigmentation on both initial color intensity and long-term color stability, highlighting the importance of targeted pigmentation strategies to improve visual quality.

Together, these results underline the importance of diet formulation in aquaculture, demonstrating that both protein source selection and pigmentation strategies can be used to optimize production performance and final product quality in trout.

# T18-PLANT-BASED ADDITIVES IN TILAPIA AQUACULTURE: APPLICATIONS, CHALLENGES, AND EMERGING OPPORTUNITIES

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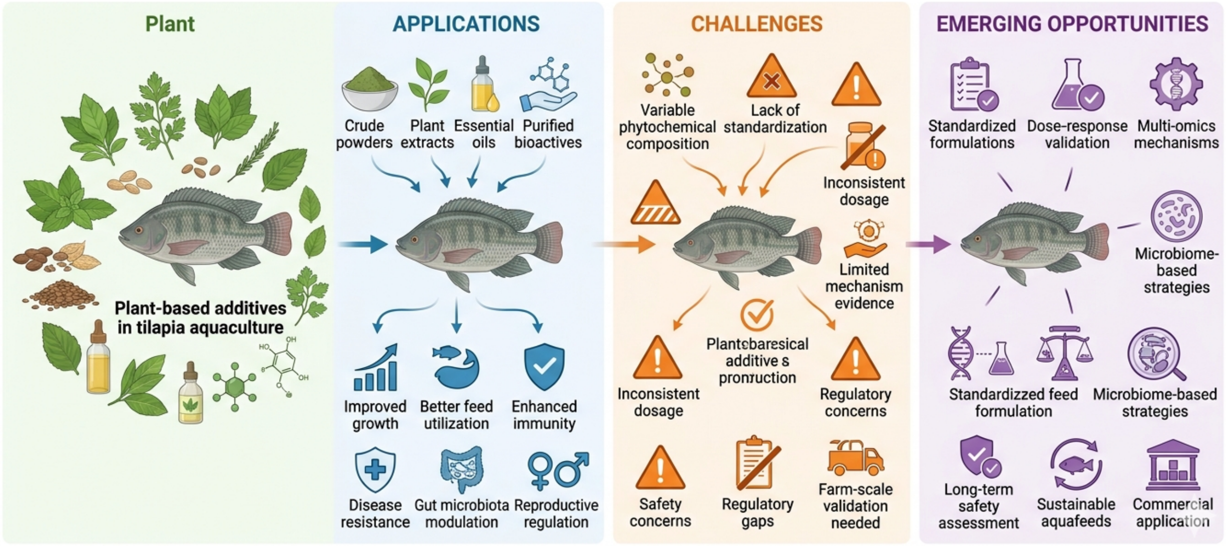
Plant-based additives are receiving increasing attention in tilapia aquaculture as natural and sustainable alternatives to synthetic growth promoters, antibiotics, and chemotherapeutic agents. This review summarizes current knowledge on the use of plant-derived products, including crude powders, extracts, essential oils, and purified bioactive compounds, in tilapia culture. Available studies indicate that plant-based additives can improve growth performance, feed utilization, immune responses, antioxidant capacity, disease resistance, and, in some cases, reproductive performance. These beneficial effects are mainly associated with bioactive compounds such as phenolics, flavonoids, terpenoids, saponins, alkaloids, and essential oils, which may support digestion, modulate gut microbiota, enhance innate immunity, reduce oxidative stress, and inhibit pathogenic microorganisms. However, the practical application of plant-based additives remains limited by variation in plant composition, differences in processing and extraction methods, inconsistent dosage recommendations, and insufficient long-term safety data. Therefore, further studies are needed to standardize preparation methods, identify effective inclusion levels, clarify mechanisms of action, and evaluate their performance under farm conditions. Overall, plant-based additives represent a promising strategy to improve productivity, fish health, and sustainability in tilapia aquaculture.

**Keywords:** Tilapia; plant-based additives; phytogenics; immunity; antioxidant capacity; sustainable aquaculture.



**References**
E. Okon et al., Fishes 10, 471 (2025).
B.A. Pudota et al., The Microbe 8, 100496 (2025).
A.A. Abou Zaid et al., Pathogens 14, 378 (2025).

# T19-How Diet, Genotype, and Environment Shape Fish Microbiota Toward Sustainable Aquaculture

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The rapid expansion of aquaculture has intensified the need for sustainable practices that optimize fish health, productivity, and environmental impact. Central to these goals is the fish microbiota, a dynamic community of microorganisms inhabiting the gastrointestinal tract, skin, and gills. This microbiota plays a crucial role in nutrient absorption, immune function, disease resistance, and overall host performance. Increasing evidence indicates that three major factors—diet, host genotype, and environment—interact in complex ways to shape microbial composition and functionality, ultimately influencing fish health and aquaculture performance.

Diet is one of the most immediate and modifiable drivers of fish microbiota. Feed composition, including protein sources, lipids, carbohydrates, and functional additives such as probiotics and prebiotics, directly alters microbial diversity and metabolic activity. The transition from traditional fishmeal-based diets to plant- or insect-based alternatives revealed significant shifts in gut microbial communities, with potential consequences for digestive efficiency and immune responses. Strategic dietary formulations can therefore promote beneficial microbes while suppressing opportunistic pathogens.

Host genotype also exerts a selective pressure on microbiota assembly. Genetic differences among fish species—and even among strains within a species—influence gut morphology, immune regulation, and host metabolic pathways, all of which influence microbial colonization. Selective breeding programs that consider host–microbiome interactions offer promising opportunities to enhance disease resilience and feed conversion efficiency, though this area remains underexplored.

Environmental conditions, including water quality, temperature, salinity, and microbial load in rearing systems, further modulate microbiota composition. Intensive aquaculture systems, such as recirculating aquaculture systems (RAS), can stabilize environmental conditions but may also reduce microbial diversity if not properly managed. Conversely, open systems expose fish to a broader range of environmental microbes, increasing microbial complexity as well as the risk of pathogen exposure.

Understanding the interplay among diet, genotype, and environment is essential for developing microbiome-informed aquaculture strategies. Integrative approaches combining nutrition, host genetics, and aquaculture system management may promote a more stable and beneficial microbiota enhancing fish health while reducing antibiotic dependence and minimizing environmental impact. Ultimately, leveraging microbial ecology may represent one of the most promising strategies for improving fish welfare, production efficiency, and environmental sustainability in modern aquaculture.

# T20-Diet, Genotype, and Environment as Drivers of Fish Microbiota: Implications for Sustainable Aquaculture.

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This study is part of a larger project that aims to improve the nutritional properties of freshwater and marine fish by the use of fortified feeds. The final aim is to deliver fish products with optimal nutritional value that fully meet consumer expectations. Within this framework, the present study investigated the effects of algal oil-enriched feeds on the physiology and health of gilthead sea bream (*Sparus aurata*). Key evaluation parameters included growth performance, fatty acid profiles in the fillets, gut microbiota composition and intestinal short-chain fatty acid (SCFA) profile.

The experiment was conducted over 15 weeks using 360 gilthead sea bream distributed across nine tanks (three tanks per feeding group) and fed a control diet or two algal oil–supplemented diets at different inclusion levels. At the end of the feeding trial, samples were collected to analyze the composition and functionality of the gut microbiota using high-throughput sequencing techniques previously described in publications by our group (Terova et al., 2021; Hasan et al., 2024; Rimoldi et al., 2025). In addition, gas chromatography was used in conjunction with mass spectrometry to SCFAs in the intestinal lumen and to evaluate the fatty acid profile of the fillets.

The inclusion of algal oil in the experimental diet led to an enrichment of omega-3 fatty acids, especially eicosapentaenoic acid (EPA) and docosahexaenoic acid (DHA), in the fillets of sea bream. Consistent with this increase, the ratio of omega-3 to omega-6 PUFAs was higher in the sea bream fillets fed the experimental diets. Overall, the fatty acid profile in the fillets matched that of the diets, which we have previously observed in a similar study (Terova et al., 2021). While the lipid composition differed, the lipid content of the fillets remained similar in the different feeding groups.

The addition of algal oil to feeds modulated the gut microbiota composition. A differential effect of the inclusion level was observed, where a higher dietary algal oil inclusion led to a decrease in the abundance of several genera within the lactic acid bacteria group. Interestingly, the concentration of butyrate and propionate in the intestinal lumen of the fish belonging to the experimental feeding groups was lower than in the fish of the control group.

This study demonstrates the importance of feed used in fish farming, extending beyond fish growth performance and health to include the nutritional quality of farmed fish for human consumption. We observed a potential trade-off between the increased omega-3 PUFA content in fillets at higher algal oil inclusion levels and shifts in microbiota status. These results provide a basis for the next phases of the I-FISH project, where different additives will be included in fish feed to improve the nutritional value of the final product, i.e., the fish fillet. Understanding how different nutritional strategies affect gut microbiota, metabolic outcomes and fillet composition is essential for the development of more sustainable and nutritionally valuable aquaculture products.

**References**

G. Terova et al., Front. Mar. Sci. **8**, 715078 (2021).
I. Hasan et al., BMC Vet. Res. **20**, 472 (2024).
S. Rimoldi et al., Aquaculture **596**, 741813 (2025).

# T21-Characterization of novel histone post-translational modifications linking, *via* the microbiota, the impact of the nutritional environment to phenotypes expressed in an agronomic model: towards an open door to new biomarkers of metabolic diseases?

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Carnivorous farmed fish such as rainbow trout are traditionnally fed with fishmeal and fish oil- based diet derived from wild marine sources. To improve sustainability,eco-friendly alternatives enriched in digestible carbohydrates are being explored. However, carnivorous fish exhibit a limited capacity to utilize dietary carbohydrates, leading to metabolic disorders that are not yet fully understood. (Polakof and Panserat, 2016). This study aims to investigate the early establishment kinetics of gut microbiota and epigenetic regulation associated with carbohydrate utilization in juvenile rainbow trout fed a high carbohydrate-to-protein ratio diet.

Following a 4-day feed deprivation period, juvenile rainbow trout were reared for 22 days and fed one of the two isolipidic and isoenergetic experimental diets: a no-carbohydrate high-protein diet (NC; ~60% fishmeal proteins) or a high-carbohydrate diet (HC; 30% digestible carbohydrates and ~40% proteins). Temporal changes in physiological parameters, gut microbiota composition, host epigenetic marks, and proteomic profiles were adressed across multiple time points (days 1, 2, 3, 4, 10, 15, and 22 following the first meal).

In trout fed a high-carbohydrate (HC) diet, the intestinal microbiota is enriched in *Lactobacillus* species, known to metabolize glucose into D- or L-lactate, alongside. All fish showed high abundance of *Mycoplasma,* independlty of the diet, in intestinal mucus, an associated fitness bacteria in salmonids and able to convert lactate CoA into lactyl-CoA via lactate co-A- transferase activity. In addition, fish fed the HC diet showed higher plasma D-lactate levels at all sampling times, whereas higher plasma L-lactate levels were observed only on Days 2 and 10. Since eucaryotes produce D-lactate only in extreme conditons through the methylglyoxal metabolism and in tiny quantity, these results suggest distinct microbial and host metabolic responses to the HC diet.

Targeting LC-MS analysis revealed a significant increase in histone H3 lactylation after 10 days in HC-fed trout compared to NC-fed fish. Histone lactylation, a recently discovered epigenetic modification, has been implicated in the regulation of metabolic pathways, including glucose metabolism (Chen et al, 2020).

These results suggest a potential microbiota-driven mechanism linking dietary carbohydrates to host epigenetic regulation via lactate-derived histone lactylation, providing new insights into the molecular basis of glucose intolerance in rainbow trout.

## References

Polakof, S., and S. Panserat. 2016. "How Tom Moon's Research Highlighted the Question of Glucose Tolerance in Carnivorous Fish." Comparative Biochemistry and Physiology Part B: Biochemistry and Molecular Biology, 2016 Sep:199:43–49. https://doi.org/10.1016/j.cbpb.2015.11.00.

Chen X, Yuan Y, Zhou F, Li L, Pu J, Zeng Y, Jiang X. Lactylation: From Homeostasis to Pathological Implications and Therapeutic Strategies. MedComm (2020). 2025 May 29;6(6):e70226. https://doi.org/10.1002/mco2.70226.

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# T22-Interactive immuno-neuroendocrine response to stress

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Both stress episodes and stress response in universal among animals. The investigation of such events of have generated a whole discipline that looks at how animals overcome such situations to maintain physiological balances and survival. Traditionally, the stress response has been addressed mainly by physiologists that described the response focusing on the activation of the neuroendocrine axes and the associated consequences of such activation. This approach has become quite useful as it could explain many of the changes in metabolism, osmoregulation and energetics. Moreover, the last decades the stress response has also incorporated the study of the molecules and pathways behind physiological and metabolic changes, thus expanding the knowledge of lower-level biological organization.

Nonetheless, the stress response is essentially a complex response that involves many, if not all, systems and levels of organization. In fact, stressors are very varied (physical, chemical, biotic, social and even symbolic), and the onset of responses may occur not only centrally or hierarchically, but sometimes peripherally and bottom-up. This is perhaps more clear in aquatic animals as fish, since the inputs of stressors or the myriad of possible stimuli may interact and enter into the body through the rich surrounding water media, hence through multiple external surfaces and mucosae of the animal. What becomes increasingly clear is that the stress response has intrinsically a coordinated and interactive nature, involving all physiological systems, and particularly all regulatory systems, neural, endocrine and immune.

Thus, besides the well-known Brain-Sympathetic-Chromafin axis and the Hypothalamus-Pituitary-Interrenal axis, we can assume that other axes are also playing a role in either short-term or long-term response, including the Brain-Pituitary-Thyroidal axis, the Brain-Pituitary-Gonadal axis or the Brain-Head kidney-Imune axis. Depending on the nature and intensity of the stressor, and the time-course, the role of all these axes may play a differential role.

It should be noted that, specifically, the neuro-immuno-endocrine axis is of high relevance in fish under stress situations, in particular under biotic stressors associated to all kinds of pathogens, opportunistic or not, or under other stressors that may induce inflammatory reactions. The coordination of neuroendocrine mechanisms and immune mechanisms are key to overcome these challenges, together with an additional coordination with the energetic axes to supply resources for such response.

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# T23-The perfect balance: trade-offs between reproduction and immunity in female rainbow trout (*Oncorhynchus mykiss*)

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Since resources are limited for organisms, they have to prioritize their distribution among competing vital functions such as reproduction and immune defense. Among vertebrates, immune-reproductive trade-offs are well documented for the homoeothermic mammals and birds, while much less information is available for poikilothermic vertebrates.

In the present study we investigated potential reproductive-immune trade-offs in a seasonally reproducing fish species, the rainbow trout (*Oncorhynchus mykiss*). To this end, we examined changes in immune and reproductive parameters over the full reproductive cycle of adult female trout. Since trade-offs can vary with the actual resource needs of organisms, we used both untreated and LPS-immunostimulated fish.

The female trout displayed a significant upregulation of reproductive parameters during the annual cycle. Immune parameters, in contrary, displayed a general downregulation during reproduction. Three months after spawning, the immune parameters were recovered, with the exception of the phagocytic activity. The immunological changes were significantly correlated with the plasma concentrations of 17β-estradiol (E2). An influence of the LPS immunostimulation on the reproductive-immune relationship was not observed.

The findings provide evidence that the natural reproductive cycle of female rainbow trout is accompanied by a downregulation of immune parameters. This may indicate that reproductive-immune trade-offs are not restricted to homoeothermic vertebrates but exist in poikothermic vertebrates species as well.

# T24-Nutritional strategies to enhance fish health and welfare

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Sustainable aquaculture requires integrated approaches that simultaneously improve fish health, welfare, and production efficiency. Among these, nutrition remains a central tool, but its impact can be significantly enhanced when combined with complementary strategies such as environmental enrichment, selective breeding, and immunonutritional priming. Together, these approaches offer a holistic framework to increase resilience, reduce stress, and support physiological robustness in farmed fish.

This keynote will address how nutritional strategies can be designed not only to meet basic dietary requirements, but also to interact synergistically with enriched rearing environments, genetically improved stocks, and early-life immunonutritional conditioning. Functional feeds containing prebiotics, probiotics, postbiotics, immunostimulants, bioactive compounds, and targeted micronutrients can help modulate gut health, immune readiness, and stress tolerance. When combined with environmental enrichment, such as species-appropriate stimuli, these diets may further promote natural behavior and welfare. In parallel, genetic selection for disease resistance, feed efficiency, and stress robustness can strengthen the long-term effectiveness of nutritional interventions. Priming strategies applied during critical developmental windows may also prepare fish for later challenges by enhancing immune responsiveness and adaptive capacity.

The integration of these tools represents a promising path toward more resilient and welfare-oriented aquaculture systems. However, success depends on species-specific biology, production context, and careful validation of combined effects across nutritional, environmental, and genetic dimensions. A systems-based perspective will be essential to translate these concepts into practical solutions for modern aquaculture.

# T25-Comparative assessment of the potential effects of EE2 and E4 on immune development in zebrafish under *Aeromonas hydrophila* challenge

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Estrogens are ubiquitous in aquatic environments and can interact with multiple physiological systems in fish, including the immune system. In zebrafish (*Danio rerio*), exposure to the synthetic estrogen 17α-ethinylestradiol (EE2) has been associated with alterations in thymus development and immune-related endpoints, indicating a high sensitivity of immune processes during early life stages. Estetrol (E4), a natural estrogen recently introduced in oral contraceptives and characterized by a safer estrogenic profile, raises questions regarding its potential effects in non-target aquatic organisms. To date, most studies have investigated estrogenic effects on immunity under basal conditions, although fish are continuously exposed to pathogens in natural environments. Immune activation induced by *Aeromonas hydrophila* provides a relevant model of bacterial challenge. Preliminary experiments have focused on estrogen exposure alone to characterize direct immunological effects. The objective of this study is to evaluate immune reactivity to a simulated bacterial infection at different stages of thymic ontogeny in zebrafish, in order to assess how EE2 and E4 modulate immune responses during immune system development.

# T26-Replacing Fish Oil with Plant Oils: Lessons from Growth, Immunity and Inflammatory Balance in Fish

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The replacement of fish oil by plant oils in aquafeeds is increasingly driven by sustainability demands, yet its implications for fish health extend beyond growth performance. This keynote synthesizes a coherent series of studies investigating how dietary lipid sources regulate growth, nutrient utilization, innate immunity, and inflammatory homeostasis in common carp (Cyprinus carpio). Using a stepwise experimental framework, we first demonstrated that common carp efficiently digest and utilize several plant oils, with no adverse effects on protein digestibility and only moderate, oil-dependent differences in lipid and energy digestibility. Subsequent feeding trials showed that complete replacement of fish oil by selected plant oils does not compromise growth performance, feed efficiency, survival, or basal immune parameters, indicating a high degree of nutritional and metabolic flexibility. However, mechanistic analyses revealed that dietary lipid composition markedly reshapes tissue fatty acid profiles, particularly the balance between n-3 and n-6 long-chain polyunsaturated fatty acids (LC-PUFAs), which are key precursors of inflammatory mediators. To elucidate the functional consequences of these changes, in vitro and in vivo lipopolysaccharide (LPS) challenge models were employed. Head kidney leukocytes and whole-fish responses demonstrated that diets based on single plant oils tend to bias inflammatory signaling toward a prolonged pro-inflammatory state. In contrast, mixed plant oil diets or plant oils supplemented with LC-PUFAs (arachidonic acid or docosahexaenoic acid) promoted a more balanced and timely resolution of inflammation, comparable to fish oil-based diets. Collectively, these findings indicate that the principal challenge in fish oil replacement is not growth limitation, but the maintenance of immune homeostasis. Strategic combinations of plant oils, together with targeted LC-PUFA supplementation, emerge as effective nutritional tools to regulate inflammatory responses while preserving sustainability. This body of work provides a mechanistic framework linking dietary lipid composition to immune regulation and offers practical guidance for the development of next-generation, health-oriented aquafeeds.

Keywords: Plant oil replacement, Immune regulation, Inflammatory balance

# T27-Use of dietary phytogenic feed additives as an effective approach to reduce *Vibrio anguillarum* infection incidence in European sea bass (*Dicentrarchus labrax*) juveniles

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Aquaculture expansion increasingly challenges fish health and production stability. From a One Health perspective, farming intensification, species diversification, and climate-driven environmental changes are reshaping host–pathogen–environment interactions and disease dynamics. These conditions may promote pathogen emergence and persistence, highlighting the need for preventive strategies that enhance host resilience. That at the same time will reduce antimicrobial use to address antimicrobial resistance, while relying on improved husbandry, vaccination, biosecurity, and nutritional approaches within the framework of sustainable and innovative feed formulations. These combined pressures affect key physiological systems, including immune function, stress regulation, oxidative balance, and mucosal health. Disruption of these interconnected processes can compromise host defenses and increase susceptibility to disease. Consequently, aquaculture health management is increasingly focused on preventive strategies that support immunomodulation and help maintain mucosal integrity. In this context, functional ingredients such as phytogenic feed additives (PFAs) represent promising tools to enhance disease resistance in farmed fish, although their precise modes of action remain insufficiently understood due to the complexity of interactions among their bioactive compounds.

Therefore, the aim of the present study was to determine the role of a phytogenic blend (AL) on disease resistance, host–pathogen interactions, and oxidative stress–related processes in European sea bass (*Dicentrarchus labrax*). Experimental diets were formulated with AL at 200 ppm (AL200) and 1000 ppm (AL1000). Fish (9.4±0.1g) were fed for 60 days and challenged with *V. anguillarum* (ip; $10^5$ cfu/fish). Tissue samples were collected at 0-, 2- and 7-days post-infection for analysis. Fish fed diet AL1000 presented reduced ($p<0.05$) hepatocyte area compared to fish fed the control diet, which correlated the enzymatic activity and relative expression of genes related to oxidative stress response ($p<0.05$). Furthermore, fish fed both AL dietary levels showed improved disease resistance ($p<0.001$) against *V. anguillarum* after 60 days of feeding. This finding was correlated with the modulation of genes involved in the orchestration of the immune response during the development of the infection, in which the diet clearly affected the response pattern over time, with a significant interaction between both factors. Bacterial growth curves revealed notable differences in growth dynamics among plasma samples depending on dietary treatment, particularly for fish fed the AL1000 diet, whereas plasma soluble protein concentrations remained relatively stable throughout the experimental period among dietary treatments or sampling times ($p>0.05$).

Overall, dietary AL supplementation improved resistance to *V. anguillarum* infection in sea bass juvenile, supporting its potential as a functional strategy to enhance disease resilience through the modulation of oxidative balance, immune-related responses, and plasma antimicrobial activity.

# T28-Antioxidant, antibacterial, and immunostimulatory potentials of terrestrial and marine extracts from by-products and low-value biomass: An ex vivo study in gilthead seabream (*Sparus aurata*) head kidney leukocytes.

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The expansion of aquaculture and the drive toward more sustainable ingredients have promoted the incorporation of alternative and novel raw materials as alternatives to traditional marine raw materials, which can provide bioactive functions in addition to fulfill fish nutritional requirements. In this context, agro-industrial by-products and low-value marine biomass emerge as promising sources of antibacterial, immunomodulatory, and antioxidant bioactive compounds. Valorizing these raw materials within a circular economy framework offers the dual benefits of reducing waste and improving fish resilience. This study evaluated nine natural extracts of terrestrial and marine origin as potential functional ingredients for aquaculture. Terrestrial by-product extracts (TE) included pomegranate peel (rich in punicalagin or ellagic acid), citrus fruits, and grape seeds, whereas marine included marine macro- and micro-algal extracts (ME) (*Rhodomonas lens*, *Desmodesmus sp.*, *Osmundea pinnatifida*, *Gracilaria sp*., and *Dictyota sp*.). Extracts were characterized by determining their total phenolic and flavonoid contents. Antioxidant activity was evaluated using two methods: 2,2′-Azino-bis-(3-ethylbenzothiazoline-6-sulfonic acid (ABTS) and Ferric Reducing Antioxidant Power (FRAP) assays. Antibacterial activity was assessed against *Vibrio anguillarum, V. harveyi*, and *Photobacterium damselae* subsp. *piscicida*. To assess the effects of extracts at cellular level, *ex vivo* assays were performed on head kidney leukocytes from gilthead seabream (*Sparus aurata*), evaluating cytotoxicity, respiratory burst, phagocytic activity, and peroxidase activity. TE showed higher levels of both phenolic compounds and flavonoids than ME, which are usually related to higher antioxidant activity (Dudonne *et al*., 2009). In addition, TE showed stronger antibacterial effects against the three pathogenic bacteria tested. However, ME in general terms, presented higher immunomodulatory potential, causing respiratory burst activation or higher peroxidase activity in leukocytes, which may be associated with the presence of bioactive polysaccharides found in marine algae (Petit *et al*., 2024). These findings suggest that combining terrestrial and marine extracts could represent an interesting strategy to enhance antioxidant defense, control bacterial pathogens, support fish immune function, and serve as functional ingredients for aquaculture marine species like *S. aurata*.

## References

S. Dudonne *et al., J. Agric. Food Chem*. 57, 1768 (2009).
J. Petit *et al., Comp. Immunol. Rep.* 6, 200128 (2024).

# T29-Using small fish models to assess phytobiotic-based feed additive for skin health

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Skin health plays a critical role in aquaculture by providing both physical protection and immune defense in farmed fish. Functional feed additives have been widely used to maintain skin integrity under farming conditions. However, testing these additives directly in commercial species is expensive and time consuming. Small laboratory fish such as guppy (*Poecilia reticulata*) and zebrafish (*Danio rerio*) offer a practical alternative. They share similar skin structure, immune responses, and regenerative capacity with major farmed fish species such as salmon, seabream, and seabass. This makes them useful models for evaluating dietary strategies for skin health.

To evaluate how dietary strategies strengthen skin defenses, a phytobiotic based additive (APEX, Adisseo) was assessed using three experimental models. First, a controlled guppy-*Gyrodactylus turnbulli* ectoparasite challenge model was used to assess resistance to infection. Guppies were fed the supplemented diet for 14 days prior to challenge. Each fish was infected with two parasites, and parasite loads were recorded every 48 hours for 17 days. Dietary supplementation reduced mean parasite burden by 58%. Survival increased from 59% in control group to 88% in treated group.

To better understand the protective mechanism, the skin samples were analyzed using shotgun proteomics. A total of 1,332 differentially expressed proteins were identified in supplemented fish. Results showed activation of immune pathways, including the complement system, and increased skin regeneration. These changes strengthen the skin barrier, reduce parasite attachment, and promote faster removal of pathogens.

Finally, a zebrafish laser ablation model was used to evaluate wound-healing capacity. Adult zebrafish were fed the supplemented diet for 14 days before the induction of skin wounds. Treated fish reached 50% wound closure in 16.2 days, compared with 26.7 days in control fish, showing nearly 40% faster recovery. Histological analysis confirmed improved re-epithelialization and more advanced tissue remodeling in treated fish.

Together, these three small-fish models demonstrate that the phytobiotic based feed additive reinforces skin barrier function, enhances immune defenses, and accelerates tissue repair. These findings support the use of guppy and zebrafish as cost-effective and biologically relevant tools for high-throughput screening of functional feed additives aimed at improving skin health and resilience in aquaculture.

# T30-The Carp and Its Herpesvirus: A Fascinating Journey into Immune System Discoveries

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The infection of common carp by Cyprinid herpesvirus 3 (CyHV-3) represents a remarkable homologous host-virus model to study host-pathogen-environment interactions. In this talk, we will illustrate some of the discoveries made in our lab using this model such as the ability of the virus to delay the expression of behavioral fever by its host and how the virus is able to prevent the detection of its nucleic acids by the cell autonomous immune system.

## References

K. Rakus *et al. Cell Host and Microbe,* **21**, 244-253 (2017).
M. Diallo *et al. Nucleic Acids Research,* **51**, 806-830 (2023).
S. Pirotte *et al. Nucleic Acids Research,* conditionnaly accepted (2026).

# T31-Physiology of stress and its connections to Operational Welfare Indicators (OWIs) in aquaculture

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Operational Welfare Indicators (OWIs) are increasingly applied in aquaculture to monitor fish welfare under commercial conditions (Noble et al., 2026). Many OWIs rely on animal-based measures, particularly behavioural observations and assessments of external body damage, due to their practicality and non-invasive nature. However, the extent to which these indicators reflect underlying physiological stress responses and negative subjective experiences of fish remains unclear (Pietsch 2025). Links between OWIs, stress physiology, and affective states are often assumed rather than empirically validated and might strongly differ depending on the time of assessment (e.g. recent lesions versus old lesions). As a result, the capacity of OWIs to accurately represent welfare and chronic or acute stress is often uncertain. This keynote will review current knowledge, highlight key gaps in validation, and discuss the need for integrative approaches that account for inter-individual variability in stress responses and welfare outcomes in farmed fish.

## References

C. Noble *et al.*, Rev. Aquac. 18:e70109 (2026).
C. Pietsch*, Animals 15:2367* (2025).

# T32-Heart rate and acceleration biologging of yellowtail kingfish *Seriola lalandi* in a commercial marine RAS environment

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Yellowtail kingfish is a fast-growing athletic fish that needs to swim constantly in order to have sufficient water flow over the gills to meet the oxygen demands (Palstra et al., 2015, 2024). In line with this are the highest heart rates ever measured among larger fishes (Palstra et al., 2024) in order to pump the oxygen-rich blood to the tissues and organs. The species is successfully farmed in marine RAS but it can be challenging to answer to its specific lifestyle conditions. In this study, we investigated the effects of varying farming conditions on heart rate (HR) and activity (acceleration, AC) as monitored by implanted biologgers. Sentinel fish were part of a population in two production tanks, one under regular conditions and one under enriched flow. HR values were on average 107 ± 37 beats per minute bpm, ranging from 26 to 246 bpm. AC values were on average 13.0 ± 7.3 milli-g, ranging from 1 to 212 milli-g. HR and AC were strongly positively correlated (+0.414 bpm milli-$g^{-1}$/+0.00596 milli-g $bpm^{-1}$). Fish under flow had lower HR (−5.34 bpm) and lower acceleration (-1.23 milli-g) than fish under regular conditions, though not significantly. HR and ACC were not significantly affected by feeding period nor photoperiod. Significant effects were created by temperature (+5.67 bpm $°C^{-1}$, +0.10 milli-g $°C^{-1}$) and weight (−0.016 bpm $g^{-1}$). Temporal weekly and daily fluctuations in HR and AC occurred. Fluctuations over the day in HR ranged from a minimum of on average 100 bpm at 4 h up to an average maximum of 120 bpm at 11 h without flow effects. AC was on average 12 milli-g under flow and 14 milli-g under regular conditions. AC increased up to 15 milli-g under flow and 18 milli-g under regular conditions during an active period between 9.20 up to 11 h, preceding HR peaking between 11 and 12.20 h. From these findings we can conclude that biologgers in sentinel yellowtail kingfish provide unique and essential biotic data that inform us about the welfare condition of kingfish and can assist with precision farming under marine RAS conditions.

## References

A.P. Palstra *et al.*, Front. Physiol. **5**, 506 (2015)
A.P. Palstra *et al.*, Biology **13(3)**, 189 (2024)

# T33-The stress response of European seabass (*Dicentrarchus labrax*) at harvest

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This study evaluated the effects of industrial-scale harvest and slaughter practices on the stress response and muscle quality of European seabass. Multiple harvest-slaughter protocols were compared, from low-stress hook-and-line and pithing (ikigun) to intensive crowding with brailing, and live chilling in ice-slurry. Harvest intensity was the primary driver of physiological disturbance, with intensive handling resulting to significant endocrine, metabolic, and osmoregulatory disruption (de la Rosa et al., 2021; Santos et al., 2010). These responses were not mediated by the application of electrical stunning. Ikigun induced a rapid loss of behavioural responses (LBR), whereas the application of electrical stunning accompanied by ice-slurry resulted in faster time to LBR than ice-slurry alone (Gräns et al., 2015). Intensive harvest accelerated post-mortem muscle pH decline and rigor mortis development (Nathanailides et al., 2011). Pre-slaughter handling therefore remains the dominant determinant of both fish welfare and product quality under commercial conditions.

## References

de la Rosa *et al.*, Animals **11**, 2164 (2021).
Gräns A et al., Animal **10**, 294 (2016).
Nathanailides C et al., Procedia Food Sci. **1**, 1099 (2011).
Santos G.A. et al., Aquaculture **299**, 73 (2010).

# T34-New strategies to evaluate and encourage fish welfare in aquaculture

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Consideration of fish welfare is becoming increasingly important in both aquaculture research and commercial production. First, improving fish welfare in aquaculture relies on the precise control of environmental parameters, ensuring that water quality, temperature, lighting conditions, stocking density, and other external factors are adapted to the biological requirements of each species. Among these environmental factors, the use of environmental enrichment (e.g., physical, sensory, or social enrichment) represents a promising strategy to promote the expression of natural behaviours and reduce stress in fish. However, thorough investigation is still required before such approaches can be widely implemented, as the effects of enrichment may vary according to species, developmental stage, or production system. Second, factors associated with human practices, including handling, transport, and slaughter procedures, also play a major role in fish welfare. Optimizing these practices can substantially reduce stress, pain, and discomfort, thereby improving overall welfare. When potentially painful or stressful procedures are unavoidable, the administration of appropriate compounds, particularly analgesic molecules, may constitute a promising future strategy to mitigate discomfort and physiological stress responses in fish. Nevertheless, further research is necessary to validate the efficacy, safety, and species-specific effects of these compounds. Third, intrinsic animal-related factors may also strongly influence fish physiology and welfare status. These factors include reproductive maturation, disease occurrence, parasitic infections, genetic background, and individual physiological condition. Together, environmental, human-related, and animal-related factors constitute complex and interconnected sources of welfare variation. Their appropriate management contributes to reducing physiological stress while supporting healthy growth, survival, and overall biological functioning.

To further improve fish welfare, it is essential to develop and validate a sufficient number of adapted and species-specific welfare indicators. These indicators include zootechnical, physiological, molecular, and cellular markers, while behavioural observations are becoming increasingly important due to their ability to reflect the animal’s direct response to its environment. In recent years, several welfare assessment grids have been developed to guide welfare evaluation in aquaculture systems. In parallel, emerging sensor technologies are helping to detect signs of stress, disease, or unsuitable environmental conditions in real-time. These standardized tools facilitate the early detection of welfare issues and promote more consistent welfare assessment across facilities for a given fish species. However, additional research remains necessary to identify novel welfare indicators, particularly those that are specific to a species, developmental stage, or production system.

By combining optimized environmental conditions, improved human practices, and careful consideration of animal-related factors, aquaculture systems can substantially enhance fish welfare. Ultimately, the integration of reliable welfare indicators into routine management practices will support the continuous improvement of fish care and husbandry strategies. Such approaches are beneficial not only for producers, by improving zootechnical performance and production sustainability, but also for scientists, by strengthening experimental reproducibility and ethical standards in animal research. Most importantly, these efforts contribute to limiting negative experiences in fish while promoting conditions that favour positive welfare states.

# T35-Reading stress through animal behaviour

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Stress is an inevitable component of life in both natural and aquaculture environments. Understanding how fish perceive and respond to stressors is therefore fundamental to improving animal welfare and production sustainability. While physiological indicators such as endocrine, metabolic, and immune responses have greatly advanced our understanding of stress biology, behaviour provides a particularly valuable perspective because it reflects the integrated outcome of processes occurring across multiple levels of biological organization.

In recent years, technological and analytical advances have enabled increasingly detailed assessments of fish behaviour, ranging from high-resolution laboratory tracking to the continuous monitoring of individuals and groups under more realistic conditions. These approaches offer new opportunities to detect subtle changes in behavioural patterns, assess individual variation in stress responsiveness, and evaluate resilience in the face of environmental challenges.

In this talk, I will discuss how behavioural observations can contribute to our understanding of stress physiology in fish and how behaviour can serve as an integrative readout of animal state. Drawing on examples from both fundamental and applied research, I will explore the links between behaviour, physiology, and welfare, highlighting how behavioural approaches can support the development of more sustainable and welfare-conscious aquaculture systems.

# T36-Which phenotypes for selective breeding in aquaculture?

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Selective breeding, as for all animal productions, is a key component of performance in aquaculture systems. Selection methods have been developed for all species, starting from simple individual selection to now reach the most up to date genomic selection methods, with proven efficiency. However, a key question remains the phenotypes to which these methods are and will be applied. As selection always has a cost, these phenotypes have to give a benefit, be it economic, in most cases, or of wider interest (product quality, fish welfare).

Historically, the most selected trait has always been and remains growth rate, often measured as harvest body weight. However, in many cases, it has been shown that growth has very little if any economic impact. Moreover, measuring it as final body weight may indeed favor early fast-growers, which may not be the fish of interest for production farms. Rather than output-based traits, efficiency traits (processing yields, survival and disease resistance, feed efficiency) have a much better potential to improve economic gains and environmental sustainability. However, these traits are more difficult to select for than growth rate, mostly because they are more difficult to measure, and/or because measurement is lethal – which may require specific selection methods or indirect selection. I will review the progress done and the remaining challenges to improve these traits in fish culture.

In addition to these efficiency traits, in the context of global change, adaptation and robustness traits also become more and more interesting. Can we help fish pass through heatwaves? What should we measure to improve this? Can we find genotypes which have stable performance in variable environments? Can we improve fish tolerance to the more and more used plant-based diets?

A last category of traits are the ones related to animal welfare. Fish welfare is more and more a concern for the consumers, and there is certainly a genetic basis to traits linked to behaviour, personality and welfare. However, working on those raises both ethical issues and technical difficulties.

While it is clear that in evolved breeding programs the breeding objective now always integrates traits other than growth rate, there are still many issues for measuring and understanding more subtle phenotypes, which may be more important both for their direct economic gains and for preparing aquaculture to a changing world. Good phenotypes are the key for selective breeding.

# T37-Genomic selection in aquaculture: current status, challenges and prospects

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Rapid and continuous progresses in molecular biology techniques have impacted many fields in the discipline, including the selection of better animals. Parallel improvements in the acquisition of new phenotypes nowadays extend largely the possibilities in the selection process: in addition to the traditional traits measured and evaluated in aquaculture, traits hard to measure like disease resistance, feed efficiency, stress tolerance or product quality benefit from the technical and statistical advances in the selection procedures. Inclusion of DNA information in the selection models have led to marker assisted selection and to genomic selection, with demonstrated positive impacts on the accuracy of the estimators, the efficiency of the selection and the generation intervals for the breeders. Although new genomic models are still developed, new challenges arise: can we include additional information from other molecular levels (transcriptome, proteome, metabolome) to improve the prediction? How can we take into account potential genotype x environment interactions? Could potential non-linear genomic effects be modelled?

Machine learning is currently proposed to attempt to provide answers to such questions. Data driven approaches, such as multilayer perceptron and deep learning, have been investigated, not only as a new improved tool for genomic selection, but also in the context of genomic annotation – which indirectly could benefit to genomic selection – among other applications. Other methods, such as ensemble methods, are also tested. The objective of the talk is to introduce some of the recent methodologies aiming at pushing the estimation of risk scores for diseases and breeding values for production traits one step further.

## References

T. Chen, H. Zhang, R. Mazumder, X. Lin, PNAS Vol.121, (2024), https://doi.org/10.1073/pnas.2403210121
W. Ma, W. Zheng, S. Qin, C. Wang, B. Lei, Y. Liu, *GigaScience*, Vol. 14, (2025), https://doi.org/10.1093/gigascience/giaf083

# T38-Zootechnical and transcriptomic profile of non-eating Eurasian perch larvae

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The onset of exogenous feeding is a critical phase in early fish larval development and is often associated with high mortality, posing challenges for aquaculture (Yúfera & Darias, 2007). In Eurasian perch (*Perca fluviatilis*), larvae show considerable variability in their ability to initiate foraging (Pepin et al., 2014), with some individuals feeding immediately (early eaters), others starting days later (late eaters), and some never feeding at all (non-eaters). The current study aimed at investigating the differences between eaters and non-eaters under optimal rearing conditions using a combination of zootechnical and transcriptomic approach. Six families were produced by crossing one female with one male, and larvae were reared until the weaning stage. Starting at first feeding (5 days post-hatching, DPH), eaters (early eaters) and non-eaters were manually selected and reared in separate tanks. Subsequent selections at 6 and 7 DPH enabled the identification of larvae that later initiated foraging (late eaters), thereby ensuring accurate classification of true non-eaters. Results indicates that the failure in foraging was the primary cause of early mortality, accounting for up to 50% of larval deaths. Eaters were larger in both length and weight compared to non-eaters, indicating that body size may influence the ability to initiate foraging. RNA-seq analysis of larvae at 6 DPH identified 3,117 differentially expressed genes (DEGs; $padj < 0.01$, $|\log_2 FC| > 1$). Principal component analysis revealed a strong separation between late eaters and non-eaters along PC1, accounting for 86% of the variance. Functional annotation indicated that these DEGs are largely involved in DNA replication and cell cycle pathways. Notably, non-eaters showed down-regulation of genes associated with lipid metabolism (e.g., *dhcr24*, *sqle*, *sc5d*). Together, these results suggest that failure to initiate foraging is associated with growth and metabolic processes, reflecting differences in physiological condition during early larval stages. This study provides a first framework for understanding the biological basis of early foraging ability in fish larvae.

## References

M. Yúfera, MJ Darias. Aquaculture, 268 (2007)
P. Pepin, *et al.* ICES Journal of Marine Science; 72 (2014)

# T39-Gene expression and growth in bighead catfish (*Clarias macrocephalus*) exposed to varying salinity levels

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Bighead catfish is important for freshwater aquaculture in the Mekong Delta, where are extremely vulnerable to climate change and saline intrusion. This species is also a good model for investigating transgenerational variation in growth and response to salinity. This study aimed to test whether parents raised in different salinities resulted in variation in growth and saline-stressed gene expression of offspring for bighead catfish. Juveniles produced from three groups of parents cultured in 0, 4 and 8 ppt were reared in 0, 4, 8, 12, and 16 ppt. Fish were sampled for gene expression (gills and intestine) on day 9th (after 8 days of salinity acclimatization) and day 24th, and for growth on day 30th. Growth indices such as final weight, daily weight gain, and specific growth rate of the three fish groups significantly declined starting from 12 ppt and further deteriorated when exposed to 16 ppt. Survival rate was markedly higher in offspring whose parents previously reared at 8 ppt, with highest survival observed at 4 ppt and sustained tolerance at 16 ppt. The group-dependent variation in survival could be attributed to parental acclimation history which is consistent to the principle of transgenerational plasticity. Transcriptional responses showed highly tissue-specific expressions and revealed marked variation with both salinity levels and exposure time. However, no correlation was observed in the relative gene expression on day 9 and day 24, suggesting non-consistent expressions between sampling intervals. Intestinal mRNA expressions of *nka1a* and *ghrb* generally decreased with duration exposure among fish groups and salinities, while relative quantity of *hsp70* displayed increasing pattern with exposure time across salinity treatments except at 0 ppt. Opposing trend was observed in the gill tissue, with longer exposure elicit slight increase in the mRNA levels of *nka1a*, *hsp70*, *ghra* across fish groups and salinity conditions. *Nka1a* expression in the intestines tend to contribute to osmoregulation driven by significantly higher expression at fish exposed to 16 ppt even after prolonged exposure. However, mRNA levels of this gene in the gills marked no variation among fish groups and salinity treatments at the end of salinity challenge. The observed lower mRNA levels at high salinities in the intestine and gill tissues were likely to be due to energy trade-off between stress response system maintenance and osmoregulation under severe environment. Regarding growth receptor hormones, *ghra* expression in the gill was significantly higher under moderate salinities after prolonged exposure, regardless of fish groups. Parallel patterns were also notably observed in *ghrb* mRNA levels in the intestine with notable expressions observed at 8 ppt on D9 and 4 ppt at D24 among three fish groups. Interestingly, the expression of these receptor genes corroborates with growth indicators having significant higher values in fish reared at 0–8 ppt. This consistency implies that *ghra* and *ghrb* may functionally contribute to the physiological adaptation of bighead catfish supporting growth under moderate salinity regimes. Taken together, bighead catfish displayed salinity-dependent and tissue-specific osmoregulatory and stress responses, with positive effects on growth and survival under intermediate salinity conditions. Beyond this, the study also provides preliminary information integral to improve the farming practices to mitigate climate-induced threats.

# T40-Sturgeon embryos as a model for genotoxicity screening

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Sturgeons (Acipenseridae) represent a unique group of fish, as they are on the verge of extinction in the wild while remaining economically important in aquaculture as a source of black caviar. In addition, they constitute an attractive model for research on DNA damage and repair. Sturgeons possess one of the highest chromosome numbers among vertebrates (up to approximately 500) and exhibit exceptional genomic plasticity, which enables spontaneous polyploidization and interspecific hybridization. However, this genomic plasticity is also associated with increased sensitivity to DNA damage from external sources, as demonstrated in our previous studies (Dey et al., 2024).

Notably, sturgeon embryos show a limited capacity to activate DNA repair mechanisms and apoptosis during early development, up to approximately 24 hours post-fertilization (hpf). In contrast, teleost species such as common carp and zebrafish are capable of initiating apoptosis and the DNA damage response (DDR) as early as 6 hpf (Ikegami et al., 1999; Dey et al., 2024). These observations led us to conclude that sturgeons at early embryonic stages may serve as a promising model for genotoxicity screening.

Accordingly, we used sterlet (*Acipenser ruthenus*) embryos to investigate the effects of common water pollutants with known genotoxic modes of action. Embryos were exposed between 2 and 24 hpf to compounds such as bisphenols (BPA, BPS, BPF) and terbuthylazine (TBA) at environmentally relevant concentrations. DNA fragmentation, survival, hatching rates, oxidative stress indices, and gene expression were assessed. The lowest xenobiotic concentrations used in this study were based on levels reported in the Danube River, a natural habitat of sterlet (Maric et al., 2023).

Specifically, exposure to TBA did not cause changes in embryo viability or malformation within the concentration range of 3–3000 μg/L. However, exposure to concentrations above 12 μg/L TBA led to early hatching and a significant increase in the expression of genes associated with neurodevelopment and primordial germ cell development. These changes were accompanied by slightly increased DNA damage at concentrations above 12 μg/L TBA, as indicated by the comet assay.

Similarly, exposure to BPA within the concentration range of 0.5–1000 μg/L resulted in significant embryo lethality only at the highest dose. Nevertheless, DNA fragmentation was observed at concentrations above 10 μg/L BPA, and changes in gene expression were detected at 1–1000 μg/L. Exposure to BPS and BPF at environmentally relevant concentrations did not affect sturgeon embryo development.

Overall, the obtained results demonstrate that sturgeons at early developmental stages are highly sensitive to water pollution, even at environmentally relevant concentrations. Although these pollutant levels do not lead to immediate embryo mortality, their effects on gene expression may have long-lasting impacts on organismal survival and reproduction.

## References

Dey A*, et al.*, Environ Toxicol Pharmacol. **110**, 104501 (2024).
Ikegami R, *et al.* Dev Biol. **215(2)**, 344 (1999).
Maric JJ, *et al.,* Mutagenesis **38,** 21 (2023).

# T41-Epigenetics in Aquaculture: recent developments and prospects

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The application of epigenetics in aquaculture has generated much interest since it can potentially provide novel, non-pharmacological approaches to induce desired phenotypes through environmental manipulation. In contrast to their terrestrial counterparts, farmed aquatic animals are well suited for these applications because their external fertilization and early development make them highly susceptible to environmental cues (Piferrer, 2023). Using the European sea bass as a model, recent research has identified epigenetic biomarkers related to domestication (Anastasiadi and Piferrer, 2019) as well as biomarkers with not only diagnostic but also prognostic value that can detect early-life thermal stress before transcriptomic changes become apparent (Valdivieso et al., 2022). A landmark advancement is the successful integration of epigenetic selection into traditional breeding programs; specifically, utilizing DNA methylation markers in the sperm to select broodstock, which resulted in a 1.4-fold increase in production yield (Sánchez-Baizán et al., 2025). Studies should take advantage of the epigenetic-sensitive windows —being, in order of importance, early development, gametogenesis and metamorphosis— to establish permanent and beneficial epigenetic marks through environmental or nutritional programming. Current research priorities include the identification of pure epialleles that are independent of the underlying genotype and heritable, ensuring their utility across diverse genetic backgrounds, as well as non-invasive monitoring tools, such as blood-associated DNA methylation marks that mirror epigenetic changes in other tissues, or circulating microRNAs (c-miRNAs) detectable in mucus and plasma, which can act as systemic messengers reflecting stress and reproductive status. The potential of epigenetics in aquaculture would be fully realized when quantitative epigenetics becomes more developed, employing epigenome-wide association studies (EWAS) and models to partition phenotypic variance into genetic, epigenetic, and environmental components. This will allow for better resolution of the "missing heritability" problem and will likely improve the prediction of breeding values. Despite this potential, many challenges remain. The most important and obvious one is that it needs to be convincingly shown that epigenetics adds value to aquaculture production. Also, using multi-omics approaches will help in moving epigenetic markers from exploratory tools to routine components of precision aquaculture. In conclusion, since epigenetics bridges the gap between the genome and the environment, it has the potential to significantly contribute to enhancing the resilience and sustainability of aquaculture in a changing climate.

## References

D. Anastasiadi, F. Piferrer. Mol. Biol. Evol**. 36**: 2252 (2019).
F. Piferrer. *Epigenetics in Aquaculture*. Eds: Piferrer, F. and Wang, H.P. (2023). John Wiley & Sons.
N. Sánchez-Baizán *et al.* Env Epigenetics, **11**, dvaf027 (2025)
A. Valdivieso *et a*l., Aquaculture, **563**, 738918 (2023).

# T42-Domestication of new fish species for sustainable aquaculture: current status, challenges and prospects

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Aquaculture, particularly fish farming, is an economic sector that has been experiencing rapid growth for the past half-century. It plays an increasingly important role in feeding the world's population. However, the sustainability of its development model is increasingly being questioned for various reasons (management of water resources and raw materials, animal welfare, antibiotics, climate change etc.) (Garlock *et al*., 2024). In this context, using the rich aquatic animal biodiversity presents a real opportunity to promote new aquaculture practices and develop aquaculture systems that are more resilient to climate, economic, and societal challenges, through an agroecological approach. Thus, more sustainable fish farming could draw on the abundant ichthyological biodiversity available (more than 36,000 species). However, such a prospect requires the domestication of new species, a slow and ongoing process with multiple definitions (Lord et al., 2025) which, overall, has only recently extended to aquatic species. The great majority of aquatic animal species currently farmed, representing only a small fraction of available biodiversity, have undergone a domestication process over the past century. However, in this context, even though the domestication of fish is a very recent phenomenon, numerous phenotypic changes have been rapidly observed as a result of maintenance in captivity. These fish phenotypic modifications during domestication vary greatly amongst species and physiological function (Milla *et al*., 2021).

Given the need to address emerging challenges for more sustainable aquaculture (including the development of integrated multi-trophic farming systems, the farming of low-trophic-level species, and the emergence of short-supply-chain bioeconomies to enhance food security and territorial integration) the domestication of new species remains a highly relevant strategy. However, it is necessary to promote more generic approaches to enable more efficient domestication processes. Combining biodiversity screening, functional trait databases, and model-species approaches could substantially accelerate the domestication of new fish species for sustainable aquaculture.

## References

Garlock *et al*., Nat. Commun. **15**, 5274 (2024).
Lord *et al*., PNAS. **122**, e2413207122 (2025).
Milla et al., Rev. Aquacult., **13**, 388 (2021).

# T43-Domestication of indigenous species: a significant contribution to the unprecedented development of aquaculture in the mekong river delta, Vietnam

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Vietnam has been ranked among the top four aquaculture producers in the world. Total aquaculture production reached 6.1 million tons in 2025, of which the Mekong Delta accounted for approximately 5.81 million tons. A key driver of this success is the development and widespread farming of domesticated indigenous species. More than 20 indigenous species belong to three major groups, including freshwater fish, brackish-water crustaceans, and mollusks. Among these, striped catfish (*Pangasianodon hypophthalmus*), black tiger shrimp (*Penaeus monodon*), blood cockle (*Anadara granosa*), hard clam (*Meretrix lyrata*), and giant freshwater prawn (*Macrobrachium rosenbergii*) have been the most important species for over two decades.

For instance, production of striped catfish and black tiger shrimp reached 1.94 and 0.296 million tons, respectively in 2025. Other species, such as mud crab (*Scylla paramamosain*), Asian swamp eel (*Monopterus albus*), snakehead (*Channa striata*), and euryhaline catfishes (*Pangasius krempfi* and *Pangasius conchophilus*), have also become increasingly important for aquaculture in the Mekong Delta. The domestication of indigenous species has been achieved through broodstock development in captivity, induced spawning, selective breeding, improved larval rearing, enhanced seed quality, and the standardization of farming practices. These advancements have enabled the expansion of large-scale, market-oriented aquaculture systems while maintaining adaptability to diverse farming conditions. Therefore, continued efforts in domestication, genetic improvement, and sustainable management of key species remains essential for the long-term productivity and resilience of aquaculture in the Mekong Delta., Vietnam.

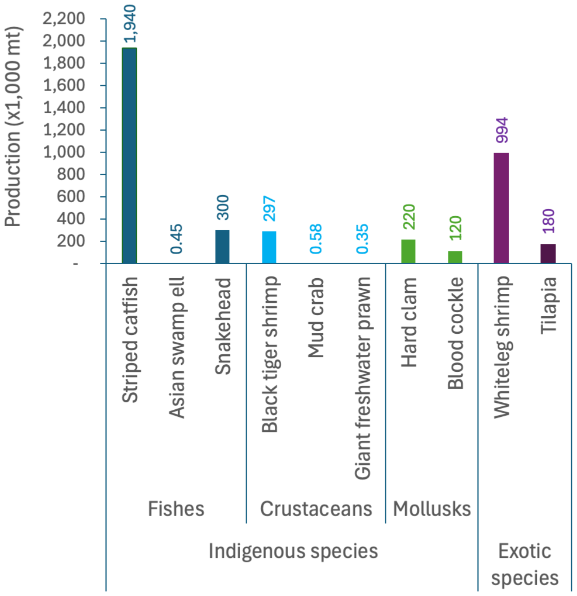

Fig. 1: Production of aquaculture indigenous and exotic species in the Mekong delta, Vietnam in 2025

# T44-Domestication starts early: physiological and molecular drivers of early-life adaptation in Eurasian perch (*Perca fluviatilis*)

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Fish domestication is a complex, multilevel process that affects phenotypic, physiological, and molecular traits determining performance under aquaculture conditions, but, the timing of its onset, particularly during early ontogeny, remains poorly understood. In Eurasian perch early development likely represents a key window for the emergence of domestication-related adaptations. For many years, we conducted comparative experimental studies on larvae originating from wild (WI) and domesticated (DO) broodstock reared under identical conditions, with no differences observed in fundamental developmental parameters (hatching, deformity rates, or swim bladder inflation). However, DO larvae exhibited higher growth rates, larger body size, and lower mortality, indicating enhanced performance under RAS conditions. At the physiological level, domestication effects were evident from the onset of exogenous feeding, with DO larvae showing reduced digestive enzyme activity and lower expression of digestive-related genes, suggesting decreased digestive plasticity and an adaptive shift toward formulated diets, reflecting early-life programming associated with aquaculture feeding regimes. In parallel, domestication influenced stress responsiveness and immune function, as well as mitochondrial processes, with DO larvae displaying attenuated stress responses, enhanced immune competence, and transcriptomic changes indicating mitochondrial function. Early-life adaptation was further shaped by parental effects, including strong maternal influence and maternal–paternal interactions. Together, these findings demonstrate that domestication begins early in ontogeny and involves coordinated changes in physiology and gene regulation, likely driven by parental programming.

## References

Palińska-Żarska *et al.*, Scientific Reports, 10:2211, (2020).
Palińska-Żarska *et al.*, Fish&Shellfish Immunology, 114, 184-198, (2021)
Debarnardis *et al.*, BMC Biology (accepted), (2026)

# T45-Early domestication alters aquaculture-related traits over the first captive-born generations in a model fish: limited evidence for sex-specific trajectories

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Domestication can induce rapid phenotypic changes through altered selection, relaxed wild pressures, and genetic drift [1,2], yet whether aquaculture potential [3], evolves differently between sexes remains untested. We investigated sex-specific phenotypic changes across four captive-born generations (F1–F4) of wild zebrafish (*Danio rerio*), analysing growth, body condition, stress responsiveness, behaviour, and reproductive performance using pedigree-based Bayesian animal models with explicit Sex × Generation interaction tests. Several traits changed significantly across generations, particularly body weight, condition factor, and reproductive traits. However, most responses were broadly parallel between sexes, and evidence for consistent sex-specific divergence was limited. These findings suggest that early captive adaptation primarily drives coordinated, sex-shared phenotypic responses, with trait-specific exceptions, underscoring the importance of sex-specific monitoring in aquaculture breeding programmes.

## References

1. S. Milla *et al*., *Rev. Aquac.* 13, 388 (2021).
2. F. Teletchea *et al*., *Fish Fish.* 15, 181 (2014).
3. L. Toomey *et al*., *Rev. Aquac.* 12, 2212 (2020).

# T46-Does species ratio matter? Survival, growth and physiology responses in pikeperch (*Sander lucioperca*) - sterlet (*Acipenser ruthenus*) polyculture in recirculating aquaculture systems

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Fish polyculture, historically practiced in ponds, is gaining increasing interest for Recirculated Aquaculture Systems (RAS) due to its documented biological, economic, and environmental benefits[1]. Its success, however, heavily depends on the species ratio, which modulates interspecific interactions and potentially influences the biological responses of the reared species[2]. This study evaluated five pikeperch (S)/sterlet (A) ratios (100/0, 0/100, 75/25, 50/50, 25/75) in triplicate over 90 days. Growth performance (weight, total length, fulton condition factor and specific growth rate), stress variables (cortisol and glucose in plasma; cortisol in mucus), immune variables (alternative complement pathway hemolytic, lysozyme, and peroxidase activities in plasma), and hepatic antioxidant variables (catalase [CAT] and superoxide dismutase [SOD] activities) were assessed at the end of experiment. All results were compared between each polyculture ratio and the respective monoculture for each species.

In the balanced ratio (50/50, SA), both species displayed higher growth (pikeperch: 111.0 g vs 71.5 g; sterlet: 200.3 g vs 169.8 g) than in monoculture. Stress, immune, and antioxidant variables did not differ significantly in both species. In the pikeperch-dominant ratio (75/25, Sa), sterlet growth was significantly enhanced (211.8 g vs 169.8 g) with 100 % survival, while pikeperch growth did not differ significantly. In pikeperch, antioxidant activities were differentially modulated with an increase of CAT (1.32 vs 0.19 $\mu mol.min^{-1}.mg^{-1}$ protein) and a decrease in SOD (10.1 vs 21.8 $U.min^{-1}.mg^{-1}$ protein), while no changes were measured in sterlet. In the sterlet-dominant ratio (25/75, sA), growth of the two species did not differ significantly (pikeperch: 98.0 g vs. 71.5 g; sterlet: 173.9 g vs 169.8 g). However, pikeperch survival was lower (77.3% vs 95.4%). Antioxidant activity was higher in both species: CAT for pikeperch (2.51 vs 0.19 $\mu mol.min^{-1}.mg^{-1}$ protein), and SOD for sterlet (18.9 vs 3.5 $U.min^{-1}.mg^{-1}$ protein). On the other hand, stress and immune variables remained stable, without any significant difference between treatments.

These findings highlight species ratio as a key management lever for optimizing polyculture systems in RAS, with balanced configuration emerging as the most favorable for both species.

## References

1. M. Thomas et al., Aquaculture, 559 (2022).

2.T. Pěnka et al., Aquaculture, 593 (2024)

# T47-Integrative Research to Improve Atlantic Salmon Health and Fitness Supporting Restocking Program in the Meuse Basin

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Atlantic salmon (*Salmo salar*) is an emblematic species of our river systems, yet it has experienced a marked decline across Western Europe and the entire North Atlantic. Although widely present in the Belgian Meuse during the 19th century, anthropogenic pressures, including overfishing, river channeling, and water pollution, led to its local extinction by 1942. The “Saumon Meuse” restoration program, initiated in 1987, aims to sustainably restore both habitats and populations, ultimately enabling the species to re-establish natural reproduction in the wild. The current restocking strategy implemented in Wallonia relies heavily on the large-scale release of emergent parr. However, several bottlenecks persist, notably the reduced survival of stocked individuals during early freshwater life stages and downstream migration, as well as low and highly variable adult return rates.

To support this restoration program, research has focused on improving the quality of eggs and juveniles produced in hatcheries. This includes optimizing breeding protocols to maximize the efficient use of precious gametes while maintaining high level of genetic diversity, as well as developing sperm cryopreservation techniques (Erraud et al., 2022). A focus was provided to cryopreservation effects on fertilization success and offspring performance. Further work has investigated early developmental conditions, from egg incubation to first feeding stages, demonstrating that rearing environments (type of incubator systems, lipid quantity and content in feed) significantly influence larval quality, survival, growth and swimming performances (Cornet et al., 2021). In addition, recent studies highlight the role of early nutritional strategies in shaping growth trajectories, swimming capacity, and metabolic performance of juveniles, which are key determinants of post-release survival (Cornet et al., 2026).

To these husbandry challenges, the impacts of climate change must also be addressed. As an ectothermic and stenothermic species, Atlantic salmon is particularly sensitive to elevated temperatures, especially in river systems where daily fluctuations may reach 12 °C between the coldest and hottest hours. Our studies have shown that such thermal variability affects fry produced using cryopreserved sperm and suggests that these individuals are less well adapted to strong daily temperature fluctuations. In addition, by studying how climate change may alter sperm quality and reproductive success, we demonstrated several deleterious effects of high temperature (+4°C compared to reference river temperature) on growth and sexual maturation. Using aquaculture techniques combined to molecular analyses, behavioral and swimming performance measurements, we’ve highlighted the need to integrate hatchery optimization and climate resilience into Atlantic salmon restoration strategies to improve reproductive success and post-release survival.

## References

Cornet *et al*. Fish Physiol. Biochem. 47, 979 (2021).

Cornet *et al.* Aquaculture 612 (2026).

Erraud *et al*. Aquaculture 549 (2022).

# T48-Effects of Sperm Cryopreservation on Offspring Fitness and Environmental Stress Tolerance in Atlantic Salmon (*Salmo salar*)

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The Atlantic salmon (*Salmo salar*) has undergone a severe decline across Western Europe and the North Atlantic, leading to the loss of natural populations in several countries, including Belgium. Listed as "Near Threatened" by the IUCN (2023), the species has disappeared from nearly 300 rivers, primarily due to overfishing, habitat fragmentation, river regulation, and pollution. In Belgium, ongoing restoration programs aim to re-establish self-sustaining salmon populations through habitat rehabilitation and supportive breeding. Within this context, sperm cryopreservation has emerged as a key tool for ensuring annual fertilization and maintaining genetic diversity when the number of returning anadromous males is insufficient. However, its potential effects on early life stages and juvenile development remain insufficiently documented. This research integrates two complementary projects designed to evaluate the developmental, physiological, and molecular consequences of sperm cryopreservation under environmentally realistic conditions at both early and later stages of ontogeny. The first project focuses on early development and examines the resistance of fry originating from fresh versus cryopreserved sperm to thermal stress (constant 9 °C, moderate fluctuations 7–12 °C, and high fluctuations 3–15 °C), followed by exposure to the bacterial pathogen *Aeromonas salmonicida*. The second project investigates potential impacts of sperm cryopreservation on later developmental stages (alevin to parr), assessing metabolic rate (respirometry), behavioral stress responsiveness (startle stress test), oxidative stress, and genes expression. Progeny derived from cryopreserved sperm exhibited reduced growth and yolk-sac reserves under high thermal fluctuations, as well as elevated expression of antioxidant and metabolic genes, indicating increased oxidative stress and higher energetic costs. Following bacterial challenge, immune competence was maintained only in fry that had not previously experienced strong thermal stress, suggesting reduced resilience to cumulative stressors. For later developmental stages, analyses of behavioral responses, metabolic rate, and transcriptomic profiles are ongoing; preliminary observations indicate potential differences between progeny groups, although definitive trends have not yet been established. Together, these studies constitute the first comprehensive evaluation of how sperm cryopreservation may influence multiple developmental stages and stress responses in Atlantic salmon, providing key insights for conservation strategies and the sustainable management of restored populations.

# P01-Effect of 17β-estradiol on ovarian development and physiological changes during different sexual maturity stages in Siberian sturgeon

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The present study was conducted to comprehensively investigate the effect of sustained-release 17beta-estradiol (E2) injection on somatic growth indices, metabolic and ionic profiles, hormonal responses, and histomorphometric changes of ovarian tissue at different sexual maturity stages of Siberian sturgeon (*Acipenser baerii*). For this purpose, 30 female Siberian sturgeon broodstock were divided into three distinct groups based on gonadal status, including sexual maturity stages II (pre-vitellogenesis), III (vitellogenesis), and IV (late vitellogenesis). Each stage consisted of two subgroups: control (receiving 0.2 mL/kg body weight of pure coconut oil) and treatment (receiving 2 mg/kg body weight of E2 dissolved in coconut oil). Injections were administered intraperitoneally in two doses over a 120-day period. The results showed that the increase in plasma E2 concentration was significant only in stage IV, but cortisol levels were not affected by the treatment. The results of this study demonstrated that using the sustained-release E2 system with coconut oil is an efficient and safe tool for managing reproductive physiology in Siberian sturgeon.

## References

Akhavan, S.R. et al., Anim. Rep. Sci. 157, 1 (2015).
Falahatkar, B. et al., Comp. Biochem. Physiol. 195A, 91 (2017).
Zhang, M. et al., Fish Physiol. Biochem. 48, 1365 (2022).

# P02-Nutrient utilization and growth performance of Nile tilapia (Oreochromis niloticus) in biofloc systems under reduced dietary protein levels

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Biofloc technology (BFT) is adopted in aquaculture as a sustainable approach to enhance nutrient recycling and improve feed efficiency by promoting the *in situ* production of microbial biomass (Khanjani et *al*., 2024). This study evaluated whether biofloc could contribute to nutrient utilization and growth performance in Nile tilapia (*Oreochromis niloticus*) under reduced dietary protein levels.

A 42-day feeding trial compared a flow-through control system receiving a diet with 38% crude protein (CP) with three biofloc treatments fed diets containing 38%, 32%, and 28% CP, each in triplicate. Zootechnical growth parameters were measured (survival rate, specific growth rate, feed conversion ratio, yield, and Fulton's condition factor), and stable isotope analyses were performed on fish blood at the end of the experiment to assess the assimilation of biofloc-derived nutrients by Nile tilapia.

Fish reared in biofloc and fed 32% CP exhibited growth performance and feed efficiency similar to those of the 38% CP control group. However, reducing dietary protein to 28% CP led to a significant decline in performance. Stable isotope analyses ($\delta^{13}C$ and $\delta^{15}N$) indicated preferential assimilation of biofloc-derived nutrients when dietary protein levels were moderately reduced (32% CP). These results demonstrate that biofloc microbial biomass can partially compensate for dietary protein reduction, provided a minimum protein threshold is maintained to support optimal growth (Zablon et *al*., 2022).

The results highlight the partial dietary compensation achieved through biofloc consumption under moderate dietary protein reduction, offering an interesting perspective for lowering feed costs and the environmental footprint of tilapia farming. However, floc quality and availability appear to be essential for maximizing dietary compensation performance, emphasizing the importance of monitoring their chemical and nutritional composition.

## References

M. H. Khanjani *et al.,* Aquac. Nutr. 1, 7496572 (2024).

W. O. Zablon *et al.,* Aquac. fish fish. 2(2), 94 (2022).

# P03-Water Governance in Madagascar: Bottlenecks to the Sustainability of Aquaculture Systems: The Case of the Rural Municipalities of Amboditandroho and Antetezambaro (Atsinanana Region)

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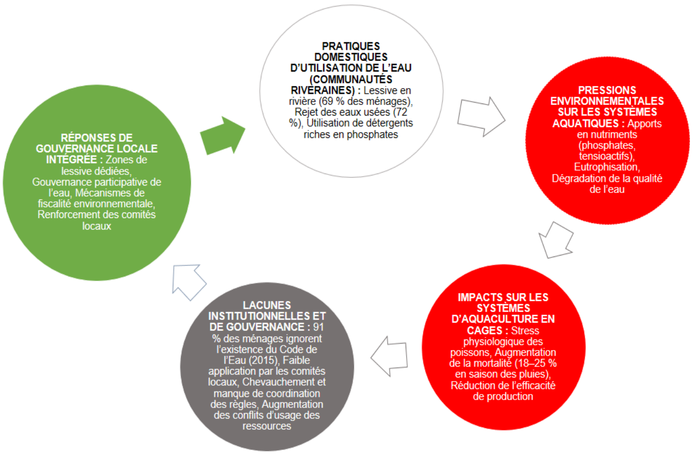
Aquaculture, a cornerstone of global food security (FAO, 2018), represents a major development priority in Madagascar (PNDEA III, 2019–2030). However, the sustainability of cage-based aquaculture systems is threatened by unregulated management of water resources. In the rural communes of Antetezambaro and Amboditandroho (Atsinanana Region), more than 620 riparian households (MEEF, 2022) depend on the same water bodies, and a large majority (78%) engage in laundry and dishwashing activities, generating diffuse pollution. Locally used industrial detergents, containing up to 22% phosphates and 12–18% anionic surfactants (Ranarijaona et al., 2021), contribute to eutrophication and induce physiological stress in fish. Our survey indicates that 69% of households wash directly in the river (4.2 times per week), and 72% discharge wastewater into it, resulting in a reported 18–25% increase in fish mortality during the rainy season, according to aquaculture producers. The primary bottleneck is institutional: 91% of households are unaware of the Water Code (2015), and community committees lack the capacity to enforce regulations, exacerbating use conflicts. This exploratory study, to be complemented by physicochemical analyses, proposes an integrated local governance framework combining participatory regulation, designated washing areas, and environmental taxation to enhance the socio-ecological sustainability of aquaculture systems.

Figure 1: cadre conceptuel des interactions socio-écologiques entre usages domestiques de l'eau, impacts environnementaux et gouvernance des systèmes aquacoles



**PRATIQUES DOMESTIQUES D'UTILISATION DE L'EAU (COMMUNAUTÉS RIVERAINES) :** Lessive en rivière (69 % des ménages), Rejet des eaux usées (72 %), Utilisation de détergents riches en phosphates

**PRESSIONS ENVIRONNEMENTALES SUR LES SYSTÈMES AQUATIQUES :** Apports en nutriments (phosphates, tensioactifs), Eutrophisation, Dégradation de la qualité de l'eau

**IMPACTS SUR LES SYSTÈMES D'AQUACULTURE EN CAGES :** Stress physiologique des poissons, Augmentation de la mortalité (18–25 % en saison des pluies), Réduction de l'efficacité de production

**LACUNES INSTITUTIONNELLES ET DE GOUVERNANCE :** 91 % des ménages ignorent l'existence du Code de l'Eau (2015), Faible application par les comités locaux, Chevauchement et manque de coordination des règles, Augmentation des conflits d'usage des ressources

**RÉPONSES DE GOUVERNANCE LOCALE INTÉGRÉE :** Zones de lessive dédiées, Gouvernance participative de l'eau, Mécanismes de fiscalité environnementale, Renforcement des comités locaux

## References

Li Y. *et al.*, Sci. Total Environ. **804**, 150125 (2022).
Kestemont, P., Aquaculture **129**, 347 (1995).
Imorou Toko, I. *et al.*, Int. J. Biol. Chem. Sci. **7**, 1298 (2013)

# P04-Dietary supplementation of *Thuja orientalis* L. leaf extract improves immune responses and resistance to bacterial infection in striped catfish (*Pangasianodon hypophthalmus*)

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This study investigated the effects of dietary supplementation with *Thuja orientalis* L. leaf extract on innate immune parameters, and disease resistance of striped catfish (*Pangasianodon hypophthalmus*). A completely randomized design was applied with four dietary treatments containing 0% (control), 0.25%, 0.5%, and 1% *T. orientalis* extract, each in triplicate, over a 4-week feeding trial. Hematological and immunological parameters were assessed at weeks 2 and 4. After the feeding period, fish were experimentally challenged with *Edwardsiella ictaluri*, and cumulative mortality was recorded. The results showed that dietary supplementation with *T. orientalis* extract significantly enhanced hematological parameters in striped catfish. Fish fed supplemented diets exhibited significantly higher total red blood cell and total white blood cell counts, as well as increased proportions of lymphocytes, monocytes, neutrophils, and thrombocytes compared with the control group ($p < 0.05$). In addition, innate immune responses, including lysozyme activity, macrophage phagocytic activity, and complement activity, were significantly elevated in the supplemented treatments relative to the control. The 1% *T. orientalis* extract treatment showed the highest enhancement of immune parameters ($p < 0.05$). Following *E. ictaluri* challenge, cumulative mortality was significantly lower in fish fed diets supplemented with 0.5% and 1% *T. orientalis* extract compared with the control group ($p < 0.05$). Overall, these findings demonstrate that dietary *T. orientalis* extract effectively enhances innate immune responses and improves resistance against *E. ictaluri* infection in striped catfish, highlighting its potential as a functional immunostimulant in striped catfish industrial culture.

# P05-Improving pikeperch (*S. lucioperca*) farming in ras trough polyculture with european catfish (*S. glanis*)

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This study is part of the POLYRAS project (Interreg GR), which aims to optimize the sustainable production of locally important fish species through polyculture in recirculating aquaculture systems (RAS). Polyculture may enhance feed efficiency, increase production, reduce labour and support animal welfare (Thomas et al., 2020). This study evaluates, in RAS, whether co-culturing pikeperch (*Sander lucioperca*) with European catfish (*Silurus glanis*) could maintain or enhance the growth of both pikeperch and catfish, reduce feed waste, and support species welfare. Results on growth performance are presented in this poster, while feed utilization and fish welfare will be addressed in future work. The experiment took place over a period of 174 days in a RAS with seven 1 $m^3$ tanks at 23°C under a 12 L:12D photoperiod. Three conditions were evaluated: pikeperch monoculture, European catfish monoculture, and pikeperch – catfish polyculture (ratio 1:1). The initial stocking density was 8 $kg.m^{-3}$. Initial mean body weights were 167g for pikeperch and 182g for catfish. Pikeperch were fed with floating pellets to satiation, while catfish received sinking pellets at a restricted rate of 1.5% of biomass. Growth was monitored monthly by individually weighing 20 fish per species and tank, and total biomass was assessed at the start, mid-point, and end of the experiment. Survival rates were up to 95% for all batches. Final mean body weights were similar between mono- and polyculture for pikeperch (respectively 612 ± 152g ; CV=24.1% and 602 ± 145g ; CV= 23.8%) and catfish (respectively 1186 ± 303g ; CV = 25.1% and 1218 ± 335g ; CV = 27.1%) with no significant differences ($P > 0.05$). Specific growth rates (SGR) were similar between mono- and polyculture for pikeperch (respectively 0.71 and 0.72) and catfish (respectively 1.05 and 1.08). Food conversion ratio (FCR) in polyculture (0.87) was intermediate between those observed in pikeperch monocultures (1.01) and catfish monoculture (0.82). Period-specific SGR analysis highlighted higher growth in polyculture under specific conditions. Our results indicate that pikeperch–catfish polyculture in RAS can sustain favorable growth performance without compromising survival of both species. Based on our observations, we suggest that the performance of this polyculture may be enhanced through implementation of cohort management and increased initial stocking density.

## References

M. Thomas *et al.,* Aquac. Rep. **17**, 100333 (2020).

# P06-DNA reprogramming in early development and its alterations under salinity and selection programme in striped catfish (Pangasianodon hypophthalmus)

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Striped catfish (*Pangasianodon hypophthalmus*) is a freshwater species intensively farmed in Vietnam and other Southeast Asian countries, where salinity intrusion associated with climate change is increasingly affecting aquaculture systems. This study investigated DNA methylation reprogramming during early development of striped catfish under freshwater conditions and evaluated the impact of salinity exposure and selective breeding on this process. Global CpG methylation levels increased markedly from fertilization to early blastula stages, indicating dynamic epigenetic reprogramming. The expression of key epigenetic regulators, including *dnmt1, dnmt3, mecp2, and tet3*, showed significant stage-specific variations during early development. In addition, exposure to salinity of 2.5 psu significantly enhanced dnmt gene expression in 6 dph larvae. Furthermore, offspring derived from a salinity-tolerant selection program exhibited moderate changes in the expression of *dnmt1, gh1, and igf1*. These findings demonstrate that DNA reprogramming in striped catfish is highly dynamic and responsive to salinity conditions, suggesting an important role of epigenetic mechanisms in early development and adaptation to brackish water environments.

### References

Fellous A., *et al.*, Ecol Evol **8**:6016 (2018).
Zhou M., *et al.* J Fish Biol **99**:1755 (2021).

# P07-Dietary supplementation of guava (*Psidium guajava*) leaf extract modulates hematological, digestive, antioxidant, and immune parameters in asian swamp eel (*Monopterus albus*)

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The inclusion of herbal extracts in aquaculture feeds has been shown to exert diverse effects on the performance of aquatic animals, including improvements in growth as well as the stimulation of hematological, digestive, and immune functions. This study performed feeding trials to determine the efficacy of guava *(Psidium guajava)* leaf extract (GE) on the hematological (RBC count, hemoglobin level, hematocrit), digestive enzyme (amylase, pepsin, trypsin), antioxidant (catalase, lipid peroxidation) and immune responses (WBC count, lysozyme activity) of Asian swamp eel *(Monopterus albus)*. Eels were fed in quadruplicate with experimental diets containing 0%, 0.25%, 0.5%, 1%, 1.5% and 2% GE. The study lasted for four weeks under optimal conditions. Biological samples were collected at weekly intervals throughout the study duration to determine the most effective concentrations.

Under optimal conditions, significant improvements in key physiological parameters were observed in eels fed diets containing 0.25% and 0.5% GE. Hematological data indicated enhanced responses in eels fed with 0.25% GE diet, with significantly higher RBC counts at day 28 and hemoglobin concentrations at day 21 compared to all treatments. Hematocrit values were also higher in day 21 relative to other GE, though not significantly different from control. Digestive enzyme activities generally increased over time and were consistently higher in GE supplemented groups compared to control group. The 0.5% GE diet stimulated significantly higher pepsin activity, while 0.25% GE diet increased intestinal amylase and trypsin at day 28, suggesting better digestive efficiency. Antioxidant capacity was improved in 0.5% GE fed eels, with significantly elevated hepatic catalase compared to the control. Muscle catalase also showed minimal increase but was not statistically significant. In addition, the 0.5% GE diet slightly reduced lipid peroxidation in both liver and muscle. Lastly, the 0.25% GE diet exhibited significantly higher WBC counts compared to other treatments, while the 0.5% GE diet showed elevated lysozyme activity relative to 0%, 1.5%, and 2% GE groups, indicating enhanced non-specific immune responses. The results highlight the potential of guava leaf extract as a natural feed additive in Asian swamp eel aquaculture.

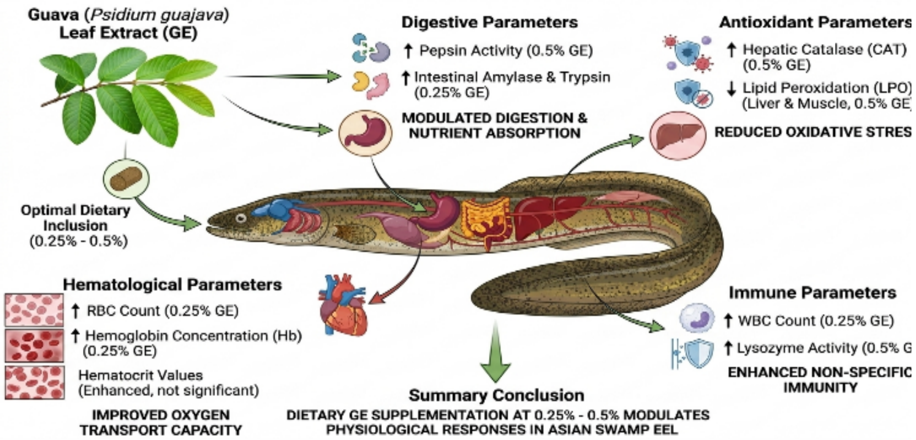

***Figure 1.*** *Schematic overview of the modulating effects of Psidium guajava leaf extract (GE) on physiological and immune parameters in Monopterus albus*

# P08-Performance evaluation of hatchery-origin fish in the Laurentian Great Lakes basin

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Fish reared in artificial environments (i.e., hatcheries) often develop behaviors best suited to those specific conditions. These behaviors can be retained after fish are stocked into natural systems, which can reduce performance compared to natural-origin (i.e., wild) conspecifics (Blouin *et al.*, 2021). Such adaptations to hatchery environments have been identified as potential impediments to fisheries management strategies aimed at supplementing and rehabilitating self-sustaining populations (Claussen & Philipp, 2023). Despite these concerns, stocking practices remain common and have been extensively implemented in the Laurentian Great Lakes (hereafter, the Great Lakes) where they have reestablished extirpated populations of native fishes and have been maintained to support those species (e.g., Dunlop et al., 2018). We evaluated the physiological performance of cisco *Coregonus artedi* and lake trout *Salvelinus namaycush*, two native species in the Great Lakes region, based on two diet-based parameters: lipid content and fatty acid profiles. Egg samples were obtained from hatchery-origin and wild cisco that were collected from the Jordan River National Fish Hatchery and Lake Huron, respectively. Ventral muscle samples were obtained from lake trout that were collected from Lake Champlain with hatchery-origin fish distinguished from wild conspecifics by a hatchery mark (i.e., fin clip). Percent total lipids were determined for all samples and percent contributions of approximately 25 fatty acids were quantified in neutral lipids and phospholipids for egg samples, and in total lipids for muscle samples. Cisco eggs had comparable lipid content between wild and hatchery-origin fish (10.2% vs 10.0%, respectively). Fatty acid profiles, however, differed significantly between the two groups for both neutral lipids and phospholipids, primarily driven by greater contributions of docosahexaenoic acid (DHA) in eggs of hatchery fish, while eicosapentaenoic acid (EPA) and arachidonic acid (AA) were higher in eggs of wild individuals. In contrast to the trends observed for cisco, wild lake trout in Lake Champlain had significantly greater lipid content than hatchery-origin fish, but fatty acid composition was largely similar between the two groups. However, variability among individual fish fatty acid profiles was greater among hatchery-origin lake trout compared to wild fish. Together, these results demonstrate that hatchery rearing can influence fish physiology by altering fatty acid profiles as shown with the hatchery cisco and can continue to impact fish behavior and performance years after stocking demonstrated by lower lipid content and potentially more generalized foraging by hatchery-reared lake trout.

## References

M. Blouin *et al.*, Plos One **16**, e0257407 (2021).
J. Claussen & D. Philipp., Fish. Manage. Ecol. **30**, 583 (2023).
E. Dunlop *et al.*, J Great Lakes Res. **44**, 735 (2018).

# P09-Immunological responses, hematological parameters and plasma enzymes activity of Siberian sturgeon (*Acipenser baerii*) fed dietary flaxseed meal

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Flaxseed is the richest source of polyunsaturated fatty acids and lignans making it an important phytoestrogen. In this study, the effects of dietary flaxseed meal (FSM) on immunological responses and physiological changes in Siberian sturgeon Acipenser baerii, were evaluated. Thirty two farmed fish (955.06 ± 53.38 g) were randomly distributed into 8 tanks (500 L) and fed diets with different levels of FSM including 0 (control), 5% (F5), 10% (F10), and 15% (F15) of diet for 180 days. Growth performance, plasma enzyme activity, hematological and immunological indices were determined at the end of the experiment. The results showed that growth indices did not change significantly after feeding with FSM ($P > 0.05$). The lowest alkaline phosphatase, aspartate aminotransferase and alanine aminotransferase activities were found in the F10 and F15 treatments ($P < 0.05$). The highest and lowest lactate dehydrogenase activity were found in the control and F15 groups, respectively ($P < 0.05$). The number of red blood cells, hematocrit, and number of white blood cells increased, while lymphocyte and neutrophil counts decreased in the F15 group ($P < 0.05$). Lysozyme activity was highest in the F10 group and lowest in the control ($P < 0.05$). Moreover, the complement C3 and C4 significantly increased in the F15 group compared to the other treatments ($P < 0.05$). Immunoglobulin M levels showed a significant increase in all FSM treatments compared to the control diet ($P < 0.05$). These results suggest that dietary FSM may affect physiological parameters and increase key innate immunological indices in Siberian sturgeon.

## References

Ghiasi, S. et al., Anim. Feed Sci. Technol. 295, 115546 (2023).
Staykov, Y. et al., J. Agric. Sci. 211, 169 (2015).
Wiesenfeld, P.W. et al., Food Chem. Toxicol. 416, 841 (2003).

# P10-Complete replacement of fish meal by black soldier fly meal in Nile tilapia juvenile’s diet: effect on growth performances and feed efficiency

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Four experimental diets were formulated to be isonitrogenous (46.4 to 52.7% crude protein) and isoenergetic (16.2 to 16.5 kJ $g^{-1}$) to test three experimental diets in which 33.3, 66.6 and 100% of fish meal (FM) was replaced with black soldier fly (*Hermetia illucens, L.)* larvae meal (BSF1, BSF2, BSF3) *versus* a control diet (FM) containing 180 g FM/kg for feeding Nile tilapia (*Oreochromis niloticus*) juveniles (11.8±0.2g).

The fish fed with the BSF diets had significantly ($P>0.05$) higher final growth performances than the fish fed the FM diet. The Apparent Digestibility Coefficient (ADC) of crude protein, Feed Conversion Ratio (FCR), Hepatosomatic Index (HSI) as well as muscle protein and lipid composition of fish muscles were not significantly different whatever the diet.

BSF meal is a good source of protein and lipids for Nile tilapia juveniles and could successfully replace FM up to 100% in their diets with improved growth performances.

## References

Azaza MS et al., Aquac. **287**:174 (2009).
Fontes TV et al., Animals **9** (4):181 (2019).
Henry, M. et al., An. Feed Sci. Technol. **203**:1 (2015).

# P11-Comparative assessment of acute toxicity and histological changes in liver of African catfish *Clarias gariepinus* exposed to cotton insecticides

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This study investigated the acute toxicity in *Clarias gariepinus* to insecticides currently used in Benin cotton fields, including Thalis 112 EC (Emamectin benzoate 48 g $L^{-1}$, Acetamiprid 64 g $L^{-1}$), Vizir C 92 EC (Cypermethrin 72 g $L^{-1}$, Abamectin 20 g $L^{-1}$), Pyrinex Quick 212 EC (Deltamethrin 12 g $L^{-1}$, Chlorpyrifos 200 g $L^{-1}$) and Pyro FTE 472 EC (Cypermethrin 72 g $L^{-1}$, Chlorpyrifos 400 g $L^{-1}$) with emphasis on liver histopathological effects. A set of 180 juveniles of *C. gariepinus* (5.21 ± 3.22 g) was exposed for 96 h to increasing concentrations of each pesticide. The values of 96-hLC50 were 4.778, 0.002, 0.004, and 0.012 mL $L^{-1}$ for Thalis, Vizir, Pyrinex, and Pyro, respectively, indicating that Vizir, Pyrinex, and Pyro were very highly toxic to *C. gariepinus* juveniles. During the experiments, the morphological and behavioral responses (discoloration, hyperactivity, lethargy, etc.) were observed in exposed fish, hypothesizing the neurotoxicity of these pesticides. Histopathological alterations observed in liver of contaminated fish were regressive changes, such as necrosis, vacuolation, bleeding, nuclear degeneration, hepatocytes degeneration, sinusoids dilatation, etc. Vizir induced the highest histological alteration indices while the lowest were induced by Thalis, confirming the highest toxicity of Vizir. These results indicate that acute concentrations of these insecticidal molecules have destructive effects on the liver of *C. gariepinus*.

Keywords: Toxicity; pesticides; bioassay; African catfish; behavioral responses; liver histological changes.

## References

Agbohessi, P. *et al*., J. Environ. Sci. Health B, **58**, 31-44 (2023).
Guedegba, N. L. *et al*. J. Environ. Sci. Health B, **54**, 580–589 (2019).
Douny, C. *et al*. Arch. Environ. Contam. Toxicol. **81**, 367–385 (2021).

# P12-Evaluation of acute toxicity and histology effect on liver of glyphosate and atrazine in the African catfish *Clarias gariepinus* (Burchell 1822)

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Aquatic organisms are exposed to chemical pesticides including glyphosate (Sharp 480 SL) and atrazine (Atraforce), two phytocidal molecules used for agriculture purposes in Benin. In this study, we assessed the acute toxicity of these two herbicides with emphasis on their histopathological effects on the liver of catfish *Clarias gariepinus*. One hundred and eighty juveniles of *C. gariepinus* (mean length 7.26 ± 0.59 cm and mean weight 5.21 ± 3.22 g) were exposed over 96 h to increasing concentrations of each phytocide. The values of 96 h-LC50 were 6.175 x $10^3$ and 3.165 ppm, respectively for Sharp 480 SL and Atraforce. This indicates that Sharp 480 SL was nontoxic, while Atraforce displayed a moderate toxicity to *C. gariepinus* juveniles. During the tests, the behavioral responses (hyperexcitation, lethargy, loss of balance, discoloration of skin, etc.) that usually precede death were observed in exposed fishes, confirming the neurotoxicity of these phytocides. Histological alterations observed in liver of contaminated fishes were regressive changes, such as necrosis, hepatocyte vacuolation, nuclear degeneration, hepatocytes degeneration, sinusoids dilatation, etc. These results indicate that exposure to these herbicides had destructive effects on the liver of *C. gariepinus*.

KEYWORDS: Toxicity; herbicides; bioassay; *Clarias gariepinus*; behavioral responses; liver histological; mortality.

## References

Agbohessi P. *et al*. J. Environ. Sci. Health B, **58**, 21-30 (2023)
Guedegba, N. L. *et al*. J. Environ. Sci. Health B, **54**, 580–589 (2019)
Douny, C. *et al*. Arch. Environ. Contam. Toxicol, **81**, 367–385 (2021)

# P13-Effects of herbal extract-supplemented diets on growth, immunity and resistance to streptococcus agalactiae in nile tilapia (*Oreochromis niloticus)*

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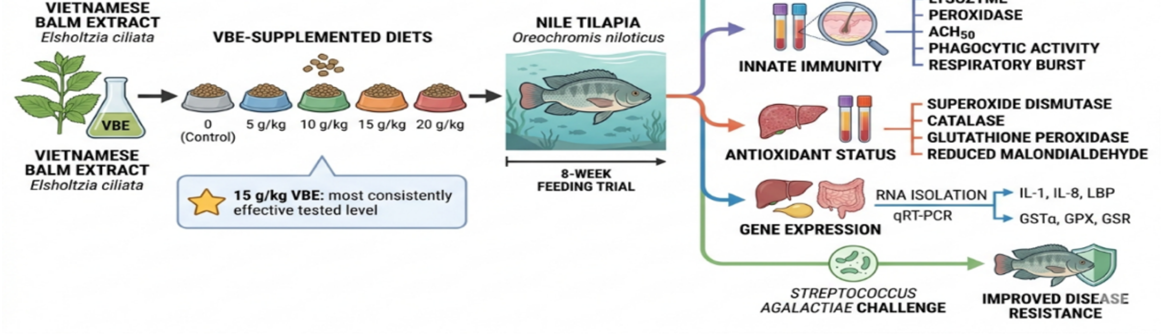
This study evaluated the effects of dietary Vietnamese balm extract (VBE) on growth performance, feed utilization, innate immunity, antioxidant status, disease resistance, and immune- and antioxidant-related gene expression in Nile tilapia. Fish with an initial body weight of 14.81 ± 0.03 g were stocked at 20 fish per tank and fed diets supplemented with 0, 5, 10, 15, and 20 g/kg VBE for 8 weeks. Dietary VBE improved final body weight, weight gain, specific growth rate, and feed conversion ratio, particularly at 10 and 15 g/kg, without markedly affecting somatic indices. Innate immune responses in skin mucus and serum, including lysozyme, peroxidase, alternative complement, phagocytic, and respiratory burst activities, were enhanced in VBE-fed fish, with the most consistent responses observed at 15 g/kg. Antioxidant status was also improved, as indicated by increased superoxide dismutase, catalase, and glutathione peroxidase activities, together with reduced malondialdehyde levels in serum and liver. Dietary VBE further modulated the expression of immune-related genes (*IL-1*, *IL-8*, and *LBP*) and antioxidant-related genes (*GSTα*, *GPX*, and *GSR*) in both liver and intestine. In addition, VBE improved resistance to *Streptococcus agalactiae* infection. Overall, 15 g/kg VBE was the most consistently effective tested level, suggesting its potential as a natural feed additive for improving health and disease resistance in Nile tilapia.

## References

F. Dadras et al., Vet. Med. (Praha) 68, 449 (2023).
L. Pudziuvelyte et al., Molecules 25, 1153 (2020).
D.T.T. Phuong et al., J. Ilm. Perikan. Kelaut. 16, 399 (2024).



# P14-Specific stressors induce differential immuno-physiological responses in fish mucosae

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Main mucosal tissues, (gills, skin, and gut) constitute an interface between the environment and the organism so they play a central role in the early detection of stressors and in orchestrating endocrine, physiological and immunological modulation. Different types of stressors, such as salinity, nanoplastic exposure, hypoxia, and crowding, and the duration and / or the intensity of them can produce different stress response outcomes. For the present study, the selected species was the gilthead seabream (Sparus aurata) that was subjected to two chronic stressors: salinity, nanoplastics (NPs), and two acute stressors, acute crowding and anoxia. Mucosal response was assessed by analysing the expression of relevant endocrine and immune genes in mucosal barriers (skin, gills, and intestine), as well as haematological and biochemical parameters in plasma. The results showed that gills and skin were more heavily affected by exposure to salinity and PSNPs alone respectively, and in both cases the combination of both challenges had a major impact compared with individual stressors. Similarly, significant haematological [white blood cell (WBC) and platelet (PLT) count] and biochemical [adenosine deaminase (ADA)] alterations occurred upon exposure to both stressors combined. Overall, different stressors tested produced distinct levels of upregulation of glucocorticoid receptors, demonstrating that the endocrine sensitivity of fish varies depending on the nature and intensity of the challenge. Similarly, the immune response varied across treatments, with each stressor eliciting a characteristic pattern of mucosal activation. Importantly, results showed that each mucosal tissue exhibits a specific response profile, indicating a tissue dependent modulation of both endocrine and immune pathways. The intensity of these responses was closely related to the type of stressor applied, highlighting the importance of mucosal differences and considering stressor specific impacts when assessing fish welfare. This work was supported by PID2020-117557RB-C21 and PID2023-149326OB-C21 (Agencia Estatal de Investigación, Ministerio de Ciencia, Innovación y Universidades, Spain).

## References

Ruiz et al., Frontiers in Endocrinol. Vol. 17 In Press (2026).

# P15-Evaluating Thiamine Treatment Schedules to Improve Hatchery Steelhead Trout Egg Viability

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Thiamine Deficiency Complex (TDC) affects salmonine species globally, causing recruitment failure (Balk et al. 2016). Thiamine deficiency is often diet-induced, stemming from females feeding on low-quality prey that are low in thiamine, rich in polyunsaturated fatty acids, and high thiaminase activity (Futia et al. 2019). Therefore, females allocate less thiamine to their eggs prior to spawning, resulting in high offspring mortality. For stocks supported by hatchery supplementation, a common mitigation practice is to immerse fertilized eggs in a thiamine bath for two hours post-fertilization. However, thiamine baths are not practical in all hatchery systems, particularly those unable to hold eggs in treatment baths for the full duration due to elevated water temperatures or operational constraints (e.g., California hatcheries). In this study, we aimed to identify an optimal thiamine treatment schedule that improves offspring survival while remaining compatible with hatchery conditions. Steelhead trout eggs were collected at the Salmon River Fish Hatchery (Altmar, NY) during the spawning period in March 2025. Eggs were submersed in a thiamine bath (1000 ppm thiamine mononitrate) for varying durations: 30 seconds, 1 minute, 1 hour, and 2 hours, beginning at fertilization. A standard treatment group (2 hours initiated post-fertilization) and an untreated control group were also included for comparison. Eggs were sampled at multiple development stages (48 h post-fertilization, eyed stage, hatching, and after yolk resorption) for thiamine analysis using high-performance liquid chromatography (Brown et al. 1998, Futia et al. 2019). Results indicated that a 2-hour treatment, initiated either at fertilization or post-fertilization, was the most effective to increase egg thiamine concentrations. Thiamine concentrations declined across developmental stages in most experimental groups, highlighting the high demand for thiamine during early life. These findings suggest that hatcheries unable to maintain appropriate conditions (e.g. water temperature) during a 2-hour egg thiamine bath should consider alternative strategies, such as thiamine injections of females prior to spawning, to improve offspring survival.

## References

L. Balk *et al.*, Sci. Rep. **6**, 38821 (2016).
S.B. Brown *et al.*, Am. Fish. Soc. **21**, 73 (1998).
M. Futia *et al.*, J. Great Lakes Res. **45**, 934 (2019).

# P16-Chronic MDMA exposure modulates physiological and behavioural responses during early development in zebrafish

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Psychoactive substances (PAS) are increasingly detected in aquatic environments due to widespread human use and incomplete removal in wastewater treatment systems (Zhang et al., 2024). Many of these compounds are neuroactive at low concentrations and may affect aquatic organisms under chronic exposure. Prolonged exposure to PAS has been shown to alter gene expression related to neurodevelopment and stress pathways (Subedi et al., 2021). Among them, 3,4-methylenedioxymethamphetamine (MDMA) is frequently detected in European surface waters at nanomolar levels (Muñiz-Bustamante et al., 2022), yet its effects during early vertebrate development remain poorly understood.

This study used zebrafish (Danio rerio) to assess the developmental and behavioural effects of chronic MDMA exposure from fertilisation to 32 days post-fertilisation at 0.1 nM (environmentally relevant) and 100 nM concentrations. Developmental endpoints included hatching success, survival, cardiac function, and growth, while behavioural analyses focused on habituation, locomotion, and social interaction using automated tracking.

MDMA exposure significantly reduced hatching success and altered cardiac function, indicating sensitivity during early development, while survival, growth, and morphology were unaffected. Behavioural responses showed subtle, phase-specific changes consistent with altered sensorimotor plasticity, without affecting social behaviour.

Overall, chronic MDMA exposure at environmentally relevant concentrations induces subtle developmental and behavioural effects without overt toxicity. These findings, together with evidence of PAS-induced gene expression changes (Subedi et al., 2021), suggest early neurofunctional disruption and support the use of behavioural endpoints as sensitive indicators in environmental risk assessment.

## References

Zhang *et al.*, Water Research, 263, 122165. (2024).
Subedi *et al.*, Environmental Pollution, 278, 116777. - 92 (2021).
Muñiz-Bustamante *et al.*, Environment international, 164, 107281. (2022).

# P17-Applied feed formulation and fish model testing as a service for Aquaculture

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At TRANSfarm, we offer a flexible in-house feed development and testing platform that enables rapid formulation and evaluation of custom animal feeds for aquaculture applications. Using our food kitchen facilities, we can produce experimental feeds with tailored compositions, including alternative protein sources, functional additives, and novel ingredients, as well as modified versions of standard commercial feeds. These feeds are subsequently evaluated in useful fish models, including rainbow trout (*Oncorhynchus mykiss*) and killifish (*Nothobranchius furzeri*), allowing controlled assessment of growth performance, feed efficiency, health parameters, and product quality traits.

This platform enables aquaculture companies and ingredient suppliers to conduct cost-effective service trials to screen new formulations, optimize ingredient inclusion levels, and generate independent performance data prior to large-scale commercial testing. By combining rapid prototyping of feeds with biologically relevant fish models, we provide industry partners with a practical tool to de-risk innovation, accelerate product development, and support evidence-based decision making.

This poster will highlight the capabilities of the platform, example application areas, and opportunities for collaboration with feed producers, ingredient suppliers, and aquaculture operations seeking tailored service trials and applied research support.

# P18-Growth performance of common carp (*Cyprinus carpio*) along an altitudinal gradient in Rwanda

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A 120-day experiment was conducted to assess the growth performance of common carp cultured in three agro-climatic zones of different altitudes (low, middle, and high) in Rwanda. Juveniles with an average body weight of 30.4 ± 2.30 g and length of 14.4 ± 1.34 cm were randomly stocked at a density of 200 fish per 100 m² pond at each experimental site. Growth indicators, including total weight gain (TWG), daily weight gain (DWG), relative growth rate (RGR), specific growth rate (SGR), and condition factor (Km), were evaluated and analyzed using one-way analysis of variance (ANOVA). Fish reared in the low-altitude zone exhibited significantly higher TWG, DWG, RGR, and SGR ($p < 0.05$) compared with those cultured in the middle- and high-altitude zones. DWG ranged from 1.16 ± 0.03 to 1.62 ± 0.02 g/day, while SGR ranged from 1.43 ± 0.02 to 1.66 ± 0.05 %/day across the three sites. Despite these differences, satisfactory growth performance was recorded in all zones, demonstrating the adaptability and culture potential of common carp across diverse agro-climatic conditions in Rwanda.

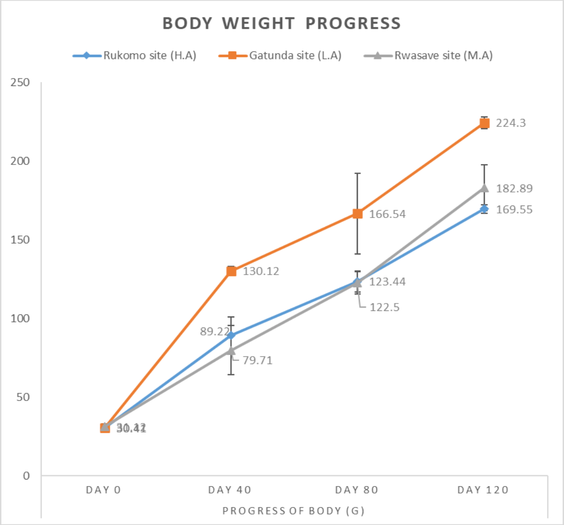

Fig.1. Body weight progress of carp fishes for 120-day study period in the conditions of three agro-climatic zones of Rwanda (H.A: High Altitude, L.A: Low Altitude, M.A: Middle Altitude)

## References

Majid M. T. *et al.* Basrah Journal of Agricultural Sciences. 40 (2018)
Mugo B.J., *et al.*Global Journal of Advanced Research, 263 (2018).
Ondhoro, *et al.*. Journal of Applied Sciences, 23 (2023).

# P19-Evaluation of the effect of preventive and therapeutic agents on biofilter efficiency in small-scale Recirculating Aquaculture Systems (RAS)

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This study systematically evaluated the impact of selected chemical substances [sodium chloride (NaCl), tosylchloramide sodium (TC), peracetic acid (PAA), and hydrogen peroxide ($H_2O_2$)] on the nitrification process in small-scale, controlled biofilter systems. Each consisted of 8 L jars containing 2 L of biocarriers extracted from a biofilter in operation for over a year, along with aeration stones. To simulate fish culture conditions, $NH_4Cl$ was added twice during the 8-hour test to mimic fish waste input. Temporal profiles of ammonium ($NH_4^+$) and nitrite ($NO_2^-$) concentrations were monitored in triplicate, including a negative control (without any substance) and a positive control (without nitrifying microbiota) for each chemical tested. All substances delayed the nitrification process, measured as the time required for $NH_4^+$ and $NO_2^-$ to return to pre-exposure levels, with $H_2O_2$ exerting the most pronounced inhibitory effect. Statistical analyses revealed that the temporal profiles of PAA and $H_2O_2$ differed significantly from the negative control. These findings advance understanding of microbial resilience and vulnerability under commonly used chemical treatments in Recirculating Aquaculture Systems (RAS), with practical implications for system management and optimization. Furthermore, the study proposes a safe methodology for evaluating the effects of chemical substances prior to their application in operational RAS.

## References

Bartelme, R. P., McLellan, S. L., Newton, R. J. Front Microbiol. 30 (2017)
Fredricks, K. T., Schleis, S. M., Smerud, J. R., Gaikowski, M. P., Erickson, R. A., Hebert, J., Fisher, G. J., Holmes, K., Hartleb, C. *Aquac Res.* 53(1),1 (2022).
Qi, W., Skov, P. V., de Jesus Gregersen, K. J., Mousavi, S., Pedersen, L. F., Mota, V. C. *Aquaculture.* (2025)

# P20-Oocyte maturation in European eel: Comparing boosting treatments with gonadotropin releasing hormone-agonist loaded implants combined with eticlopride injection, and with human chorionic gonadotropin, vs. carp pituitary extract

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After a 3 to 6-month period of weekly injections with carp pituitary extract (CPE) to complete vitellogenesis in eels, oocyte maturation is usually boosted with an extra CPE injection, if the oocyte hydration response results in an increase in body weight index (BWI) of more than 10%, and oocytes show germinal vesicle migration. If this boosting results in further BWI increase reaching more than 20% with oocytes showing germinal vesicles in a peripheral position, an injection of 17α,20β-dihydroxy-4-pregnen-3-one (DHP) is used to induce further oocyte maturation, ovulation and egg release after 10 to 12 hours. As CPE has a short half-life and contains several hormones, in the present study the efficacy of different pure hormone treatments was examined on the oocyte maturation and ovulation response. Thirty migratory silver eels were pretreated, first with hCG injection, then with a 17β-estradiol implant, and were subsequently treated weekly with CPE injections to induce vitellogenesis. At the moment of boosting oocyte maturation, the females were assigned to one of the three experimental groups (n=10) including (a) CPE as a positive control, (b) slow-release implants loaded with gonadotropin releasing hormone-agonist (GnRHa) combined with eticlopride injection as dopamine antagonist (GnRHa+E), which act upstream in the reproductive axis on the pituitary, and (c) human chorionic gonadotropin (hCG) as a luteinizing hormone (LH) analogue with longer half-life. All females matured fully, but one died before egg release. Twenty-one females gave larvae (6 of the CPE treatment, 7 of the hCG treatment and 8 of the GnRHa+E treatment), up to 12,000 larvae per batch, that stayed alive up to 17 days. The females in the GnRHa+E group took longer to reach the right status for DHP injection than eels of the hCG and CPE groups indicating the slow release of GnRHa. Eels in the GnRHa+E and hCG groups had higher egg weights than eels in the CPE group reflecting a more significant absorption response and possible higher egg quality. This was further supported by a larger number of females giving high larvae yield in the GnRHa+E group. Our results suggest that the GnRHa+E treatment represents a promising improvement to induce oocyte maturation in eels.

# P21-Effect of vaccination on growth performance and feed efficiency of Atlantic salmon (*Salmo salar*)

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Fish diseases are considered a persistent threat to aquaculture and one of the major reasons for limiting the expansion of the aquaculture industry worldwide. In this context, vaccination is the most effective solution, since it is the most efficient tool for disease prevention. The majority of aquaculture vaccines are administered via injection, which can be either intraperitoneal (IP) or intramuscular (IM). IP injections have been shown to provide the most effective and long-lasting immunity when compared to other methods. However, IP vaccination has been associated with some side effects, including reduced growth, abdominal adhesions, and vertebral deformities. A vaccination trial was conducted on Atlantic salmon (*Salmo salar*) to evaluate the effect of intraperitoneal (IP) injection on growth performance, feed utilization, and survival rate. Atlantic salmon in the freshwater phase, weighing 34.43 ± 0.81 g, were separated into two groups with two replicates each (N= 182 fish/replicate). One group was vaccinated against *Aeromonas. salmonicida* ssp. *salmonicida* (ALPHA JECT® 3000, Pharmaq, Norway) and the other remained unvaccinated. The fish were grown to an average weight of 90.25 ± 3.13 g before transferring them to seawater. Once in seawater, fish were fed for 81 days with a commercial standard diet for this fish species and challenged against *Aeromonas. salmonicida* ssp*. Salmonicida*. After the 81 days of feeding, growth performance data such as body weight, standard length, and fork length showed higher values ($p < 0.05$) for unvaccinated fish. However, there were no significant differences in K factor ($p > 0.05$). Regarding feed efficiency parameters, non-vaccinated fish showed significantly higher biomass gain and feed intake, and consequently a significantly lower FCR ($p < 0.05$). After the challenge test, as expected, higher survival rates were observed in vaccinated fish. The results indicate that vaccination had negative effects on fish growth and feed efficiency, while provided protection against *Aeromonas. salmonicida* ssp. *salmonicida*. These results suggest that the vaccination process influences fish metabolism and performance, likely due to the energy requirements associated with the immune response.

# P22-Thermal acclimation and heritable differences in ion and water transport pathways in the intestine of European sea bass (*Dicentrarchus labrax*) lineages.

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The European Sea bass, *Dicentrarchus labrax*, a major species for aquaculture, is found along the Atlantic coast, the Mediterranean Sea and the Black Sea, where a strong thermal gradient occurs along this transect. Distinct *D. labrax* genetic lineages have been characterized previously in the Atlantic and Mediterranean region [1]. They have evolved under different environmental conditions, potentially resulting in local adaptation and/or in distinct plastic responses to temperature [2]. In seawater, teleosts are exposed to a continuous dehydration which requires intestinal water uptake following active ion uptake ($Na^+$ and $Cl^-$ mainly) [3]. However, the molecular mechanisms underlying solute-coupled water uptake in response to long-term temperature exposure remain largely unexplored. Whereas intestinal water absorption has been investigated mainly via the transcellular routes involving ion transporters and water channels, much less studies have focused on the paracellular route involving junctional complexes. We investigated ion uptake mechanisms in Atlantic and East Mediterranean *D. labrax* following a two-year acclimation to three thermal regimes reflecting the natural habitats of the species. We used a common garden experiment to investigate acclimation as well as heritable differences in gene expression between lineages. Overall, we observed a similar acclimatory response in both lineages with downregulated gene expression related to solute-coupled transcellular water uptake. In contrast, the vha pump shows an inverse gene expression pattern. Interestingly, we revealed lineage-specific differences, mainly in the warmest regime, where the East Mediterranean lineage favours transcellular water uptake (*aqp8ab*) within a leaky epithelium (pore-forming claudins 2 and 15a) whereas the Atlantic lineage overexpresses barrier-forming claudins (3d, 7b) that promote epithelial tightening. Increased water uptake capacity in the Mediterranean lineage could be a strategy to face warmer and more saltier environments. This study highlights physiological diversity as a key factor in shaping fish resilience to ongoing global warming.

## References

[1] Duranton et al., Nat Commun **9**, 2518 (2018).
[2] Jensen et al., Proc Biol Sci **275**, 2859 (2008).
[3] Grosell et al., J Exp Biol **209**, 2813 (2006).

# P23-Effect of autochthonous yeast administration on digestive functionality and survival of cobia (*Rachycentron canadum*) larvae

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The use of host-derived probiotic yeasts is a promising strategy to enhance larval performance, but their effects during and after supplementation remain poorly understood. This study evaluated three autochthonous yeast strains: *Candida haemuloni* C27, *Debaryomyces hansenii* C10, and *D. hansenii* C28, isolated from cobia (*Rachycentron canadum*) (Reinoso et al., 2023). A well-known strain, *D. hansenii* CBS8339 (isolated from rainbow trout) (Tovar-Ramírez et al., 2004), was included for comparison. Their effects on growth, survival, digestive functionality, and immune response of cobia larvae were evaluated. Prior to the nutritional trial, yeast biomass production, viability after stocking, and the enrichment protocol for live food were optimized to ensure the delivery of high numbers of viable yeast cells to the digestive tract of live prey (Figure 1).

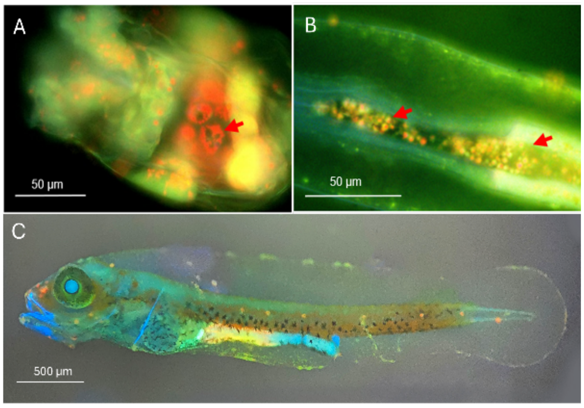

**Figure 1.** Fluorescence microscopy of yeast cells stained with acridine orange in the digestive tracts of (A) rotifer, (B) Artemia, and (C) cobia larvae.

Larvae were fed for 14 days (2–15 days post-hatch, dph) with rotifers and *Artemia* metanauplii enriched with each yeast strain. A total of 75,000 larvae (2 dph; ~3 mm) were randomly distributed into 15 tanks, with three replicates per treatment: three groups received autochthonous yeasts, one group received *D. hansenii* CBS8339, and a control group received non-enriched live food.

All strains except *D. hansenii* C10 remained viable in the larval gut until 24 dph (9 days after the last supplementation). During supplementation, larvae fed *C. haemuloni* C27 and *D. hansenii* CBS8339 showed higher acid protease activity. After supplementation, *D. hansenii* C28 enhanced the activity of eight of nine digestive enzymes analyzed, while all yeast-fed groups showed increased α-amylase and lipase activity. In addition, *C. haemuloni* C27 upregulated *il-1β* and *tnf-α* expression. Survival was higher in larvae supplemented with *C. haemuloni* C27 and *D. hansenii* C28 (~31%) compared with the control (~22%). No differences in growth or intestinal histology were detected among treatments. These findings indicate that *C. haemuloni* C27 and *D. hansenii* C28 improve survival, digestive functionality, and immune response in cobia larvae, with effects that persist beyond supplementation, likely due to yeast persistence in the digestive tract.

## References

Reinoso, *et al.* (2023).
Tovar-Ramírez *et al.* (2004).

# P24-Optimizing larval sea lamprey culture: effects of diet composition and feeding regime on growth and body composition

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The collection of larval, metamorphosing, and juvenile sea lamprey (*Petromyzon marinus*) for Great Lakes Fishery Commission (GLFC)-funded research in the Great Lakes has become increasingly difficult due to effective population suppression through lampricide treatments. This limitation is particularly critical for early life stages and individuals >100 mm total length, which are needed to support emerging research on supplemental control strategies, genetic biocontrol, and next-generation pesticides. To address this challenge, the Sea Lamprey Aquaculture and Procurement Program (SLAP) was established to develop a closed life-cycle culture of sea lamprey, with an initial focus on optimizing larval rearing conditions. Here, we present results from two controlled experiments evaluating the effects of diet composition and feeding frequency and ration on larval growth and body composition, contributing to the development of best practices for sea lamprey culture.

In Experiment 1, larvae (80–99 mm TL) were assigned to four diet treatments (yeast; yeast + Otohime; yeast + fish meal; yeast + wheat flour) under replicated flow-through conditions at two locations: a laboratory facility supplied with Lake Huron water and a mobile rearing trailer supplied with river water. Growth metrics (length and mass) and proximate composition were assessed over a three-month period. Diet composition did not significantly affect larval growth rate or proximate body composition; however, diets exhibited distinct fatty acid profiles, and these signatures were reflected in larval tissues, indicating dietary fatty acid assimilation.

In Experiment 2, larvae were fed a yeast + wheat flour (50:50) diet and assigned to one of four feeding regimes ($3 \times 2.5$ g week$^{-1}$, $3 \times 5$ g week$^{-1}$, $3 \times 7.5$ g week$^{-1}$, and $1 \times 15$ g week$^{-1}$) under the same replicated conditions. Feeding frequency and ration influenced growth, with the lowest ration ($3 \times 2.5$ g week$^{-1}$) resulting in reduced growth, while feeding regimes comprising a larger ration size produced higher growth rates. Feeding frequency also affected fatty acid profiles, but showed no clear effect on proximate body composition.

Overall, these results indicate that while diet composition has limited effects on growth in terms of length and weight, feeding regime and environmental conditions are key drivers of larval performance (e.g., lipid content and fatty acid signatures), providing important guidance for the development of effective sea lamprey culture protocols.

# P25-Growth performance and feeding strategy of common carp reared in biofloc system

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Biofloc technology (BFT) is an alternative aquaculture approach that relies on microbial aggregates to improve water quality and potentially provide a supplementary healthy food source for cultured fish. Usually applied under tropical water temperature (from 25-30°C), the functioning of Biofloc under lower temperature is still unknown. However, the use of this rearing system in continental conditions with lower temperature could really have an important impact on inland aquaculture diversification in Europe. As fish growth, feeding strategies, and Biofloc composition and quality are strongly influenced by temperature, the aim of this study was to evaluate the functioning of Biofloc system in different rearing temperature with common carp (*Cyprinus carpio*) as fish model.

Therefore, we investigated the growth performance and feeding strategy of common carp juvenile reared in BFT across a temperature gradient ranging from 15 to 30°C, and determined the contribution of microbial flocs to fish nutrition using stable isotope analysis.

Juvenile common carp (initial mean body weight: 15 g) were reared for 12 weeks in BFT systems at four temperatures (15, 20, 25 and 30°C) in triplicate. Fish were reared at an initial stocking density of 5 kg $m^{-3}$ and fed with a commercial carp diet, with daily ration adjusted according to rearing temperature and stocking density. A control group was reared in a recirculating aquaculture system (RAS) throughout the experimental period and fed the same commercial diet. Water physico-chemical parameters (temperature, oxygen, pH, conductivity, TAN, alkalinity, nitrate) were daily monitored throughout the experiment. Carp growth was monitored six times during the 12-week experimental period. At the end of the experiment, carbon and nitrogen stable isotope ratios were measured in fish muscle.

Growth performance increased with temperature, with the highest final body weight recorded at 30°C. In contrast, specific growth rate was highest at 15°C (0,90) and lowest at 30°C (1,14). Feed conversion ratio was lowest at 15°C (1,34), indicating the best feed efficiency, whereas the highest FCR was observed at 25°C (2,09). Stable isotope analyses are currently underway and will provide further insight into the relative contribution of biofloc particles to carp nutrition under the different temperature conditions.

Overall, our results show that BFT remained efficient at temperatures lower than those usually reported for this technology (25–30°C), maintaining stable water quality and therefore acting effectively as a biological treatment system. Common carp also exhibited satisfactory growth under all tested conditions, demonstrating their good adaptation to BFT. These findings suggest that BFT could represent a promising diversification strategy for production in continental Europe.

# P26-Modulation of growth, hepatic metabolism, and the somatotropic axis by nutritional status in longfin yellowtail, *Seriola rivoliana*.

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Seriolid fishes are among the most valuable finfish groups for aquaculture development. In Hawai’i, the longfin yellowtail, *Seriola rivoliana*, or kanpachi, is reared in both open-ocean and nearshore aquaculture facilities. However, there are major constraints on increasing captive production, as hatchery-produced offspring generally show poor fecundity and low larval viability. To optimize rearing strategies and characterize nutrient delivery and utilization in this species, first-generation hatchery-bred *S. rivoliana* juveniles were reared for 52 weeks in two nearshore facilities under distinct dietary regimes. The diet treatments consisted of an 8-mm pellet diet (control) and a gelatinized mixture of homogenized fresh seafood and vitamins (gel), which was subsequently transitioned to a whole fresh diet of chopped fish and squid (whole). Weights were recorded monthly for fish at both sites, and feed conversion ratios (FCR) were adjusted for biomass removal and corrected for moisture content. A two-week fasting trial was also conducted on fish fed the pellet diet to identify physiological traits associated with growth performance. Initial analyses of morphometric data indicate a consistent effect of diet at both study sites. Fish fed the gel diet grew more slowly, had higher FCRs, and had a lower hepatosomatic index (HSI) than those fed a commercial pellet diet. Due to their low performance, fish on the gel diet were transitioned to a whole diet. Over the following 6 months, growth rates of fish fed the whole diet were higher than those of fish fed a gel diet and similar to those of pellet-fed controls at each site (Figure 1). Two weeks of fasting did not change body weight, condition factor, or plasma glucose but lowered HSI and hepatic glycogen. Moreover, the upregulation of pituitary *growth hormone* (*gh*), a response that promotes lipolysis during starvation, and the downregulation of hepatic *gh receptor 1* and *insulin-like growth factor 2*, indicated a state of ‘Gh-resistance’ during catabolism. These findings, together with future characterizations of the relationships among diets, growth performance, and physiological growth regulators, will lay the foundation for optimal rearing practices for this species. [Supported by NOAA (Award no. NA22OAR4170108)]

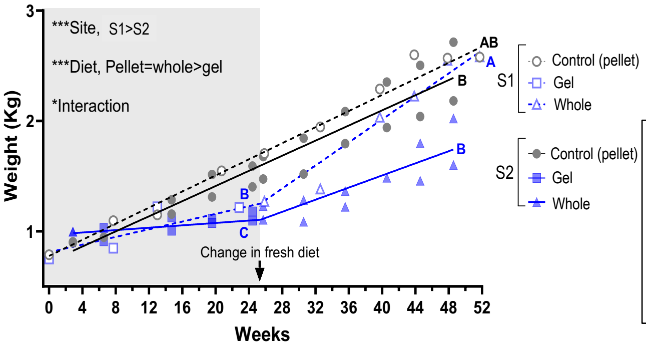

Figure 1: Linear regressions of average fish weights at two study sites (S1 and S2). Dots represent fish weights at each tank treatment and corresponding lines indicate the slope of each regression at each site. Different letters indicate significantly different slopes, one-

# P27-Impact of global change on growth and gene transcription of three-spined stickleback (*Gasterosteus aculeatus*)

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Worst-case IPCC climate change scenario, RCP8.5, projects a warming of ~ +3°C associated with a decrease of ~ −0.4 pH of surface waters by 2100, which will impact aquatic species such as teleost fishes (Nagelkerken *et al.*, 2023). Three-spined sticklebacks (*Gasterosteus aculeatus*) were reared for two years in freshwater under two climatic conditions: a first group experiencing temperature and pH fluctuations similar to those of the watercourses of the Oise (France); and a second group subjected to a ΔT of +3°C and a ΔpH of −0.4. A significant slowdown in growth was found after 128 days post-fertilisation and persisted until the end of the experiment (730 days) in both females and males exposed to the RCP8.5 climate change scenario (Figure 1). Transcriptomes were extracted from the fish livers in order to investigate the hepatic gene transcription profiles after two years of exposure to these climatic conditions. Females showed a broader transcriptional response than males, with the two sharing few differentially abundant transcripts (DATs). Among those DATs, the fish show a deregulation of oxidative phosphorylation proteins associated to an up-regulation of genes related with lipid catabolism and glycolysis. Together with the increased abundances of a wide range of angiogenesis-related growth factors, these changes in the fish transcriptome suggest the involvement of Hypoxia-Inducible Factors (HIFs) (Nikinmaa and Rees, 2005), whose activity could have been increased by the slight drop in dissolved oxygen caused by higher temperatures during two years. This leads us to conclude that sticklebacks are oxygen-limited in their energy production, which means they are unable to sustain their growth whilst supporting an accelerated metabolic rate by higher temperatures.

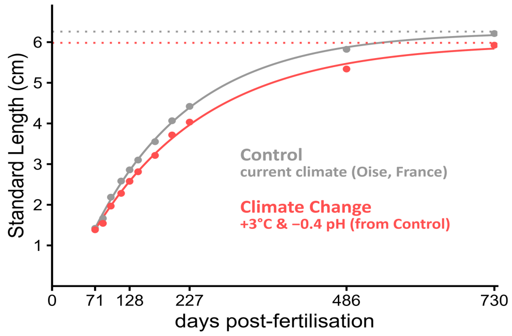

Figure 1: von Bertalanffy growth curves of Control (grey) and Climate Change (red) exposed sticklebacks. Points: means at each measured time. Horizontal dotted lines: asymptotic lengths.

## References

Nagelkerken *et al.*, PLOS Climate **2**, e0000258 (2023).
Nikinmaa and Rees, Am J Physiol Regul Integr Comp Physiol **288**, R1079 (2005).

# P28-Genomic diversity and population connectivity of *Pangasius krempfi*: a baseline for domestication programs

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*Pangasius krempfi* is an anadromous catfish native to the Mekong River. Its adaptations to habitats with varying salinities give it a high potential for aquaculture diversification and domestication under changing environmental conditions, especially in regions with saltwater incursion. Despite nacscent husbandry programs, information on its population structure and genetic diversity remains limited. This study aims to assess genome-wide genetic diversity and connectivity of *P. krempfi* across its natural distribution range. Samples were collected from upstream spawning grounds in Laos and from estuaries of the Mekong River Delta (Vietnam), where juveniles naturally occur. We are using genome-wide single nucleotide polymorphisms (SNPs) generated using a ddRAD-seq approach to quantify within-population genetic diversity, including heterozygosity, allelic richness, nucleotide diversity, and inbreeding levels. Genetic differentiation and population structure will be evaluated using pairwise F_ST, AMOVA, and clustering analyses. This will allow us to present estimations of effective population size (Ne) and to assess the demographic stability of wild populations. These results are valuable to understand the past and ongoing impact of fishing on this species, to support conservation management, and to further ongoing selective breeding programs for climate-resilient aquaculture.