



Ph.D. thesis topics 2026/2027

DSP Rybářství / Fishery

Výzkumný ústav rybářský a hydrobiologický / Research Institute of fish Culture and Hydrobiology

Vodňany 2

Supervisor: Assoc. Prof. Martin Bláha 3

Fishpond farming and its impact on surrounding ecosystems 3

Supervisor: Prof. Otomar Linhart 5

Studying AMPK ULK1 Pathways and Autophagy Regulation in Zebrafish and Common Carp Gametes: Impacts on Sperm and Egg Survival and Function 5

Supervisor: Oleksandr Malinovskyi, Ph.D. 8

Enhancing performance of intensively reared pikeperch (*Sander lucioperca*) through controlled exposure to natural environmental signals 8

Supervisor: Veronika Piačková, DVM 11

Critical moments of pond aquaculture in relation to infectious diseases of common carp (*Cyprinus carpio* L.) 11

Supervisor: Assoc. Prof. Martin Pšenička 13

Maternal contribution to oocyte biogenesis: tracing the origin of biomolecular and cellular components of the egg 13

Supervisor: Assoc. Prof. Martin Kocour 16

Novel approaches to selective breeding and genetic improvement of common carp 16

Hydrobiologický ústav BC AV ČR / Institute of Hydrobiology CAS České Budějovice 18

Supervisor: Prof. Jan Kubečka 19

Competitive interactions strengths at different stages of freshwater invasions and impacts on Eltonian niches of native species 19

Supervisor: Prof. Jan Kubečka 21

Spatiotemporal dynamics of fish movement: The role of orientation, temperature, and hydrology in habitat selection 21

Ústav akvakultury a ochrany vod / Institute of Aquaculture and Protection of Waters České

Budějovice 24

Supervisor: Prof. Andrea Vetešníková Šimková 25

Parasite susceptibility, immune defense, role of microbiota and its food-based stimulation in the breeds and crossbreeds of common carp in pond aquaculture 25

Supervisor: Radek Gebauer, Ph.D. 27

Perfluoroalkyl and polyfluoroalkyl substances in sustainable aquaculture 27

Supervisor: Ewumi Azeez Folorunso, Ph.D. 30

Microbial ecology and plant protection in soilless systems: plant-mediated interactions and crop health 30



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Fishpond farming and its impact on surrounding ecosystems

Hospodaření na rybnících a jeho dopad na okolní ekosystémy

DSP: Rybářství / Fishery

Annotation

Central European fishponds represent unique, manmade freshwater ecosystems that are important and integral to the landscape. Fishponds used mostly for fish production represent the predominant form of standing water bodies in Central and Eastern Europe (from < 1 ha to several hundred ha, depth 1–4 m). Long-term excessive nutrient loading in the last century led to both enhanced fish production and significant environmental degradation of fishpond ecosystems. Such environmental degradation has manifested in impaired fish production, frequent cyanobacterial blooms, and hypoxic events (mostly in deep water layers) with periodic fish kills alongside direct effects on eco-services, such as degraded recreational uses or biodiversity support. Recently, climate change has deepened some of these negative processes. Consequently, the current fishponds have become less predictable regarding production processes and, therefore, less cost-efficient, more stochastic, and highly unstable systems.

In recent years, water quality in fishponds has come under scrutiny and pressure from the public. However, there are scarce studies suggesting that fishponds can serve as an effective nutrient sink in the landscape, which, under the right conditions, can transform nutrients into fish biomass while maintaining the eco-services and the profitability of fish farming. With the continued tightening of EU rules regarding open-water quality conditions, close collaboration between scientific institutions and fish producers is necessary. The ongoing PhD project aims to assess fishpond farming as an integrated production–ecosystem system, with a primary focus on fish production efficiency and economic performance in relation to its impacts on surrounding aquatic and terrestrial ecosystems.

The main hypothesis

- Reasonable fish stocking can keep both economic profitability and eco-services in fishponds.
- Seasonal nutrient imbalances and stoichiometric constraints shape primary productivity and natural food availability, which ultimately affect fish production efficiency and feed utilisation.

Aim(s) of the Ph.D. thesis

- Find equilibrium and evaluate trade-offs between maximising fish yield and maintaining ecosystem functions.
- Provide a holistic evaluation of pond farming under contemporary environmental and market conditions.
- Suggest smart management based on size, position and historical data.

Possible approaches to reach the aims / to verify the hypotheses

- Integration of historical production records with environmental data to quantify relationships between fish yield, production efficiency, and nutrient outputs from fishponds.
- Analysis of data from fishponds under contrasting management strategies, examining how



stocking practices, feeding intensity, and water management influence both production performance and ecosystem functions.

- Applied production-oriented experiments aimed at testing how modifications in fishpond management affect fish production outcomes and the magnitude of ecological impacts on adjacent water bodies.

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RP4 Freshwater ecosystems in the era of global change



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Studying AMPK ULK1 Pathways and Autophagy Regulation in Zebrafish and Common Carp Gametes: Impacts on Sperm and Egg Survival and Function

Studium AMPK ULK1 cest a regulace autophagie v gametách zebřičky pruhované a kapra obecného: dopad na přežití a funkci spermií a jiker

DSP: Rybářství / Fishery

Annotation

Autophagy is a conserved cellular process responsible for degrading damaged organelles and proteins, essential for maintaining cellular homeostasis. In gametes, autophagy protects sperm and oocytes from oxidative stress, nutrient deprivation, and aging. The AMPK ULK1 signaling pathway is a central regulator of autophagy, where AMPK activates ULK1, initiating autophagosome formation, reducing reactive oxygen species (ROS), and maintaining mitochondrial function. The aim of this project is to investigate how AMPK ULK1 mediated autophagy affects the survival and function of gametes in zebrafish (*Danio rerio*). By combining pharmacological modulation, genetic manipulation, and advanced imaging in transgenic zebrafish lines (GFP Lc3), the study will examine how autophagy preserves gamete quality and fertility. Functional assessments will include sperm motility, DNA integrity, ROS levels, oocyte fertilization success, and embryo viability. This research will provide the first comprehensive analysis of AMPK ULK1 regulation of autophagy directly in zebrafish gametes, with potential implications for aquaculture, reproductive biology, and understanding gamete aging.

The main hypothesis

- Activation of AMPK ULK1 increases autophagy in gametes → reduces ROS and improves mitochondrial function.
- Inhibition of AMPK or ULK1 decreases autophagy → increases gamete damage → reduces fertilization success and embryo viability.
- Specific genes involved in mitophagy, ROS response, and gamete survival are regulated by AMPK ULK1 signaling.

Aim(s) of the Ph.D. thesis

- Molecular Objectives:
 - Characterize AMPK ULK1 activation in zebrafish sperm and oocytes.
 - Determine how AMPK ULK1 modulation affects autophagic flux and mitochondrial function in gametes.
- Functional Objectives:
 - Assess sperm survival and function (motility, DNA integrity, ROS levels).
 - Assess oocyte quality (fertilization success, embryo viability, mitochondrial status).
- Mechanistic Objectives:
 - Identify key genes and proteins regulated by AMPK ULK1 in gametes.



- Compare effects of pharmacological activation or inhibition of AMPK and ULK1 on gamete quality.

Possible approaches to reach the aims / to verify the hypotheses

- To investigate the role of AMPK ULK1 signaling and autophagy in zebrafish gametes, a combination of molecular, cellular, and functional approaches will be employed. The study will integrate pharmacological, genetic, and imaging techniques to comprehensively evaluate the impact of autophagy on sperm and oocyte survival and function.

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RP1 Reproductive and genetic procedures for fish biodiversity conservation and aquaculture



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Enhancing performance of intensively reared pikeperch (*Sander lucioperca*) through controlled exposure to natural environmental signals

Zvýšení efektivity intenzivního chovu candáta obecného (*Sander lucioperca*) prostřednictvím řízené expozice přirozeným environmentálním stimulům

DSP: Rybářství / Fishery

Annotation

Intensive culture of pikeperch (*Sander lucioperca*) often results in compromised stress resilience, suboptimal feeding behaviour, and poor adaptation to natural conditions, particularly when fish are released for restocking or grown in semi-natural environments (Molnár et al., 2023; Holubová et al., 2025). Unlike pond-reared juveniles, fish produced entirely in controlled RAS lack exposure to the natural environmental signals that shape behavioural reflexes, predator awareness, and physiological robustness during early ontogeny (Malinovskyi et al., 2023). This PhD project aims to identify, quantify, and experimentally apply key natural environmental signals—such as variable photoperiod, spectral light composition, turbidity, structural complexity, predator cues (chemical/visual), and live-prey-based trophic stimuli—to improve growth, welfare, stress physiology, and post-release adaptability of pikeperch produced under intensive conditions (Barry et al., 1995; Hermelink et al., 2017). The work will combine behavioural assays, stress-physiology biomarkers (HPI axis, glucose, lactate, oxidative stress enzymes), feeding dynamics, and performance indices (growth, FCR, survival) to uncover the mechanisms by which natural cues affect fish phenotype. Controlled manipulations will be conducted in RAS and pond-in-pond units, enabling mechanistic understanding and scaling towards practical conditions. The final outcome will be the development of validated rearing and adaptation protocols integrating natural environmental stimuli into intensive pikeperch production, with transferability toward restocking programmes, welfare-oriented aquaculture, and alternative hybrid culture systems. The project creates a framework where bio-inspired stimulation becomes an integral tool for increasing the robustness and ecological competence of intensively reared pikeperch.

The main hypothesis

- Controlled exposure of intensively reared pikeperch to selected natural environmental signals (such as variable photoperiod, spectral light cues, turbidity, structural complexity, predator- and prey-related stimuli) enhances physiological robustness, feed conversion, stress resilience, and predictability of reproductive performance, ultimately improving growth, welfare, and post-release adaptability compared to fish reared under conventional intensive conditions.

Aim(s) of the Ph.D. thesis

- To identify and characterise natural environmental signals that most strongly influence physiological robustness, feeding behaviour, welfare indicators, and reproductive predictability in pikeperch.



- To elucidate the physiological, hormonal, and behavioural mechanisms by which controlled exposure to selected natural stimuli enhances growth performance, stress resilience, and the consistency of reproductive processes in intensively reared pikeperch.
- To design, test, and validate practical rearing and adaptation protocols incorporating natural stimuli to improve growth, welfare, stress resilience, and reproductive predictability in intensive pikeperch production.

Possible approaches to reach the aims / to verify the hypotheses

- Conducting controlled rearing experiments with pikeperch exposed to different natural environmental signals (e.g., dynamic photoperiod, spectral light cues, turbidity levels, structural enrichment, predator/prey chemical cues) within replicated RAS or pond-in-pond systems.
- Collecting comprehensive datasets on: performance parameters (growth rate, feed intake, FCR, survival, condition indices), physiological and biochemical markers obtained through blood sampling (cortisol, glucose, lactate, triglycerides, hematology profiles), reproductive parameters (gonadosomatic index, gamete quality, hormonal profiles, spawning synchrony and effectiveness), and basic environmental and husbandry variables (temperature, dissolved oxygen, turbidity, light regime, structural complexity).
- Assessing reproductive predictability and effectiveness by monitoring timing of gonadal maturation, variability in GSI, ovulation/spermiation rates, fertilisation success, hatching rate, and larval viability under different environmental-stimulus regimes.
- Performing repeated blood sampling and physiological profiling to evaluate endocrine responses (HPI axis activity, reproductive hormones), metabolic status, stress resilience, and adaptive responses to applied natural cues.
- Recording behavioural indicators (feeding motivation, activity patterns, predator-avoidance behaviours, stress responses) using video tracking or direct observation to link natural stimuli with adaptive behavioural mechanisms.
- Applying statistical data analysis such as GLM, ANOVA, ANCOVA, linear mixed models, PCA, Pearson correlations, and multivariate clustering to evaluate: treatment effects, relationships between physiological markers and growth or reproductive traits, predictors of robustness and reproductive consistency, and integrated performance responses across experiments.
- Synthesising findings into validated rearing and adaptation protocols that incorporate natural environmental stimuli to improve robustness, welfare, growth performance, and reproductive predictability in intensive pikeperch aquaculture.

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Funding:

Project of NAAR (NAZV) no. QL26020013 Long-term sustainable and profitable production of pikeperch juveniles in recirculating aquaculture systems aiming higher adaptability during restocking and improved water quality in water reservoirs.

CENAKVA Research program

RP3 Sustainable aquaculture with a responsible water and nutrient management



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Critical moments of pond aquaculture in relation to infectious diseases of common carp (*Cyprinus carpio* L.)

Kritické momenty rybníčního chovu ve vztahu k infekčním chorobám kapra obecného (*Cyprinus carpio* L.)

DSP: Rybářství / Fishery

Annotation

The common carp is a major aquaculture species among cyprinids worldwide, and its culture in ponds in the Czech Republic dates back to the 12th century (Kocour et al., 2005; Prchal et al., 2018). The global aquaculture of common carp is increasing (FAO, online; Kocour et al., 2005) and is expected to remain one of the most significant sources of high-quality protein for human nutrition in the future.

One of the primary factors that can threaten the success of carp farming in ponds is the presence of infectious diseases. Farmers can influence the food supply for fish and, to a certain extent, water quality, but they are virtually powerless when it comes to outbreaks of viral diseases in fish, for example. The treatment of any disease (not only viral) in pond farming is hampered by a lack of medicines registered for fish and, above all, by legislative restrictions on the application of foreign substances to water. The only option for protecting stocks is therefore prevention, which consists of preventing the introduction of pathogens into the farm (which is practically impossible in pond aquaculture), or in supporting the resistance of fish so that they are able to cope with infection themselves with as little loss as possible, and in identifying critical moments in terms of a combination of known factors that contribute to the development of infections due to the breakdown of the immune barrier of fish (Omori and Adams, 2011).

As with terrestrial animals, the first line of defense in fish is provided by components and mechanisms of innate immunity. These mechanisms are triggered immediately or shortly after antigen recognition and always respond in a consistent manner, regardless of the number of contacts. Adaptive, or acquired, immunity develops later, is directed against a specific pathogen, and with each subsequent contact, its onset accelerates, and its effectiveness increases. In fish, as poikilothermic organisms, all these processes are dependent on water temperature. Seasonal changes can therefore be expected and have been confirmed in several publications (Buchtíková et al., 2011). However, these changes have not yet been assessed in relation to other water quality parameters, the availability of natural and presented food, etc.

The main hypothesis

- The outbreak and subsequent dynamics and severity of infectious fish diseases depend on a constellation of certain external and internal factors.
- Identifying dependencies between the immune system of fish and specific parameters of external conditions can help prevent these critical moments and reduce fish mortality.



Aim(s) of the Ph.D. thesis

- Based on regular monitoring of water quality, examination of fish health, and measurement of selected immune response parameters, identify "immune windows" in common carp in a specific fish farm.

Possible approaches to reach the aims / to verify the hypotheses

- Regular sampling of water and fish from specific ponds, identification of pathogens (microscope, cultivation, PCR), hematological examination of fish, and measurement of selected immune response parameters.
- Analysis of measured data and search for statistically significant correlations.

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CENAKVA Research program

RP3 Sustainable aquaculture with a responsible water and nutrient management



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Maternal contribution to oocyte biogenesis: tracing the origin of biomolecular and cellular components of the egg

Mateřský příspěvek k biogenezi oocyty: původ biomolekulárních a buněčných složek vajíčka

DSP: Rybnářství / Fishery

Annotation

Maternal contributions are essential for successful oogenesis and early embryogenesis, yet the origin of many egg components remains insufficiently resolved: which biomolecules and organelles are synthesized autonomously by the oocyte and which are imported from the maternal soma during folliculogenesis and vitellogenesis. This dissertation will dissect “oocyte autonomy” versus “maternal provisioning” by exploiting germ cell transplantation and surrogate reproduction as a natural tracing strategy. In this system, the oocyte derives from donor germ cells, while the surrounding ovarian environment and systemic maternal tissues belong to a surrogate female, enabling unambiguous identification of surrogate-derived components that enter the developing egg.

The project will focus on three major classes of maternal contributions: (i) RNA species (mRNA and regulatory small RNAs), (ii) proteins (including yolk precursors and candidate transport factors), and (iii) mitochondria/mtDNA. Species- or genotype-specific markers will be used to discriminate donor versus surrogate origin in eggs and isolated oocytes, combining targeted assays (allele-specific RT-qPCR, ddPCR) with high-throughput profiling (RNA sequencing and quantitative proteomics) to map the molecular landscape of imported versus oocyte-produced components. In parallel, potential mitochondrial transfer will be examined by advanced microscopy, including live imaging with mitochondrial tracers and ultrastructural analyses by electron microscopy, to localize and characterize transfer routes at the oocyte–somatic interface.

By integrating molecular tracing with imaging across defined stages of oocyte growth, this work will provide a mechanistic and quantitative framework for maternal provisioning in fish. The outcomes will advance fundamental understanding of germline–soma crosstalk, organelle inheritance, and biomolecular trafficking in oogenesis, and will also inform applied reproductive biotechnologies, including optimization of surrogate broodstock technologies and conservation-oriented breeding programs.

The main hypothesis

- The egg contains a mixture of oocyte-derived and maternally supplied components, and their relative contribution can be unambiguously resolved using surrogate reproduction.
- Maternal somatic tissues contribute distinct RNAs and proteins to the oocyte during folliculogenesis and vitellogenesis, rather than supplying biomolecules passively or randomly.
- The majority of mitochondrial content in the egg originates from the oocyte lineage, while any maternal somatic mitochondrial contribution, if present, is limited and stage-dependent.



- The origin of egg components is developmentally regulated, with defined temporal windows during oocyte growth in which maternal provisioning predominates.
- Germ cell transplantation provides a robust biological tracing system to discriminate between intrinsic oocyte synthesis and maternal import of biomolecular and cellular components.

Aim(s) of the Ph.D. thesis

- To establish germ cell transplantation and surrogate reproduction as a biological tracing framework to discriminate oocyte-autonomous synthesis from maternal somatic provisioning.
- To determine the origin of RNAs in the egg, distinguishing transcripts produced by the oocyte from those supplied by maternal somatic tissues.
- To assess the origin and dynamics of mitochondria in oocytes and eggs, including quantitative detection of donor- versus surrogate-derived mtDNA and imaging-based evaluation of potential transfer routes.
- To evaluate maternally supplied proteins in the egg using established somatic markers as references for somatic-to-oocyte provisioning.
- To define the temporal window(s) of maternal provisioning across key stages of oocyte growth and maturation.

Possible approaches to reach the aims / to verify the hypotheses

Germ cell transplantation and surrogate reproduction

- Donor germ cells will be transplanted into sterilized recipient females to generate surrogate broodstock producing oocytes of donor germline origin within a somatic ovarian environment of the surrogate. This system will serve as a biological tracer allowing discrimination between oocyte-derived and surrogate-derived components.

Molecular discrimination of donor versus surrogate origin

- Species- or genotype-specific genetic markers (SNPs, haplotypes) will be used to distinguish donor- and surrogate-derived molecules. Allele- or species-specific RT-qPCR and ddPCR will be applied to quantify the origin of RNAs and mitochondrial DNA in isolated oocytes and eggs.

Transcriptomic analyses of maternal RNAs

- High-throughput RNA sequencing will be performed on oocytes and eggs to identify and quantify donor- versus surrogate-derived transcripts, including mRNAs and regulatory small RNAs. Bioinformatic mapping to donor and surrogate reference genomes will allow assessment of RNA origin and relative contribution.

Analysis of mitochondrial origin and transfer

- The contribution of donor- and surrogate-derived mitochondria will be evaluated by sensitive mtDNA quantification methods (ddPCR, deep sequencing). Potential mitochondrial transfer will be examined using live-cell mitochondrial tracers (e.g. MitoTracker), confocal microscopy, and ultrastructural analysis by transmission electron microscopy to localize mitochondria at the oocyte–somatic interface.

Protein origin and maternal provisioning

- Protein contribution will be assessed using targeted molecular and proteomic approaches. Established maternally supplied proteins (e.g. liver-derived yolk precursors such as vitellogenin) will be used as reference markers to validate somatic-to-oocyte transport. Where feasible, quantitative proteomics will be applied to identify surrogate-specific protein signatures in eggs.

Stage-specific sampling and temporal analysis



- Oocytes will be collected across defined stages of growth and maturation to determine when maternal RNA, protein, and mitochondrial contributions occur. This temporal framework will enable identification of critical windows of maternal provisioning.

Integration of molecular and imaging data

- Molecular tracing results will be integrated with microscopy-based observations to link quantitative contributions with spatial localization and cellular mechanisms of transfer, providing a comprehensive view of germline–soma interactions during oogenesis.

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CENAKVA Research program

RP1 Reproductive and genetic procedures for fish biodiversity conservation and aquaculture



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Novel approaches to selective breeding and genetic improvement of common carp

Nové přístupy k selektivnímu šlechtění a genetickému zušlechťování kapra obecného

DSP: Rybářství / Fishery

Annotation

Despite one of the largest aquaculture productions of common carp worldwide (FAO, on-line), its selective breeding and genetic improvement programs are not well developed, and they are far behind the situation in other fishes (e.g. Atlantic salmon, rainbow trout) (Janssen et al., 2017) or livestock (Yáñez et al., 2022). The situation is given by the intensification level of common carp production technologies. Still, a progress has happened with respect to estimating i) genetic parameters of various quantitative traits and ii) potential of selective breeding for common carp genetic improvement under semi-intensive fishpond management (Rasal et al., 2024).

It has been repeatedly shown that selective breeding has high potential for genetic improvement of common carp stocks (Prchal et al., 2024). On the other hand, little is known about potential of different selective breeding approaches (e.g. mass selection vs. selection based on breeding values or pedigree vs. genomic breeding value estimates).

Common carp aquaculture in Europe has been declining for last few years, still the Czech Republic is one of the leading countries in EU aquaculture of this species. The common carp aquaculture is heading to many challenges and keeping the common carp culture sustainable and stable should be the governmental priority otherwise the existence of fishponds in the present appearance may be endangered. Deeper understanding of potential of more sophisticated selective breeding and biotechnological approaches for efficiency of common carp culture may help the Czech Republic to keep its leading position in this industry in Europe.

The main hypothesis

- Selection of common carp based on estimating the breeding values is more effective than the one based on the phenotypic values.
- Genetic interactions between fishpond culture and fishpond-RAS-fishpond culture before selection challenge may affect the selection process of the best candidates for selective breeding program set up for semi-intensive fishpond management.
- Higher carp mass and mass yield with appropriate supplemental feeding may not affect the water quality parameters in fishponds.
- Gene editing may solve the problems with intramuscular bones in common carp and increase the muscle building of the fish.

Aim(s) of the Ph.D. thesis

- to improve the knowledge about potential of novel approaches in selective breeding and genetic improvement of common carp



- to compare the effectivity of breeding values and phenotypic values for selective breeding programs
- to verify the potential of utilization of fishpond-RAS-fishpond rearing before selection challenge to accelerate the selective breeding program for semi-intensive fishpond management
- to better understand of effect of common carp stocking density in fishponds and type of supplemental feeding on the functioning of the fishpond ecosystem with respect to water quality
- to focus also on a controversial topic in Europe and to verify a potential of gene editing techniques for elimination of intermuscular bones in common carp or for increasing the muscle hypertrophy

Possible approaches to reach the aims / to verify the hypotheses

- Collecting the data about i) carp performance (weight, weight yield and survival), ii) production parameters (carp mass and mass yield received), iii) type and amount of distributed supplemental feed, and iii) water quality parameters in fishponds with different common carp stocking densities.
- Comparing the ranking of candidates for selection of different quantitative traits based on phenotypic values or breeding value estimates (including the phenotypic value and the pedigree or low-density SNP information) and statistical verification of accuracy of each method.
- Comparing the genetic variation of different traits of fish cultured in fishpond only or in fishpond-RAS-fishpond system and estimating the genetic correlations and environmental interactions using appropriate software (DMU, R-package etc.).
- Application of CRISPR-Cas9 technique in common carp to knock out the genes that may be responsible for intermuscular bones or muscle building in fish and observation the effect of this technique on the appropriate and other traits.

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CENAKVA Research program

RP1 Reproductive and genetic procedures for fish biodiversity conservation and aquaculture



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Competitive interactions strengths at different stages of freshwater invasions and impacts on Eltonian niches of native species

Síla konkurenčních interakcí v různých fázích sladkovodních invazí a jejich dopady na eltonovské niky původních druhů

DSP: Rybnářství / Fishery

Annotation

Invasive species fundamentally alter species composition and energy pathways in ecosystems, but their impact varies depending on the invasion stage of the taxa. Pressure on sensitive taxa in the ecosystem builds gradually until carrying capacity is reached (Blackburn et al. 2011, Soto et al. 2023). The impact of invasive species on native taxa can be assessed by examining changes in life table characteristics, such as reproductive rates and condition (Tapkir et al. 2022, Šmejkal et al. 2025a), or by applying the food niche concept, which explores isotopic niche space and food sources (Tapkir et al. 2023).

The Eltonian niche concept emphasises species interactions, trophic position, and food sources. This functional perspective is crucial for understanding ecosystem dynamics, food webs, and how invasive species interact with native taxa. Yet little is known about how this niche changes during stages of invasion in freshwaters, or how endangered taxa might benefit from invasive species reduction programmes.

This PhD topic will explore the impact of two model invasive fish species, the gibel carp (*Carassius gibelio*) and the topmouth gudgeon (*Pseudorasbora parva*), on native taxa, with emphasis on: i) temporal shifts in invasive species abundance due to the progression of invasion, and ii) reduction of invasive species by 90% through trapping measures. These species cause significant declines in wetland native taxa of functionally similar species, making it relevant to investigate the underlying mechanisms (Šmejkal et al. 2025b). Given the focus on temporal trends in this thesis proposal, data collected over the past three years will also be analysed to extend the data series.

The main hypothesis

- Realized isotopic niche of native taxa will be shrinking with increase of invasive species population
- Invasive species reduction is a powerful tool to restore original niches of endangered taxa

Aim(s) of the Ph.D. thesis

- To understand Eltonian niche dynamics under invasive species pressure at various stages of invasion success
- To investigate the interplay of niches sizes and overlaps between invasive and native species with reduction population programmes
- To conduct a bibliometric study assessing the current knowledge of this topic in scientific literature and define future directions



Possible approaches to reach the aims / to verify the hypotheses

- Stable isotope analysis using fish scales, fins as non-lethal approach and analysis of potential prey items
- Flushing out stomach content
- Setting up controlled competitive interactions at varying densities in mesocosm
- Field sampling of sites with varying CPUE of invasive and native fishes

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Spatiotemporal dynamics of fish movement: The role of orientation, temperature, and hydrology in habitat selection

Časoprostorová dynamika pohybů ryb: role orientace, teploty a hydrologických poměrů na výběru habitatu

DSP: Rybářství / Fishery

Annotation

River fragmentation caused by dams, weirs, and hydropower plants represents one of the most critical threats to freshwater biodiversity globally (Birnie-Gauvin et al., 2017). While engineering solutions such as fishways and bypass channels are widely implemented to restore longitudinal connectivity, their biological effectiveness is often surprisingly low (Birnie-Gauvin et al., 2017). A major reason for this failure is the discrepancy between hydraulic design and fish behavior. Traditional management focuses on "swimming performance" (can the fish physically swim through?) (Castro-Santos & Haro, 2010), ignoring the critical aspect of "orientation and navigation" (can the fish find the entrance?). Without understanding the mechanisms determining how fish select and utilize their environment (Nathan et al., 2008), conservation efforts in regulated rivers like the Danube remain inefficient.

To improve passage efficiency, we must first understand the baseline spatial strategies of fish in unfragmented or semi-natural environments. Current knowledge of how fish perceive space, maintain headings, and select specific habitats is limited, often relying on coarse-scale data (Hussey et al., 2015). This thesis utilizes high-resolution telemetry from lentic systems (reservoirs) to establish a fundamental understanding of how navigation underpins habitat selection (Rodríguez et al., 2021). By analyzing fine-scale trajectories of model species (e.g., pikeperch *Sander lucioperca*, wels catfish *Silurus glanis*, pike *Esox lucius*), it is possible to define the natural rules of habitat use (how fish search for resting or foraging sites and respond to environmental cues), which serves as a necessary control for understanding their behavior in anthropogenically altered systems (Edelhoff et al., 2016; Říha et al., 2022).

In regulated rivers, these natural selection strategies confront artificial barriers. The complex hydro-morphology of the Danube (Gabčíkovo-Čunovo system) creates a "sensory trap" where altered flow regimes and depth profiles disrupt migration routes (Kubala et al., 2019). Here, the challenge shifts from theoretical orientation to practical passability. Rheophilic fish species must not only possess the motivation to migrate but also the ability to select the correct path towards bypass entrances amidst turbulent tailraces. The problem is exacerbated by the lack of knowledge regarding vertical microhabitat selection; a fish preferring near-bottom structures may simply miss a surface-oriented fishway, regardless of its motivation.

This doctoral research addresses the urgent need to integrate behavioral ecology into river management. By combining the study of fundamental navigation principles with applied telemetry of barrier crossing success, the project aims to identify the specific behavioral bottlenecks limiting connectivity. The analysis of depth selection, thermal habitat preferences, and passage efficiency at key obstacles will provide direct recommendations for optimizing fishway attraction flows. Ultimately, the thesis demonstrates that



successful restoration of migration corridors requires a holistic approach that considers not just the physical permeability of barriers, but the spatiotemporal dynamics of habitat selection of the species attempting to cross them.

The main hypothesis

- In featureless lentic environments, fish rely on allocentric cognitive maps. We hypothesize that navigation towards known habitats is precise and goal-directed regardless of the starting position, significantly exceeding the efficiency of random walk or simple beaconing models.
- In lotic systems, vertical space use is determined by species-specific ecomorphological traits. We hypothesize strict vertical niche partitioning: while pelagic predators as asp (*Leuciscus aspius*) utilize the upper water column, benthic species as starlet (*Acipenser ruthenus*) or barbell (*Barbus barbus*) are obligatorily bound to the riverbed boundary layer, causing them to approach migration barriers at significantly different depth strata. It can caused species-specific differences in barrier permeability.

Aim(s) of the Ph.D. thesis

- To characterize fine-scale movement trajectories and homing precision of different fish species in reservoirs, aiming to confirm the existence of map-like navigation and identify the behavioral rules used for orientation in the absence of flow.
- To assess the spatiotemporal dynamics of rheophilic species (*Acipenser ruthenus*, *Leuciscus aspius*, *Barbus barbus*) in the Danube, with a specific focus on how vertical space use (depth selection) changes in response to discharge, temperature, and migration phase.
- To quantify the passability of the Gabčíkovo-Čunovo waterworks for the target species and identify behavioral bottlenecks (e.g., depth mismatch at fishway entrances) that limit successful migration.
- To quantify the passability of the Gabčíkovo-Čunovo waterworks in relation to species-specific vertical distribution, and to identify behavioral bottlenecks caused by the mismatch between the preferred swimming depths and the vertical position of fishway entrances.

Possible approaches to reach the aims / to verify the hypotheses

- Data Acquisition: Combine high-resolution 3D telemetry (reservoirs) with large-scale linear arrays equipped with depth and temperature sensors (Danube).
- Statistical Framework: Perform all analyses in R (e.g., *actel*, *moveHMM*) using Hidden Markov Models to segment behavioral states, circular statistics for navigation precision, and GLMMs to test abiotic drivers.
- Habitat Modelling: Apply Habitat Selection Models (HSM), specifically Resource Selection Functions (RSF) or Step Selection Functions (SSF), to quantify the selection of microhabitats (depth strata, flow classes) relative to their availability.
- Barrier Assessment: Evaluate passage efficiency using event-time analysis and compare fish vertical profiles with fishway hydraulics to identify migration bottlenecks.



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Parasite susceptibility, immune defense, role of microbiota and its food-based stimulation in the breeds and crossbreeds of common carp in pond aquaculture

Vnímatost k parazitům, imunitní obrana, role mikrobioty a její stimulace potravou u plemen a kříženců kapra obecného v rybníčním chovu

DSP: Rybářství / Fishery

Annotation

Common carp represents the highest fish meat production on the Czech market. Its effective farming, similarly, to other economically important fish species worldwide, is threatened by several factors, with the transmission of parasitic diseases and the introduction of new pathogens into fishpond ecosystems being among the most serious threats. Individual breeds and crossbreeds of common carp differ genetically, phenotypically (shape morphology, scale pattern), and in performance (growth rate and survival), and may differ in resistance to various pathogens. An important step in the breeding of common carp was the intentional introgression of genes from the Amur carp, the original wild form of common carp, characterized by high tolerance to environmental conditions and vitality. The genes of the Amur carp, introduced through combinatorial crossing, were also inserted into the mirror-scaled genotype with the aim of breeding the Amur mirror carp, which is a key breed used to generate highly productive F1 hybrid forms. Thanks to the genes of the Amur wild carp, the Amur mirror carp acquired high non-specific resistance that protects against pathogens.

Due to the close relationship between microorganisms and the host (both considered as one holobiont having a crucial role in the One Health concept), the application of microbial communities of fish hosts as indicators of their health status is currently emphasized, while individual components of microbial communities can have a protective or, conversely, pathogenic function. The composition of fish microbial communities is influenced by the ecophysiological characteristics of the aquatic environment (i.e., the fishpond ecosystem), interactions with parasites and pathogens, and the type of food, which affects the intestinal microbiota. The genotype of the fish host (here carp breeds and their crossbreeds) may play an important role in the composition of microbial communities in close association with susceptibility or resistance to pathogens. From the perspective of host microbial communities, increasing fish resistance to pathogens and strengthening immunity by applying immunostimulant additives to feed mixtures represents a possible effective way to protect the health of common carp in fishpond ecosystems.

The main hypothesis

- The parasite load in fishpond ecosystems and the susceptibility to specific parasite species may vary among lines and crossbreeds of common carp in relation to their genetic background (with an expected role of Amur wild carp advantageous genes playing a role in ecological tolerance and parasite resistance).
- The protective role of microbial communities may vary among lines and crossbreeds of common carp, especially if microbiota is associated with parasite susceptibility or resistance.



- Feed modification using probiotics (or other immunostimulants) may increase common carp resistance to parasites, and the capacity of common carp hosts to induce an effective immune response after food stimulation potentially differ among lines and crossbreeds of common carp.

Aim(s) of the Ph.D. thesis

- To assess the susceptibility of genotypes and phenotypes of common carp breeds and crossbreeds to overall parasite load in natural fishpond ecosystems as well as to selected pathogens, and to investigate the potential of fish hosts to induce an effective immune response over time.
- To evaluate the genetic potential of common carp breeds and their crossbreeds to respond to immune stimulation through modified feed mixtures enriched with probiotics (or other immunostimulants), which could potentially strengthen the protective components of fish microbiota against parasitic infection.

Possible approaches to reach the aims / to verify the hypotheses

- Experimental studies in breeding facilities (aquarium conditions) and in fishpond aquaculture of common carp to examine susceptibility to pathogens/parasites and infectivity rate by several fish pathogens
- Quantification of microbial communities using DNA metabarcoding
- Integrative approaches in the quantification of targeted parasites and evaluation of entire parasitic communities of common carp from pond aquaculture
- Molecular methods for assessing the immune response (e.g., gene expression analysis via qPCR)
- Data set analyses and scientific interpretation of outputs

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CENAKVA Research program

RP3 Sustainable aquaculture with a responsible water and nutrient management



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Perfluoroalkyl and polyfluoroalkyl substances in sustainable aquaculture

Perfluoralkylové a polyfluoralkylové látky v udržitelné akvakultuře

DSP: Rybářství / Fishery

Annotation

Perfluoroalkyl and polyfluoroalkyl substances (PFAS) represent a serious environmental problem. These chemicals are stable, accumulate in the environment, and can adversely affect human health. In response to identified health risks, the European Union has introduced strict limits on PFAS content in foods, including fish products. These regulations pose a significant challenge, particularly for the Czech Republic, where aquaculture is dependent on exports. The aim of the proposed Ph.D. thesis is to provide a comprehensive solution to the PFAS issue in intensive aquaculture, especially in recirculating aquaculture systems (RAS) and aquaponic systems. The project will verify options for the removal of PFAS from aquaculture sludge, which can be utilized within bioeconomic processes such as the production of organic fertilizers, biogas, or composting. Attention will also be paid to the fate of PFAS in aquaponics, particularly their potential transfer to plants and the possibility of degradation during remineralization processes. An important outcome will be the development and validation of environmentally friendly technologies to reduce PFAS levels in the system, including depuration of fish and plants before harvest to enhance the safety of final products.

The main hypothesis

- PFAS can contaminate plants in aquaponics.
- New technologies and processes can decrease PFAS concentrations in the production system.
- New technologies and processes can decrease PFAS concentrations in fish and plants.

Aim(s) of the Ph.D. thesis

- To screen the PFAS flows in the production system.
- To develop a technology to decrease PFAS concentration in the production system.
- To develop a technology to decrease PFAS concentration in fish and plants.

Possible approaches to reach the aims / to verify the hypotheses

- The screening of the PFAS flows will be performed in selected fish farms.
- Technologies such as advanced oxidation processes and biotechnology will be used to decrease PFAS concentrations.

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CENAKVA Research program

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Microbial ecology and plant protection in soilless systems: plant-mediated interactions and crop health

Mikrobiální ekologie a ochrana rostlin v bezpůdních systémech: interakce zprostředkované rostlinami a zdraví plodin

DSP: Rybářství / Fishery

Annotation

Aquaponics is increasingly becoming a potential sustainable alternative to conventional food production systems due to its efficient resource use and low demand for arable land. Globally, the adoption of aquaponics is increasing with market growth expected to reach approximately 10% by 2030 1.

Aquaponic systems co-cultivate fish and vegetables, where the aquaculture and hydroponic compartments are either configured in a single-loop or multiple loops. In these systems, nutrient-rich water is supplied from the fish compartment to grow the vegetables in the hydroponic section, after which the water may either return to the fish unit or discharged. The nutrient dynamics and the mechanisms within the systems are largely influenced by the microbiome and plant-derived exudates that interact across the systems. However, managing disease outbreaks originating from waterborne and root-associated pathogens in hydroponic unit, as well as fish-related diseases in the fish compartments remain significant challenges 2. Application of chemical treatments and antibiotics in both compartments are incessantly discouraged. Interactions between the microbiome, plant exudates, and plant pests and pathogens have been suggested to have the potential to naturally suppress pathogen proliferation 3,4. The microbiome of fish and the plant compartments are unique, and their complex interactions with plant-released exudates along with metabolites of pest/pathogens may provide a novel pathway to controlling diseases and improve nutrient utilization.

While farmers interest may majorly lie in maximizing yield with minimal inputs, understanding the interactions between indigenous microbiome, plant-derived compounds, and pathogen defense mechanisms across various cultivation systems and plant species, will provide an essential insight on the strategic integration of the system components to achieve a sustainable cultivation. However, little is known whether interactions between microbiomes and exudates have the potential to protect and fortify the systems from stressors.



The main hypothesis

- Plant exudate profiles during stress selectively shape indigenous microbial communities
- Differences in microbial community composition and function between hydroponic and aquaponic systems are reflected in plant disease or pest infestations severity and plant defense responses.
- The interactions between microbiome and plant-induced compounds are diverse across various cultivation systems

Aim(s) of the Ph.D. thesis

- To characterize and compare exudate profiles of plant grown in hydroponic and aquaponic systems under healthy and pathogen-challenged conditions.
- To determine how plant and plant metabolites influence microbial community structure and functional potential in soilless cultivation systems.
- To assess the relationship between microbial community composition, plant defense responses, and disease suppression or pest infestation.

Possible approaches to reach the aims / to verify the hypotheses

- Cultivation of plant in controlled hydroponic and decoupled aquaponic systems, including pathogen challenge experiments using *Pythium aphanidermatum* 5.
- Collection of root, rhizosphere, and plant tissue samples at defined growth stages for microbial and biochemical analyses.
- Profiling of root exudates using gas chromatography–mass spectrometry (GC–MS) and/or liquid chromatography–mass spectrometry (LC–MS).
- Analysis of microbial community structure using 16S rRNA gene metabarcoding and bioinformatics pipelines.
- Application of multivariate statistical analyses (e.g. PCA, redundancy analysis, correlation networks) to link metabolites, microbial communities, and plant health indicators.

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RP3 Sustainable aquaculture with a responsible water and nutrient management