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One of the founding and foremost principles of the NoWPaS network is that it be free to attend to all participants. Because of this we are especially grateful to the generous support and contributions from the following sponsors:



Keynote Abstracts

Salmonids population dynamics: from ecology to management, and back...

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Abstract: Salmonids are characterized by a large diversity of life histories derived from complex life cycles in contrasted environmental conditions. Yet, empirical studies are impeded by the difficulty in observing individuals with traditional tools for most of their life. Population dynamics is a field interested in modelling change in population abundance and structure across time and space. It can be viewed as an approach integrating ecological knowledge gained at individual and population levels into a unified framework. Population dynamics models are used to quantify latent demographic processes. They offer a relevant approach to investigate change in population structure and abundance in a variety of spatial and temporal scales in response to environmental change. In this presentation, I will present how population dynamics models driven by ecological knowledge can feed expertise for salmonids management, and how models developed for management purpose can eventually inform ecology. Examples of life cycle models of various complexity, for brown trout and Atlantic salmon, will be used as an illustration.

Two sides of the same coin: evolutionary and ecological processes underpinning alternative migratory tactics

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Abstract: Many intriguing examples of discrete polymorphisms occur in nature, i.e. discontinuous intraspecific variation in morphology, feeding behaviour, mating tactics, life histories, migratory tactics, etc. The processes that generate and maintain such alternative phenotypes have long intrigued evolutionary biologists, and many questions remain. In our research group, we use brown trout (*Salmo trutta*) as a model system to understand the evolutionary and ecological causes and consequences of alternative migratory life histories. Brown trout come in many different “flavours”, with migratory versus resident forms being of particular interest to anglers, fisheries managers and conservationists. Both types are spawned in freshwater, but in the case of anadromous migrants (“sea trout”) there is a period of feeding at sea, followed by return migration to freshwater; resident, on the other hand, remain all their lives within their natal stream or lake. Anadromous migration is much more common in females, who benefit more than males from larger sizes attained at sea. This sets up a potential sexual conflict, where ‘alleles for migration’ may increase the fitness of females, but decrease the fitness of males. In this talk, I will first present some experimental findings that show how these alternative tactics emerge via complex interactions between genes and environment. Next, I will present results from genomics and transcriptomics analyses that examine genetic architecture and molecular mechanisms underpinning alternative phenotypes and sex-specific gene expression. Finally, I will present outcomes from an eco-genetic simulation model that explores the interaction between sexual conflict and parasites in driving evolutionary and population dynamics.

Ocean nomads - Atlantic salmon at sea

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Key words: Ocean life stage, marine feeding migration, growth, survival

Abstract: Atlantic salmon is one of the best studied fish species in the world, but more so during the freshwater and near-coastal life stages than during their ocean life. In Europe and North America, the abundance of Atlantic salmon has generally declined since the 1970s, and one of the major hypotheses for the decline is reduced marine survival. We aim to study what impacts Atlantic salmon growth and survival at sea within the SeaSalar project. Determining the mechanisms driving range-wide reductions in marine survival is hindered by an insufficient understanding of their oceanic ecology and distribution. Hence, migration patterns and habitat use at sea are studied by using satellite tagging and genetic analyses of salmon collected at sea, and the results redefine our knowledge of the ocean distribution of Atlantic salmon at sea. Analyses of salmon collected at sea have provided new knowledge of their diet and why growth and survival have been reduced during the recent decades. Detailed growth analyses have provided a new understanding of the spatial and temporal variation in growth and survival, and how patterns are linked to ecosystem changes in the ocean. An overview of our results from studies of migrations, growth and survival of Atlantic salmon at sea will be presented.

Homing, straying, and the illusion of Alaska's pristine wild salmon fisheries

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Abstract: The homeward migration of anadromous salmonids is one of the great natural wonders of the world, connecting both the fish and the people that rely on them to specific places and times across the Salmosphere. Homing, and the behavioral alternative straying, are biological phenomena that profoundly influence salmonid ecology, evolution, management, and conservation. In the first part of the talk I will hit on the 'highlights' of what has been learned about homing and straying through the study of hatchery produced Pacific salmon in Alaska and the Pacific Northwest region of the USA. In the duration of the talk I will review a body of work underway to understand the impact of the ca. 1.5 billion juvenile pink salmon and chum salmon released each year into Alaska's marine waters on the productivity and fitness of wild salmon populations, and by doing so challenge the myth of Alaska exceptionalism.

Delegate Abstracts

Investigating the link between *vgll3* genotype and aggressive behaviour in juvenile Atlantic salmon (*Salmo salar*)

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Keywords: Aggressive, growth, Atlantic salmon, genotypes, condition

Abstract: Aggressive behaviour can affect social hierarchies and result in the unequal distribution of resources, with aggressive individuals monopolizing access to food influencing growth. In Atlantic salmon, aggression has been found to have a genetic component, and growth also influences maturation timing. Maturation timing associates with a large-effect locus around *vgll3*, which is also linked to size at maturation and body condition (fatness), with *vgll3**EE (early maturation genotype) individuals having higher condition factor than *vgll3**LL (late maturation genotype) individuals. Here, we examine the possibility that aggressive behaviour may play a role in juvenile *vgll3**EE individuals having higher condition factor by having increased food intake due to higher aggressive behaviour promoting increased food access. This prediction was tested in a social context: aggressive behavior and the amount of eaten food was recorded in four size-matched individual juvenile salmon, two with each *vgll3* genotype, over 99 independent trials. Contrary to our prediction, *vgll3**LL individuals had significantly higher net aggression than *vgll3**EE individuals. Aggression was not associated with sex or individual's size, and genotypes did not differ in their condition factor nor amount of food eaten. These results imply that aggressive behaviour may have an energetic cost impairing growth and condition, especially when food cannot be monopolized. This may have implications for individual fitness and aquaculture practices.

Contrasting effects of nutrient application method on juvenile Atlantic salmon (*Salmo salar*) density and growth

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Keywords: Atlantic salmon, conservation, fisheries management, population dynamics, nutrients

Abstract: Declining numbers of Atlantic salmon (*Salmo salar*) returning to streams to spawn have resulted in a decreased import of marine-derived nutrients, which are deposited in streams as spawner waste products and carcasses. Previous research has demonstrated an increased growth rate and biomass of juvenile salmon, alongside increased invertebrate abundance and biomass, when nutrient levels at spawning grounds were experimentally increased. In this experiment, the efficacy of two methods of nutrient application were tested using fish feed pellets as salmon carcass analogues. Across six sites in Northern Scotland, streams received either 15kg of bagged pellets or 15kg of hand-scattered pellets across a 500m² stream area, each downstream of a control area of the same size. Each control and treatment area received 2500 eggs, 100 from each of the same 25 families. The scattered pellet treatment showed significant positive increases in juvenile salmon biomass and density, though this was accompanied by a significant negative effect on fork length, body mass and body condition. There were no significant effects of the bagged pellet treatment. Scattered pellets may more effectively disperse a pulse of nutrients across a wider area, allowing for more even enrichment, as opposed to bagged pellets which may only have a localised impact. Scattered enrichment could allow increased survival through a reduction in competition, whereas bagged enrichment may create hotspots of higher quality resources that the majority of fish are excluded from. Further research is required to understand the processes underpinning this differential pattern in density and growth.

Geographical gradient in gill microbiome diversity of farmed Atlantic salmon during an Amoebic Gill Disease episode.

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Keywords: Atlantic salmon, microbiome, amoebic gill disease, qPCR

Abstract: Amoebic Gill Disease (AGD) is an economically important pathology of Atlantic salmon (*Salmo salar* L.) of growing concern. AGD may impact the gill microbiome of farmed salmon, thus altering the host-microbiome relationship as well as the defensive role against pathogens associated with the microbiome. More and better information is required to understand interactions between gill microbiomes and the causative agent of AGD, *Neoparamoeba perurans*. In this study, we compared the gill microbiome of AGD-affected Atlantic salmon farmed at different locations to also determine the impact of geography on the microbiome-AGD milieu. Gills were excised from each of five fish from each of six farms along the western coast of Ireland throughout the summer and autumn. Total microbial genomic DNA was extracted from gill samples. The bacterial community on gills was characterized and compared across locations and timepoints using universal prokaryotic (16S rRNA) PCR primers and high-throughput DNA sequencing. AGD development was determined using qPCR targeting the *N. perurans*. Additionally, key environmental parameters were tracked and correlated with the microbiome. Each fish farm was affected by AGD during the study. A clearly descending gradient from northern toward southern farms was observed in the alpha diversity descriptors. There were significant variations in the microbiome composition between locations at each timepoint. Some differences significantly correlated with AGD development. This study supports the idea that AGD and the local environmental factors impact the gill prokaryotic microbiome.
Funding of research: Department of Agriculture, Food and the Marine (Ireland).

The role of early sexual maturation in marine survival in coho salmon (*Oncorhynchus kisutch*)

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Keywords: Genomics, life-history traits, complex trait, early sexual maturation, GWAS

Abstract: Survival is a quantifiable trait whereby variation in the population results from both genetic and environmental influences. Stark changes in the environment will challenge an individual's adaptive potential, and those with advantageous genetic variants can have a selective advantage for survival. By studying the genomes of surviving individuals in a family, we can examine the associations between genetic variation, familial survival rates, and fitness traits to unravel important genomic regions associated with survival. Using hatchery coho as a model, we examined the genetic architecture of families with higher adaptive potential during a marine wave. We collected operculum punches and 13 phenotypes from parents and their surviving adult progenies for four consecutive generations (2006 to 2018, n=18,583). Pedigree data was aligned with spawning and rearing records to enumerate family-based marine survival rates. We found significant, consistent correlations between survival with smaller body size and early sexual maturation (ESM) across generations. ESM occurs predominately in male coho that return 1-year earlier than their siblings, resulting in smaller body size. To elucidate the genetic intersection between ESM and survival, we conducted a genome-wide-association-study to compare families with high frequency of ESM to high frequency of 3-year-old adults (n=716). We found five single-nucleotide-polymorphism on Okis30 that were consistently associated with sex, age-at-maturity, and length (hallmarks of ESM). Three were found in the intron of genes involved with modifying chromatin structure, regulating cell death and ion channel activity. This highlights the importance of alternate life histories strategies to ensure population resilience during challenging ocean conditions.

From genome erosion to intracellular niche – the biology of mycoplasmas in the Atlantic salmon

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Keywords: Mycoplasma, genome size, intracellular niche, shotgun metagenomics, Atlantic salmon.

Abstract: Mycoplasmas are the smallest autonomously self-replicating life form on the planet. Members of this bacterial genus are known to parasitise a wide array of metazoans including vertebrates. Whilst much research has been significant targeted at parasitic mammalian mycoplasmas, very little is known about their role in fish species and aquaculture. The aim to this study is explore the biology and evolution of mycoplasmas in Atlantic salmon, including their cellular niche, genome size structure and gene content. Using Fluorescence in-situ hybridisation (FISH), mycoplasmas were targeted in epithelial tissues across the digestive tract (stomach, pyloric caecum and midgut) from different developmental stages (eggs, parr, subadult) of farmed Atlantic salmon (*Salmo salar*). For the genomic aspect, via shotgun metagenomic sequencing from a farmed Atlantic salmon subadult, we assembled a nearly complete, albeit very small genome (~0.57 MB). Phylogenetic analysis of the recovered genome revealed taxonomic proximity to other salmon derived mycoplasmas, as well as to the human pathogen *Mycoplasma penetrans* (~1.36 Mb). We annotated coding sequences and identified riboflavin pathway encoding genes and sugars transporters, and several hypothetical proteins. Our study provides genomic insights of the ecological and functional association between *Mycoplasma* and *Salmo salar*, suggesting a high level of dependency of the microbe on its host and a potential role for *Mycoplasma* in contributing to host microbiota nutrition.

Population structure and genomic evidence for local adaptation to freshwater and marine environments in anadromous Arctic Char (*Salvelinus alpinus*) throughout Nunavik, Québec, Canada

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Abstract: The Arctic Char (*Salvelinus alpinus*) is an anadromous salmonid of great importance for traditional fisheries in the Inuit communities of Northern Canada. Arctic Char are known to migrate to coastal feeding areas in proximity to their natal rivers, which could indicate a potential for local adaptation to marine as well as freshwater conditions. In an effort to develop biologically significant management units for Arctic Char in the southeastern Canadian Arctic, we assessed genetic population structure and adaptation at a local and regional scale: 650 individuals were sampled from 23 localities in Nunavik (Quebec), Baffin Island (Nunavut) and northern Labrador, and around 18,000 SNP markers were obtained using genotyping-by-sequencing (GBS). Fish harvested in different rivers sharing an estuary could generally not be distinguished, suggesting high level of gene flow inside a catchment area. Patterns of genetic diversity show signs of hierarchical genetic structure, with the broader level of structure dividing the study area in four major regions with extent roughly matching the oceanographic basins around Nunavik (Hudson Bay, Hudson Strait, Ungava Bay and Labrador Sea). As the environment is highly contrasted between those regions, natural selection could play a role in structuring Arctic Char populations. Association between genetic markers and environmental factors were tested using both monogenic (e.g. Baypass, LFMM) and polygenic (e.g. RDA) methods, to identify potential targets for local adaption. These results will inform local and regional decision makers about conservation of Arctic Char stocks in Nunavik.

Immunostimulant baths influence expression of immune and metabolic genes in yolk-sac larvae of Atlantic salmon (*Salmo salar*)

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Keywords: Immunostimulants, innate immune system, gene expression, antiviral, metabolism

Abstract: Disease resistance of fish larvae may be improved by bath treatment in water containing immunostimulants. Among many innate immune receptors, Toll-like receptors (TLRs) have a key role in innate response. Pattern recognition receptors (PRRs), such as TLR3 and TLR7, work as an “early warning” to induce intracellular signaling and facilitate an antiviral response. By virtue of their importance, we hypothesized that the immunostimulants, astragalus, hyaluronic acid, imiquimod, and poly I:C can boost the antiviral immune and metabolic systems in the early life stages of Atlantic salmon. A single bath of newly hatched larvae with astragalus upregulated the expression of IFN α , IFN γ , ISG15, MDA5, PKR, STAT1, TLR3 and TLR7 immune genes, on day 4 post treatment. Similar patterns were observed for hyaluronic acid and poly I:C. Increased expression was observed for ISG15, MDA5, MX, STAT1, TLR3, TLR7, and viperin, on day 9 for imiquimod. Metabolic gene response was stimulated on day 1 after immunostimulant bath in ATG/ULK, C-myc, Glut1, HIF1 α , mTOR, and SIX1, in astragalus, hyaluronic acid, and imiquimod. Expression of iNOS in poly I:C was an average 4-fold above that of control at the same timepoint. Throughout the remaining sampling days, iNOS and IL-1 β were consistently overexpressed. Expression of immune and metabolic genes were correlated for HIF1 α /Mx in astragalus, mTOR/viperin in hyaluronic acid, iNOS/TLR3 in imiquimod; and ATG/ISG15, HIF1 α /ISG15, HIF1 α /ISG15, mTOR/IFN α , and mTOR/Mx in poly I:C. In conclusion, the immunostimulants induced antiviral and metabolic gene responses, indicating that a single bath at an early life stage could enable a more robust antiviral defense in fish.

Evolutionary management of intra specific diversity and hybridization dynamics between Atlantic and Mediterranean lineages of *Salmo trutta*

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Keywords: demogenetic modelling, intraspecific diversity, reproductive isolation, introgression, management

Abstract: Biodiversity variations within and between species are often the results of reproductive isolation mechanisms and can highly be impacted by anthropic activities. Human interventions have often led to the admixture of previously allopatric lineages, notably for salmonids species. In the Mediterranean area, intensive stocking of Atlantic *Salmo trutta* has led to a mosaic of outcomes regarding hybridization between the Atlantic and the Mediterranean lineages. To understand and predict this introgression dynamic we analysed the impact of parental genotype-by-environment interaction on embryonic survival and implemented the obtained results in an individual based demo-genetic model. Our aim is to represent the evolution of intraspecific diversity dynamic, and predict the impacts of various management practices by considering environmental conditions and eco-evolutionary mechanisms – as well as their genetic basis – since both should be considered for intraspecific diversity management. Studying eco-evolutionary mechanisms, we first showed that embryonic survival was highly dependent upon maternal genotype-by-environment interactions with eggs from the Mediterranean maternal lineage presenting a higher survival than eggs from any other females in colder temperatures. This advantage was disappearing with increasing temperature, suggesting, for the first time in brown trout, lineage-related patterns of local adaptation to thermal conditions. Second, simulations including this post-zygotic barrier, as well as previously demonstrated pre-zygotic isolation, indicated that evolutionary mechanisms may play an essential role in introgression dynamic and may interplay with management practices efficiency. Managers interested in native conservation should thus consider the role of both, reproductive isolation mechanisms and environmental factors in their decision-making regarding conservation actions.

Inbreeding avoidance at the gamete level in Atlantic salmon

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Keywords: Fertilisation, cryptic female choice, ovarian fluid, kin recognition, sperm competition

Abstract: Inbreeding can lead to fitness depression and reduce adaptive responses, so a range of mechanisms are recognised to limit reproduction between close genetic relatives. Here, we examine whether inbreeding avoidance exists between sperm and egg in Atlantic salmon, in a post-copulatory selection process where mechanisms are still to be unveiled. Philopatric salmon usually return to their natal streams to spawn, presenting a risk of breeding between genetic relatives, and reduced potential for females to control paternity under external fertilisation. Using in vitro fertilisation experiments, we test for the presence of gamete level inbreeding avoidance by comparing sperm behaviour and fertilisation outcomes between sibling and non-sibling crosses of farmed salmon. Using a paired breeding design, we compared sperm motility in sibling versus non-sibling ovarian fluid, fertilisation rates, and paternity outcomes following sperm competitions between sibling versus non-sibling males (assigned using microsatellites). Results showed that sperm behaviour was significantly different in sibling versus non-sibling reproductive fluid, with spermatozoa activated in sibling fluid showing reduced motility and different swimming trajectories. Males also suffered an average 18% reduction in fertilisation and hatch rates when crossed with eggs from sibling females. These findings indicate that post-copulatory pre- and post-zygotic inbreeding avoidance mechanisms have evolved at the gamete level in salmon, probably through interaction between ovarian fluid biochemistry and sperm swimming behaviour. However, our sperm competition trials did not yield a clear disadvantage for male fertilisation success when their sperm were competing for a female's eggs as a sibling, and we discuss possible reasons for this result.

Assessing the impact of river barriers on successful seaward migration of Atlantic salmon, *Salmo salar* along the River Derwent, Cumbria.

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Keywords: Atlantic salmon, smolt, acoustic telemetry, migration, river, river management

Abstract: Atlantic salmon (*Salmo salar*) smolts migration through freshwater to salt-water systems has been classified as a critical transitional phase in providing new feeding grounds and environments required for growth to ensure returning adults future reproductive success. Though downstream migration during the smolt phase has been thought to incur the highest mortality rates throughout the *S.salar* life cycle, due to the increased physiological and behavioural transformation stress and external barriers/threats to which individuals are exposed. *S.salar* smolts originating from tributaries along the west coast of England have seen a significant decline in population abundance, this has been noticeable on the Derwent river, Cumbria. Along this tributary exposure to various natural and anthropogenic stressors are unavoidable, such as weirs, large standing waters, urbanised sites, and water flow fluctuations. For this study 1) we are using acoustic telemetry to determine whether downstream migration mortality overlaps with known pressures, 2) determine where the highest rates of mortality occur, 3) determine if there where physiological differences between smolts that did/did not successfully migrate to sea, 4) analyse what barriers incur a great delay in migration and why. This project is funded by EA DEFRA, Natural England, The Derwent Owners Association, Bowland Game: Isel Fishings and is supported by University of Glasgow. The aim of this project is to help better understand the impact of river barrier presence on migrating fish, which will aid in implementing river management and policy to reduce the rate of reduction in the catchment and along north-west coast of England tributaries.

Not so faithful after all? Straying of seatrout in a fjord system

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Keywords: seatrout, straying, natal homing, partial migration, meta-population

Abstract: Natal homing is considered an essential evolutionary strategy for diadromous fishes in order to find suitable partners and habitat during spawning. However, not all individuals always return to their natal spawning grounds - behavioural trait known as straying. The aim of this paper was to investigate the extent of straying taking place in an anadromous brown trout (*Salmo trutta*) population from one donor to several recipient populations within a fjord system. 21 538 juvenile down migrating brown trout were tagged with Passive Integrated Transponder (PIT) tags in 2015 and 2016. All tagged fish were grouped according to their developmental stage as parr, pre-smolt or smolt. Out of 1815 returning seatrout, 37% were detected in non-natal rivers. Further, it was found that the longer they had been away at sea the less likely they were to stray. Additionally, the likelihood of straying was dependent on the length at tagging and the timing of juvenile migration with both being dependent on the developmental stage during tagging. The results of this study demonstrate high levels of straying that may take place in a seatrout populations, especially in areas where several suitable rivers are in close proximity. Further, the results of this study imply that in such highly connected areas multiple rivers combined form a meta-population structure. These aspects are extremely important to take into account when making management decisions about the populations.

Spatial and seasonal changes of food availability for juvenile Atlantic salmon (*Salmo salar*) in rivers of Northeast Iceland

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Keywords: Atlantic salmon, food webs, prey, food availability, River Continuum Concept, trophic levels, population dynamics, Arctic charr

Abstract: Freshwater ecosystems contain many species which depend on one another for survival. Therefore, studying food web dynamics of rivers could improve our knowledge on the state of the ecosystem, how energy is transferred between organisms, and the potential future trends of the inhabiting species. The drivers for survival and growth of Atlantic salmon (*Salmo salar*) populations in their northern limit needs to be further studied to better predict and manage the changes in population dynamics, especially as each population may respond differently to environmental variables. Additionally, the River Continuum Concept (RCC) shows that invertebrate communities will change along the river due to stream size and nutrients, and by investigating whether the invertebrate community within the river follows the RCC allows managers to better support the production of Atlantic salmon.

The purpose of this project is to determine the role of food and resources availability in juvenile Atlantic salmon growth rates and population abundances in the rivers of Northeast Iceland. In addition, other salmonids species in rivers, like the arctic charr (*Savelinus alpinus*), are also affected by prey availability and the presence of interspecific competition. The trophic relationships within the river could be described using long-term data, collected annually, on abundance of juvenile fish, stomach content, and river invertebrate abundance, and algae. Food availability may also vary spatially between and within rivers as well as seasonally. This could give a better indicator on the current feeding conditions and the population trend of Atlantic salmon in different rivers over time in Iceland.

Stability and persistence of an adaptive network of Atlantic salmon populations

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Keywords: dispersal, adaptive network, diversity, Atlantic salmon, demogenetic individual-based model

Abstract: Spatial dispersal is a ubiquitous trait in organisms. It is central in the theory of metapopulations, with potential consequences on their stability and persistence, as well as on local population dynamics. Although dispersal and metapopulation functioning have been suggested for salmonid, the consequences of dispersal are still underappreciated, likely because assessing dispersal in nature is challenging. Populations biocomplexity is also known to provide network stability through the portfolio effect. We investigate how an adaptive network of salmon populations fosters network stability and persistence by using a demo-genetic individual-based model mimicking an Atlantic salmon metapopulation. Our model depicts a complex relationship between dispersal and the metapopulation portfolio effect. In particular, we show that low dispersal rates favor metapopulation stability, via the demographic rescue of small populations and stabilizing effects of dispersal. However, higher dispersal rates tend to synchronize populations, leading to anti- rescue effects. We also show that dispersal and interpopulation genetic diversity allow quicker evolution towards optimal traits values, that can be described as evolutionary rescue. Altogether, we suggest that the spatial structure of Atlantic salmon populations should be considered in management and conservation strategies because the dynamics and capacity to respond to environmental changes of local populations rely on the whole metapopulation functioning via spatial dispersal and biocomplexity.

Assessing the migration of Atlantic Salmon *Salmo Salar* smolts through Scotland's largest Loch

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Keywords: Atlantic salmon, Acoustic telemetry, Migration, Freshwater, Lakes

Abstract: A large proportion of catchments contain free standing bodies of water that Atlantic salmon (*Salmo salar*) must navigate through before entering the marine environment. However, there is a lack of information concerning the behaviors salmon smolts exhibit through large free-standing bodies of water. The few studies assessing smolt movement through lakes have noted that in comparison to riverine migration smolts experience disorientation and undergo slow migrations. In this current study the objective was to assess drivers of salmon smolt movement throughout Loch Lomond, Scotland and compare the migratory pathways of successful and unsuccessful smolts. The preliminary results of this study indicated that smolts that did not migrate ($n = 21$) through the Loch were detected for six times longer, displayed more signs of disorientation, and had trajectories that were two times the length of successful smolts ($n = 28$). Water level and water temperature were the only environmental predictors influencing migration success. The likelihood of a smolt completing a successful migration was highest when water temperatures ranged between 8-9 °C, which is consistent with the average temperature Scottish smolts enter the marine environment. Secondly, the likelihood of successful migrants declined as Loch level increased. There is a dam located on the Leven and when it is open the water level in the Loch decreases and the flow within the river increases. During 2021, a flow meter will be placed at various locations throughout the Loch to determine if this is the main driver of movement.

Using diet to manipulate mitochondrial function, food intake and growth at high temperatures in brown trout (*Salmo trutta*)

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Keywords: temperature, mitochondria, growth, performance

Abstract: To understand how ectotherms such as fish will cope with increasing temperatures, we need a better understanding of the physiological mechanisms that determine their thermal limits. One hypothesis is that ATP production is limited at high temperatures due to decreasing mitochondrial efficiency (ATP produced per unit oxygen consumed). This may cause a reduction in growth rate due to the high associated energetic demands and lead to other effects related to ageing and survival including altered telomere dynamics. As part of this study, we aimed to experimentally alter mitochondrial efficiency in brown trout by feeding three contrasting diets (20 fish per diet) that differed in their HUFA (highly unsaturated fatty acid) levels; the aim was to alter membrane composition, leading to changes in leakiness and hence mitochondrial functioning. We predicted that with higher HUFA levels in the diet, the leakier and less efficient the mitochondria would be, resulting in reduced growth at high temperatures. Fish, acclimated to 19°C, were fed on these diets for 10 weeks, which we predicted would allow a sufficient change in membrane composition. Over the final two weeks of the experiment they were held individually to measure food intake and growth. At the end of the experiment the fish were culled, and tissue samples taken. Here we present data on the effect of the diet treatments on mitochondrial physiology in the liver and muscle. Results will be presented that relate diet to mitochondrial efficiency under elevated temperatures, and how mitochondrial efficiency relates to food intake and growth.

The role of environmental variation on the population dynamics of Atlantic Salmon (*Salmo salar*)

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Keywords: Atlantic salmon, matrix population models, metabolic theory, Iceland, population dynamics

Abstract: The anadromous Atlantic salmon life cycle can be described as stage structured due to its discrete life stages as well as its distinct river and marine phases. Such details need to be depicted when modelling the population dynamics of these species and can be therefore explored using a Matrix Population Model (MPM). MPMs are a convenient tool particularly for stage-structured populations as they are able to handle complex life cycles but can still be used to easily calculate population growth rates and generation times. However, a limitation of this approach is that through having discrete categories, parameterising Life Table rates and gathering data on each life stage can lead to a number of difficulties and often assumptions. To overcome this and create a mechanistic population model, I will incorporate metabolic traits to parameterise a MPM. The metabolic rate of an individual can be defined by its mass and temperature and such individual-level processes have been shown to be the fundamental biological rate that governs many observed patterns in ecology. Therefore, I will use metabolic theory to predict population dynamics of Atlantic Salmon, utilising metabolic-derived traits to lead to the initial development of a population model and understand the impact of environmental variability. This will enable an understanding of the fundamental drivers of Atlantic salmon populations and the first stage to predicting population dynamics. Predictions from this stage will be compared to empirical data, to validate the application of model.

Tracking fish swimming behaviour in the vicinity of a hydrokinetic turbine

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Keywords: Renewable energy, vertical axis turbine, fish behaviour, motion tracking, fish-flow-interaction.

Abstract: Hydrokinetic vertical axis turbines (VAT) are a promising alternative to traditional hydropower schemes to extract river and tidal energy. Their ability to operate in low-to-medium velocity flows with relatively low rotational speeds is thought to minimise the risk of fish collision; however, a major research gap exists in quantifying the impact of VAT on fish swimming behaviour. Small-scale experiments were undertaken in an open channel flume in the hydraulic laboratory at Cardiff University, UK, investigating the impact of a hydrokinetic VAT on spatial usage and swimming kinematics of juvenile rainbow trout (*Oncorhynchus mykiss*) for two flow discharges and turbine operational states (rotating and stationary). Fish swimming behaviour was recorded using a top-mounted camera, processed using a motion tracking algorithm, allowing the extraction of the fish's centre of mass and tail kinematics, and is linked to hydrodynamics. Hydrodynamic measurements conducted using Particle Image Velocimetry indicated a region of low mean streamwise velocity in the wake of the turbine, which was shifted towards the upstroke side and surrounded by regions of high-velocity flow on either side of the turbine. Fish swam within both low and high momentum regions of the turbine's wake, moved between the downstream and upstream section, and swam close to the turbine, presenting minimal avoidance behaviour. These experimental observations provide new insights into fish swimming kinematics and spatial preference adaptation to the presence and flow alterations caused by VATs. This new knowledge will help to inform turbine array design and operation, and to foster VAT as environmental-friendly technology.

Behavioural and physiological factors related to predation susceptibility of Atlantic salmon smolts

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Keywords: Acoustic telemetry, gene expression, migration, pathogenic microbes, *Salmo salar*

Abstract: Atlantic salmon (*Salmo salar*) population numbers have declined throughout their native distribution. The downstream migration undertaken by smolts to reach marine feeding grounds is a major mortality bottleneck in the life cycle of salmonids with predation often accounting for majority of these mortalities. Here, we pair the emerging technologies of high-throughput qPCR and predation acoustic transmitters to link prey physiology and behaviour with predator interactions to investigate mechanisms that may lead to migration failure or increased predation susceptibility. We applied this methodology to Atlantic salmon smolts migrating out of the Stewiacke River, Nova Scotia, a river system dominated by predatory striped bass. Smolts were tagged over three years, 2017-2019, with acoustic predation tags to quantify the amount of predation mortality during out-migration. Additionally, in 2019, we took gill biopsies of tagged smolts to quantify the expression levels of 57 genes related to physiology and identify the presence/absence of 18 pathogenic microbes. We investigate whether smolt physiological status or behaviour is predictive of migration fate.

Reconciling stock-assessment with MCMC - Optimizing the new ICES WGNAS Atlantic Salmon stock-assessment model

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Keywords: hierarchical Bayesian model, stage-based life cycle model, fisheries stock assessment, spatial synchrony

Abstract: Atlantic salmon stocks are widely depleted. Despite conservation measures, most of the population fail to recover. The widespread decline of marine survival rate in the recent decades is of major concern, and the underlying mechanisms are still unknown. A hierarchical Bayesian life-cycle model has been developed to improve the workflow and the scientific basis of stock assessment in the ICES Working Group on North Atlantic Salmon. The new model captures the dynamics of 25 large complex of population across the Atlantic basin. It allows for analyzing synchronicity in marine survival and probability of maturation among the different stock units. The new framework makes uses of Bayesian MCMC methods, known to be highly flexible, but at the cost of being computationally intensive and time consuming. Making such a model workable in the context of a working group workflow then requires specific development to optimize computation time and to reach MCMC convergence in a reasonable time. Here we present generic methodological guidelines to achieve better computational efficiency and apply it to this new stock assessment model to achieve a reasonable computational time. Our approach requires several steps: i) spotting model bottlenecks regarding run time and algorithmic efficiency; ii) identifying the origins of MCMC inefficiencies around those nodes; iii) adapting model structure, parameterization and/or MCMC algorithms around those bottlenecks to optimize MCMC. We finally present a model configuration answering practical requirements as well as future model developments.

Exercise swimming effects on reproductive success in farmed female brown trout (*Salmo trutta*)

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Keywords: Swimming exercise, farmed fish, aquaculture, *Salmo trutta*, reproductive success

Abstract: The reproductive migration of salmonid species is one of the most famous examples of migrations in the animal kingdom. Salmonids are also one of most used fish in aquaculture for food production but aquaculture salmonids are also used for conservation efforts with stocking programs. However, the current rearing conditions in the farms does not allow adult spawners to develop their normal migration behavior and it is unknown whether it might lead to negative effect on their offspring. Previous studies have shown that swimming improves several aspects of fish physiology such as cardiac performance, growth, and immunity system. In the current study, the aim was to study the effects of simulated migration effort, i.e. induce swimming exercise training during natural migration period, on reproductive success of aquaculture female adult brown trout (*Salmo trutta*) and on their offspring. To do that we randomly divided the spawners in two groups with two different water flow conditions, control group with normal water velocity used in aquaculture (0.2 bl/s) and exercise group with an intense water flow (0.7 bl/s) for 6h per day for 5 weeks. After 12 days of resting, the artificial reproduction was induced. To investigate the effect of swimming exercise on the reproductive success we analyzed the mass, length, condition factor, fecundity and eggs size of the spawners and hatching success, survival rate in different age classes and mass, length and condition factor of the offspring.

Evolution of maturation reaction norms along a life-history gradient in Atlantic salmon

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Keywords: age at maturity, phenotypic plasticity, evolution, Atlantic salmon, marine growth

Abstract: Age at maturity is an important life-history trait due its effects on individual fitness and population demography. In Atlantic salmon, larger, later-maturing individuals usually have greater reproductive success, but they also face a greater risk of dying before first reproduction. Marine growth conditions are considered to be an important factor influencing age at maturity, but according to the empirical evidence, there is no universal rule for how marine growth conditions influence age at maturity in Atlantic salmon. Populations that are under different selection pressures may differ in the optimal plastic response to growth conditions, and may therefore evolve different maturation reaction norms. There is a large variation in life history among Atlantic salmon populations, with some populations being dominated by small, early-maturing fish, and others being dominated by large, late-maturing fish. Population differences are to a large degree genetic, and genomic evidence indicate that these traits are selected to fit the natural environment of the population. We used a long-term scale dataset from 135 Norwegian populations to study how marine growth conditions influence age at maturity in Atlantic salmon, and whether this relationship varies among populations depending on their life history. We found that in populations dominated by early-maturing salmon, the proportion delaying maturation decreased as growth conditions improved, while maturation was less influenced by growth in populations dominated by late-maturing salmon. Our findings suggest that populations that are genetically differentiated and that have evolved different life histories, also have evolved different maturation reaction norms.

DNA methylation is not a main gene regulatory mechanism in the process of smoltification

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Keywords: DNA methylation, RRBS, smoltification, gene regulation, RNAseq

Abstract: Prior to sea migration Atlantic salmon undergoes radical physiological and behavioural changes in order to adapt to an adult life in the marine habitat. These coordinated processes are believed to be regulated by a combination of physiological status and environmental cues such as temperature and photoperiod. One well-studied physiological change during smoltification is remodelling of lipid metabolism properties of the liver, possibly an adaptation to a very different dietary availability of long-chained polyunsaturated fatty acids in the sea. However, the mechanism underlying this remodelling of tissue function is still unknown. Here we test the hypothesis that dynamic changes in regulation of DNA-methylation is important in driving smoltification related changes in liver-tissue function. To measure DNA-methylation we apply reduced representation bisulfite sequencing (RRBS) and assess whether this observed change in the liver transcriptome is reflected in the methylation landscape. We do not see an overall different methylation signal between the fish from the different stages of smoltification for our experimental set up. However, the signal might be weak but still carry information. When doing a differential methylation analysis followed by KEGG overrepresentation analysis, there seem to be some impact of photoperiod and transition to salt water in the methylation data. Still, these results do not strongly support DNA methylation as a main regulatory component of the smoltification process in the liver and during transition to sea water.

The genomic consistency of the loss of anadromy in an Arctic fish (*Salvelinus alpinus*)

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Keywords: parallelism, allopatry, landlocked, anadromy, incipient speciation, SNPs

Abstract: While many anadromous fishes are known to occasionally become trapped in landlocked lakes, the genetic consequences of this loss of anadromy and its consistency across landlocked populations are not well understood. Restricted to a freshwater environment year-round and isolated from other populations, landlocked populations may quickly genetically diverge from anadromous populations due to selection and drift. Replicate landlocked populations might demonstrate little genetic parallelism if drift hampers adaptation to consistent selective pressures. Understanding the repeatability of genetic differentiation between landlocked and anadromous populations is critical for management as gene flow may still occur between these populations if landlocked populations subsequently regain sea-access. We employed an 87k SNP array to investigate 7 replicate pairs of nearby landlocked and commercially exploited anadromous Arctic Charr (*Salvelinus alpinus*) populations across 5 drainages within Labrador, Canada. Paired landlocked and anadromous populations were characterized by high genetic differentiation. There was generally little consistency in outlier SNPs across pairs, potentially due to high levels of genetic drift in landlocked populations. However, several outlier SNPs, genes, and paralogs were detected between multiple pairs of landlocked and anadromous populations, suggesting the potential for genetic parallelism. Our results suggest that despite their isolation, selection may drive repeated local adaptation and incipient speciation in landlocked populations.

Microbial ecology, metabolism and growth in post-smolt Atlantic salmon

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Keywords: Aquaculture, metabolism, microbiome, Atlantic salmon

Abstract: In recent years, a wealth of new studies examined the variation within host microbial communities to determine its role in modulating host physiology, health and ecology. Yet, the extent of those variations and their potential drivers are still not well understood. Here, we characterized microbiomes of post-smolt Atlantic Salmon of different genetic background in an aquaculture setting. We measured potential environmental drivers of gut microbial community changes, as well as physiological parameters of the host. Our findings verify causal links between host-associated microbial assemblages and host phenotype and could eventually lay base for the use of pro- and prebiotics to increase fish health and productivity of farmed Atlantic Salmon.

Predicting the effects of environmental factors and juvenile body length on adult marine return rates of Atlantic salmon *Salmo salar*

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Keywords: Marine survival, passive integrated transponder tags, state space model, body size

Abstract: Globally, populations of Atlantic salmon, *S. salar*, have declined for decades. There are many factors thought to be contributing to this trend, including habitat degradation, over-exploitation, and climate change. As an anadromous species, adult return rates from marine habitats to freshwater are typically quite low. Recent work has shown that smolts with large body lengths at the onset of their seaward migration are more likely to survive at sea and return to freshwater as adults. Knowing that larger smolts have higher adult return rates, we tested whether this signal is robust to a suite of biotic and abiotic factors, such as sea surface temperature and sea bass abundance, in the estuary during the early part of their migration. To do so, we used data from a thirteen-year dataset where up to 600 PIT-tagged smolts were captured and measured annually during their migration down the River Frome, UK. We developed a state-space model to describe the probability of individual *S. salar* returning as one sea winter or multi sea winter adults, while accounting for imperfect detection. These results should be of interest to scientists and river managers working on salmon restoration projects.

Transcriptomic predictors of post-smolt migration fate in juvenile Canadian Atlantic salmon from multiple stocks in eastern Canada

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Keywords: Transcriptomics, telemetry, migration

Abstract: Atlantic salmon smolts experience high mortality during the marine sequence of their migration. However, the risk factors underlying marine mortality have thus far been elusive because small fish are extremely challenging to monitor in the open ocean. To determine how individual status contributed to mortality risk, we combined transcriptomic technology with acoustic telemetry to track wild smolts from four Atlantic Canadian rivers up to 800 km into the Gulf of St. Lawrence. Decision trees and multivariate ordinations were used to assess predictors of marine survival among the smolts, 15% of which were detected at receiver lines again in the Gulf of St Lawrence. Results provide some of the highest resolution data describing the gene expression profiles of wild smolts and the longest distance survival data ever to be analyzed in the context of individual variation in smolt survival.

The role of the microbiome in the gill health of farmed Scottish Atlantic salmon

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Keywords: Atlantic Salmon, microbiome, gill disease, gill health,

Abstract: Scotland is a large farmed Atlantic salmon producer, creating approximately 10,000 jobs and valued at £601 million in 2017 making salmon health vital for the industry. Gill disease is now a prominent issue, leading to major mortalities. Recently, Complex Gill disease (CGD), thought to be multifactorial in nature with a wide range of clinical presentations, has emerged, with little known about the cause or development of CGD. We aim to characterize and investigate the role of the gill microbiome in gill health and CGD outbreaks in farmed Atlantic salmon throughout production cycles from freshwater hatcheries to final harvest from seawater cages. To achieve this, we are tracking the gill microbiome of farmed salmon from four salmon farms located along the Scottish coast, from freshwater hatcheries transfer to seawater farms. This includes two Autumn (2018) and two Spring (2019) inputs over a period of up to 18 months until harvest. One farm was monitored intensely every two weeks, and three farms every 4 weeks. Characterisation of the gill microbiome will be performed by 16S rRNA gene amplicon sequencing. To-date, a total of almost 600 fish have been sampled for the study. DNA extraction and 16S rRNA primer region were optimised for the samples by compared regions of the 16S rRNA gene to identify the optimal region to reduce host DNA contamination of our 16S libraries. We are currently awaiting results from one longitudinal study and a study mapping the changes in the microbiome during transfer to seawater from hatcheries.

The influence of navigation infrastructure on the downstream movement of juvenile Atlantic salmon in a Scottish river

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Keywords: Atlantic salmon; navigation; migration; salmonids; telemetry

Abstract: Navigation infrastructure can negatively influence the migration of fish populations, yet the severity of its effects remain poorly understood. Using acoustic telemetry we investigate how a 19th century canal system in a large Scottish river influences the movement rate, delay, timing and success of seaward migrating juvenile Atlantic salmon (*Salmo salar*). Results highlight distinct patterns of movement between river sections and canal sections, with fish exhibiting slower progress and distinct temporal movement patterns whilst migrating through the canal reaches of the river. Together, these data add to the body of work showing that navigation locks and hard engineering are a potential threat to migrating salmonid species.

Long-term changes in marine growth modulates maturation schedule in Atlantic salmon

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Keywords: Atlantic salmon, life history strategy, marine growth, maturation decision, probabilistic reaction norm.

Abstract: Recent decline in abundance of Atlantic salmon and concomitant change in life history may result from a decline in the growth conditions during marine migration. Available literature suggests the existence of a sex-specific reaction norm with body length at the end of first summer at sea that modulates maturation. However, the extent to which this mechanism explains variations in age at maturity remains unclear. Individual growth measurements from historical scales collected from 5 rivers in the Channel (2001-2016) were used as proxy of body length at different life stages. Over the study period, growth over first summer at sea declined in all populations affecting length at end of first summer. Results suggest that individual probability to mature and return after one year at sea increases with growth. Response strongly differ between males and females; Females need to achieve higher growth than males for the same probability to mature. This supports the hypothesis of a sex-specific probabilistic reaction norm with river specific effects, likely to explain part of temporal and spatial variations in proportion of small early maturing fish in salmon populations. Ongoing research seeks to develop a modelling approach to integrate this new knowledge and resolve the intricate mechanisms relating growth, and size selective survival and maturation to explain the variability of abundance and age composition of returns.

Can the past explain the present? Investigating long-term trends in Atlantic salmon (*Salmo salar*) resource use, trophic position, and distribution at sea

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Keywords: stable isotopes, marine migration, compound-specific stable isotope analysis, Greenland

Abstract: Atlantic salmon (*Salmo salar*) populations have declined considerably over the last 50 years to the point where many populations are now threatened or endangered. This decline is believed to be largely attributed to low marine survival caused (in part) by changes in ocean temperature and prey abundance. To date however, research has focused heavily on the freshwater portion of the Atlantic salmon lifecycle, while the link between changes in the marine environment and Atlantic salmon growth, diet, and distribution at sea remains unknown. Studying migratory species in a marine environment presents a challenge as direct observations are difficult to make, and the setting is spatially complex. Stable isotope analysis and compound-specific isotope analysis presents a cost-effective alternative to traditional tagging studies as a consumer's isotope ratios reflect both its trophic position and the different trophic pathways through which it assimilates energy and mass. Coupling stable isotope analysis with archived Atlantic salmon scales provides an opportunity to investigate Atlantic salmon marine ecology over a large time scale. The aim of this study is to detail long-term trends in Atlantic salmon marine resource use, trophic position, and foraging locations of fish caught in Bay of Fundy rivers and the North West Atlantic Ocean around Greenland over a 50-year time period and characterize how marine primary production pathways that support these salmon populations has changed through time.

Diversity of chars in the central Canadian Arctic

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Keywords: Hybridization and introgression, *Salvelinus*, morphometrics, community-partnered research, species at risk

Abstract: The Canadian Arctic is warming at approximately three times the global rate, which has significant impacts on both local communities and aquatic species. Anadromous fishes, which are important to food security due to their abundance and availability for year-round harvest, are especially vulnerable to climate-induced change due to their life stage-specific dependency on multiple habitats. Despite this vulnerability, the genetics, ecology, and demography of these fishes – the closely-related Arctic char (*Salvelinus alpinus*) and Dolly Varden (*Salvelinus malma*) – remain understudied, making it difficult to anticipate the effects of climate change on species persistence. The community of Kugluktuk, located along the Coppermine River in the central Canadian Arctic, has historically supported a subsistence Arctic char fishery. Since 2015, community members have observed fewer char present in the river, and have reported physical variation in fish appearance. These observations, along with limited scientific evidence, have led to the belief that Dolly Varden (*S. malma*) may be present in the Coppermine River, several hundred kilometers east of their purported range. I am using next-generation sequencing technologies, as well as meristics and morphometrics, to evaluate the presence of both Arctic char, Dolly Varden, and hybrids in the Coppermine River. Meristic analyses suggest that the Coppermine River supports both Arctic char and Dolly Varden. Preliminary genetics results suggest that fish in the Coppermine River are genetically distinct from fish in surrounding river systems. These data will help inform habitat restoration and management, thereby helping to ensure the viability of a critical subsistence fishery.

ddRADSeq approach reveals hierarchical genetic population structure in Icelandic anadromous Arctic char

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Keywords: Arctic charr, anadromous, ddRADSeq, population genomics, Iceland

Abstract: Assessing genetic connectivity and differentiation within a metapopulation is one major task prior to local adaptation evaluation, evolutionary history reconstruction, resource management as well as conservation. Arctic charr (*Salvelinus alpinus*) colonized Icelandic water systems following the retreat of the ice cap around 10,000 years ago, and since then have diversified into multiple forms. In contrast to substantial interest in the adaptive diversification of landlocked charr populations, the Icelandic anadromous charr populations are largely unexplored. Here we investigate the genetic population structure in anadromous charr from 18 locations inhabiting the coast of Iceland. By using ddRADSeq we genotyped 17,946 filtered single nucleotide polymorphisms (SNPs) for 251 anadromous individuals (average sample size per location = 14) along with 134 landlocked individuals from 6 Icelandic lakes and 34 individuals from 2 abroad populations. Our results reveal that Icelandic charr populations form a clearly distinct genetic cluster from the abroad populations at a broad spatial scale. While at finer spatial scales within Iceland, Icelandic anadromous charr populations have higher heterozygosity compared to landlocked charr. Hierarchical genetic structures were observed for both anadromous charr and landlocked charr, as neighboring hydrographic systems harbor distinct populations grouped by regions.

The relationship between eDNA particle concentration and organism abundance in nature is strengthened by allometric scaling

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Keywords: Environmental DNA, eDNA, abundance, allometry, allometric scaling

Abstract: Organism abundance is a critical parameter in ecology, but its estimation is often challenging. Approaches utilizing eDNA to indirectly estimate abundance have recently generated substantial interest. However, preliminary correlations observed between eDNA concentration and abundance in nature are typically moderate in strength with significant unexplained variation. Here, we apply a novel approach to integrate allometric scaling coefficients into models of eDNA concentration and organism abundance. We hypothesize that eDNA particle production scales nonlinearly with mass, with scaling coefficients < 1 . Wild populations often exhibit substantial variation in individual body size distributions; we therefore predict that the distribution of mass across individuals within a population will influence population-level eDNA production rates. To test our hypothesis, we collected standardized body size distribution and mark-recapture abundance data using whole-lake experiments involving nine populations of brook trout. We correlated eDNA concentration with three metrics of abundance: density (individuals/ha), biomass (kg/ha) and allometrically scaled mass (ASM) ($\sum(\text{individual mass}^{0.73})/\text{ha}$). Density and biomass were both significantly positively correlated with eDNA concentration (adj. $r^2 = 0.59$ and 0.63 , respectively), but ASM exhibited improved model fit (adj. $r^2 = 0.78$). We also demonstrate how estimates of ASM derived from eDNA samples in "unknown" systems can be converted to biomass or density estimates with additional size-structure data. Future experiments should empirically validate allometric scaling coefficients for eDNA production, particularly where substantial intraspecific size distribution variation exists. Incorporating allometric scaling may improve predictive models to the extent that eDNA concentration may become a reliable indicator of abundance in nature.