Salmon Aquaculture - Case Studies

Using Standard BioTools Microfluidic Technology

Standard BioTools™
March 2023

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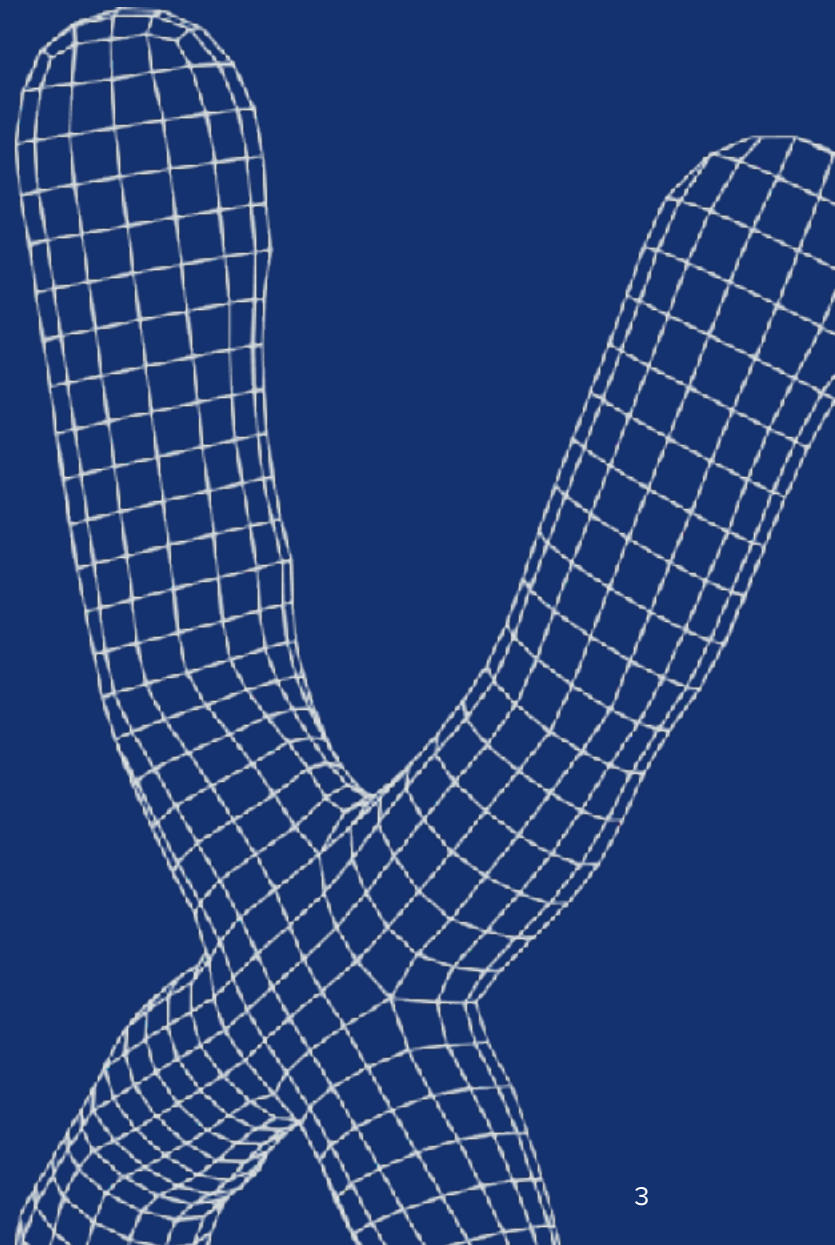
Gene Expression and Fish Welfare



Gene Expression and Fish Welfare

Any further question?

Talk to us

The Atlantic salmon's stress- and immune-related transcriptional responses to moderate hypoxia, an incremental temperature increase, and these challenges combined

Objective: To examine how moderate hypoxia and incremental temperature increase affects transcript expression in the liver of post-smolts as compared to control conditions

Utilization of Standard BioTools products:

- Biomark HD System
- 96.96 dynamic arrays

Conclusions:

- Identified extensive transcriptional changes in stress and immune-related genes in the liver of post-smolt Atlantic salmon when exposed to temperature increase alone, or in combination with moderate hypoxia
- Identified several genes to be used as markers of stress response in post-smolt Atlantic salmon

Beemelmanns, et al. "The Atlantic salmon's stress- and immune-related transcriptional responses to moderate hypoxia, an incremental temperature increase, and these challenges combined". G3 (2021)

Gene Expression and Fish Welfare

Any further questions?

Talk to us

Background

- Increasing water temperatures and de-oxygenation of the oceans as a result of global warming may negatively impact the overall health of farmed Atlantic salmon.
- Few studies have looked at the combined effects oof hypoxia and incremental temperature change on gene expression in salmonids.
- Authors measured gene expression of various stress and immune markers in the liver, which was selected for its role in stress response, nutrient metabolism, and immunity

Beemelmanns, et al. “The Atlantic salmon’s stress- and immune-related transcriptional responses to moderate hypoxia, an incremental temperature increase, and these challenges combined”. G3 (2021)

Gene Expression and Fish Welfare

Any further questions?

Talk to us

Methods

- Total RNA extracted from flash frozen liver tissue of 360 Atlantic salmon subjected to Standard BioTools reverse transcription, preamplification, and data collection workflows.
- Data collected using the 96.96 GE IFC on the Biomark HD.
- 41 gene target panel included genes related to the following categories:
  - Heat shock response
  - Stress response
  - Oxidative stress response
  - Cellular metabolism
  - Immune response
  - Transcriptional regulation (methylation)

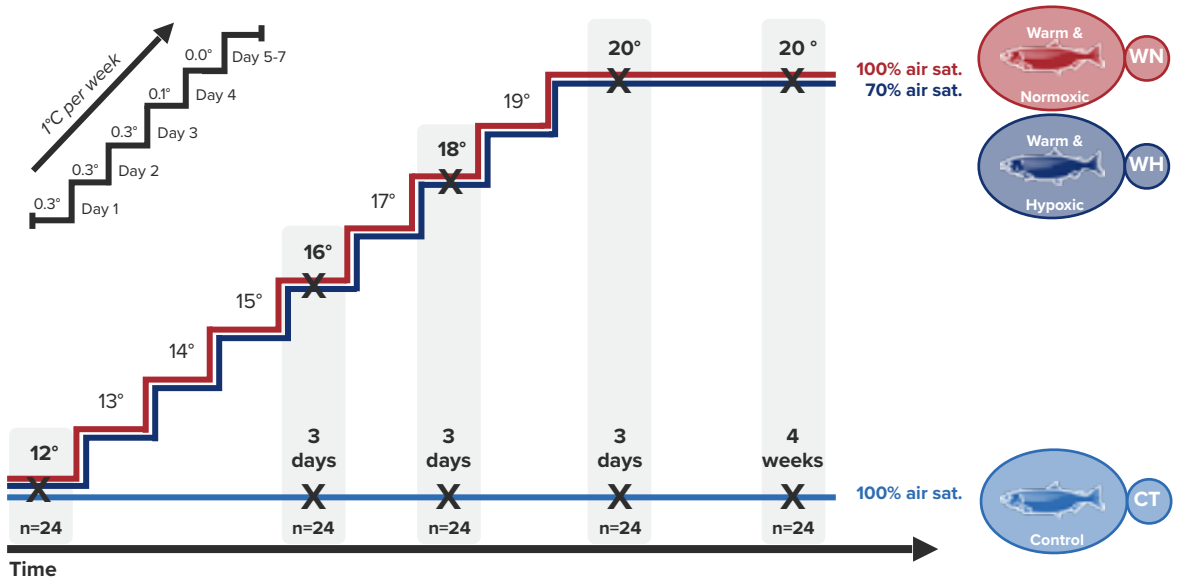


Figure 1 Schematic diagram of the experimental design. Post-smolt Atlantic salmon were either subjected to: (i) a constant water temperature of 12°C and normoxia (100% air saturation) (Control, CT); (ii) a temperature increase from 12°C to 20°C under normoxia (100% air sat.) (Warm & Normoxic, WN); or (iii) moderate hypoxia (~70% air sat.) and then the incremental increase to 20°C (Warm & Hipoxic, WH). The water temperature was gradually increased by 1°C week $^{-1}$ using the following regimen: 1st day, +0.3°C; 2nd day, +0.3°C; 3rd day, +0.3°C; 4th day, +0.1°C; 5th – 7th days no increase in temperature (see upper-left portion of the figure). The sampling of liver tissue was performed initially at 12°C, then 3 days after reaching 16°C, 18°C and 20°C, and 4 weeks after the temperature reached 20°C (20°C-4wks) (n = 8 per treatment/temperature, N = 120 total). The transcriptional responses in the liver of these fish were assessed by measuring the transcript expression of 45 biomarker genes related to the heat shock response, oxidative stress, apoptosis, immunity, metabolism and epigenetics using qPCR (Fluidigm Biomark™ HD).

Beemelmanns, et al. “The Atlantic salmon’s stress- and immune-related transcriptional responses to moderate hypoxia, an incremental temperature increase, and these challenges combined”. G3 (2021)

Gene Expression and Fish Welfare

Any further questions?

Talk to us

Results and conclusions

Results:

- High temperature initiates immune-related transcript expression changes in the liver
- Moderate hypoxia at 12°C impacts hypoxia and stress related transcript expression, but not immune related genes
- Immune transcript expression at 4 weeks was less impacted as compared to the initial 3-day exposure
- Persistent changes observed in epigenetic markers that facilitate thermal acclimation responses

Conclusions:

- Identified several genes that can be used as biomarkers to characterize transcriptional stress response

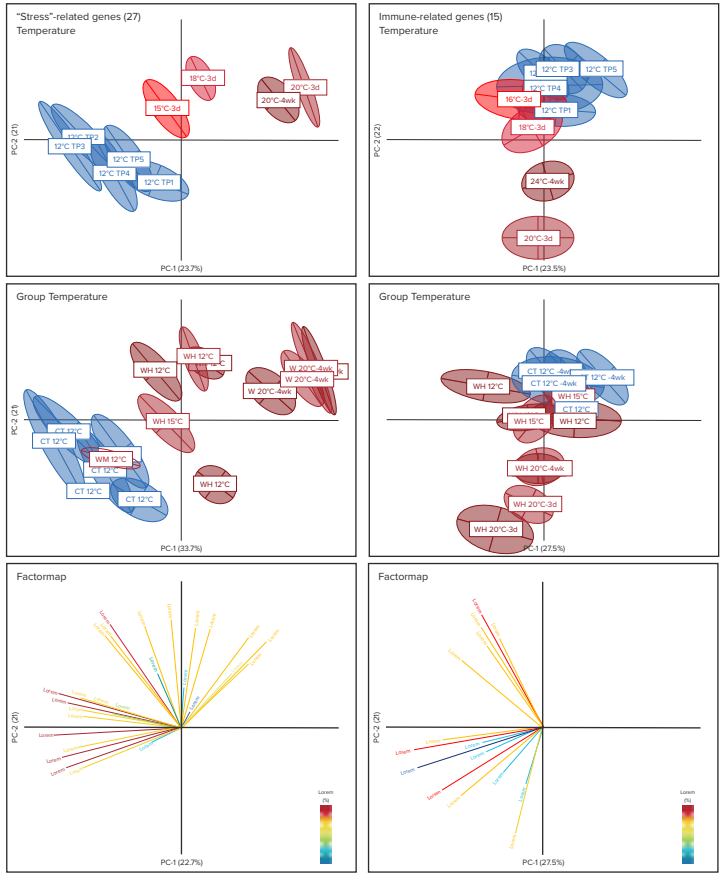
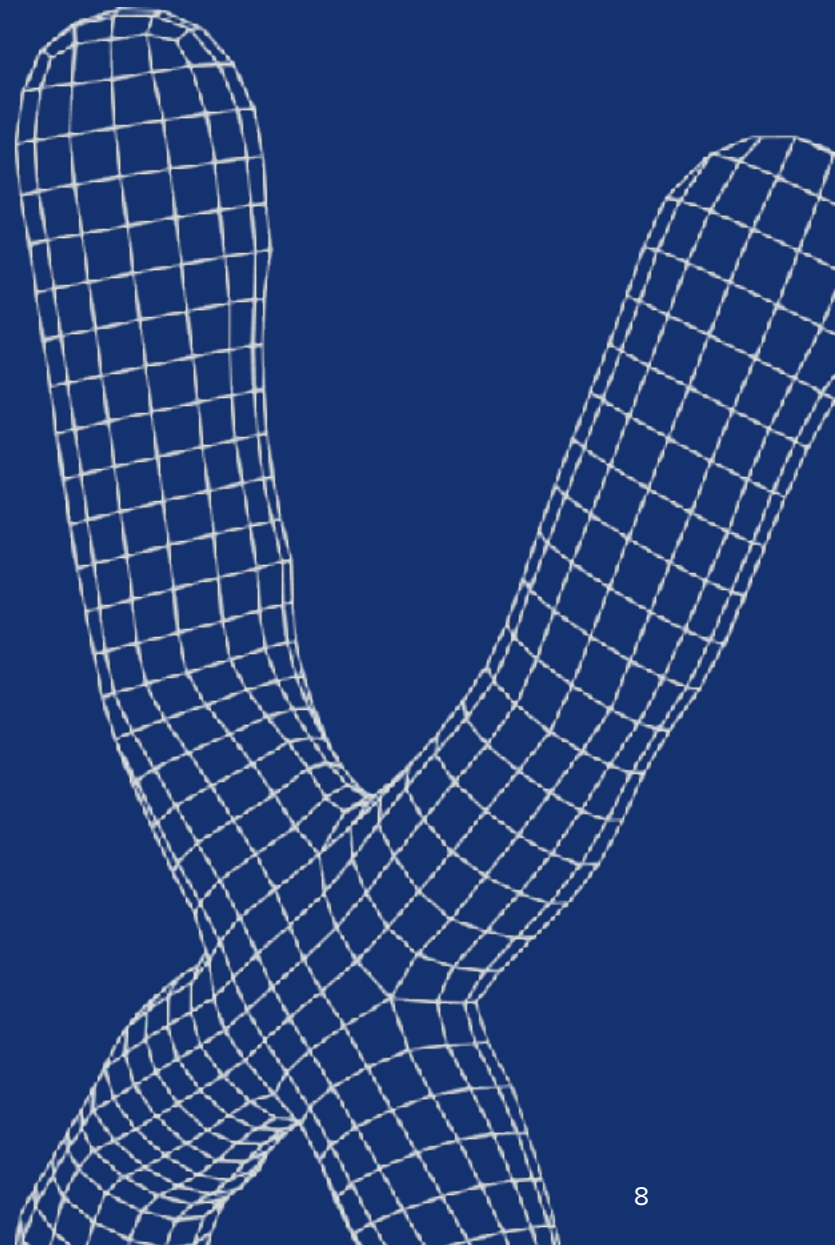


Figure 2: Transcriptional responses of stress- and immune-related genes in Atlantic salmon liver

Beemelmanns, et al. "The Atlantic salmon's stress- and immune-related transcriptional responses to moderate hypoxia, an incremental temperature increase, and these challenges combined". G3 (2021)

Gene Expression and Immune Response



Gene Expression and Immune Response

Objective: To explore the role of antimicrobial peptides β-defensins and cathelicidins in N. perurans, which causes amoebic gill disease

Utilization of Standard BioTools products:

- Biomark HD System
- 48.48 dynamic arrays

Conclusions:

- Biomark HD shows β-defensins -3 and -4 and cathelicidin 2 were upregulated in gill of parasite-challenged salmon
- Indicate potential novel roles in innate immune responses to N. *perurans*

McGrath, et al. "Antimicrobial peptide gene expression in Atlantic salmon (Salmo salar) seven days post-challenge with Neoparamoeba perurans". Developmental and Comparative Immunology (2022)

Gene Expression and Immune Response

Any further questions?

Talk to us

Background

- Amoebic gill disease (AGD) is an infection of Atlantic salmon caused by N. perurans, and is a significant contributing factor to fish mortality
- Antimicrobial peptides (AMP) β-defensins and cathelicidins, mediators of early immune response, have not yet been evaluated in relation to AGD.
- To assess the functional role that these genes play in local and systemic responses to infection, the authors measured gene expression in swim bladder, gill, and intestine from healthy and infected salmon

McGrath, et al. “Antimicrobial peptide gene expression in Atlantic salmon (Salmo salar) seven days post-challenge with Neoparamoeba perurans”. Developmental and Comparative Immunology (2022)

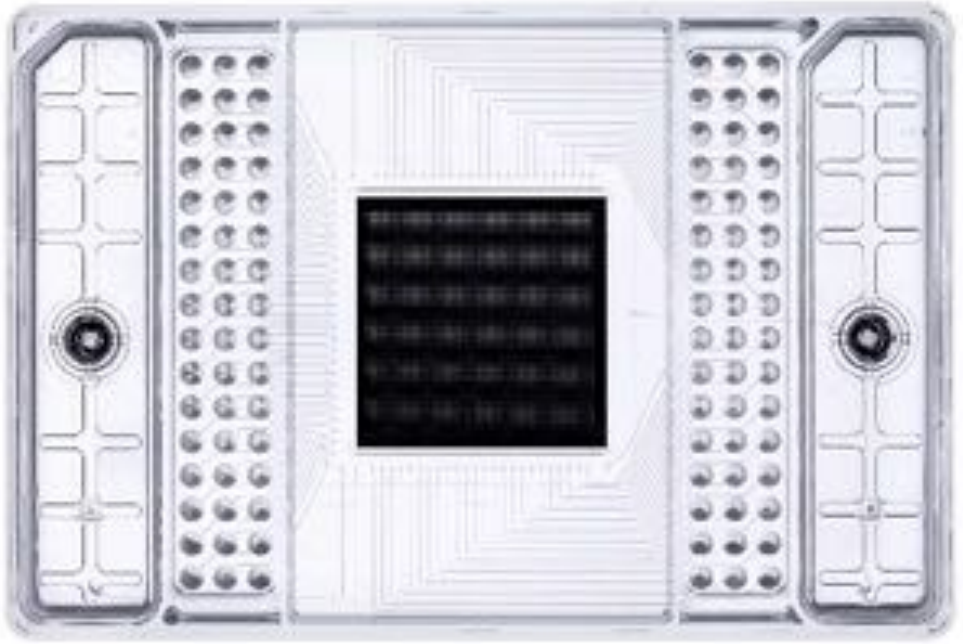
Gene Expression and Immune Response

Any further questions?

Talk to us

Methods

- Total RNA was extracted from swim bladder (n=12), whole intestine (n=12), and whole gill (n=12) in control and infected salmon.
- Standard BioTools workflows for reverse transcription, preamplification, and data analysis were followed.
- Data collected using the 48.48 GE IFC on the Biomark HD.
- Housekeeping genes elongation factor 1αa (EF1αa) and elongation factor 1αb (EF1αb) were selected as they are stable across a range of organs in Atlantic salmon.



McGrath, et al. “Antimicrobial peptide gene expression in Atlantic salmon (Salmo salar) seven days post-challenge with Neoparamoeba perurans”. Developmental and Comparative Immunology (2022)

Gene Expression and Immune Response

Any further questions?

Talk to us

Results and conclusions

Results:

- In infected salmon, β-defensin and cathelicidin expression was upregulated in the gill in response to early phase of parasitic infection, before clinical presentation was observed
- Upregulation not observed in infected intestine and swim bladder, suggesting there is just a localized immune response in the gill at early stages of infection
- β-defensin and cathelicidin expression found in healthy swim bladder for the first time

Conclusions:

- Atlantic salmon AMP genes play a novel role in early asymptomatic innate immune responses to the parasite N. perurans
- β-defensin and cathelicidin expression confirmed in both healthy and infected Atlantic salmon
- Swim bladder (whose ancillary functions are largely unexplored) may have a novel immune role

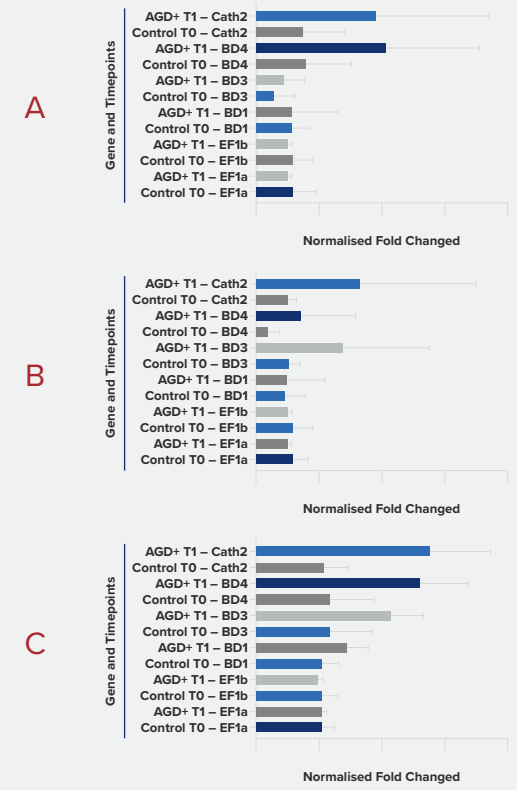
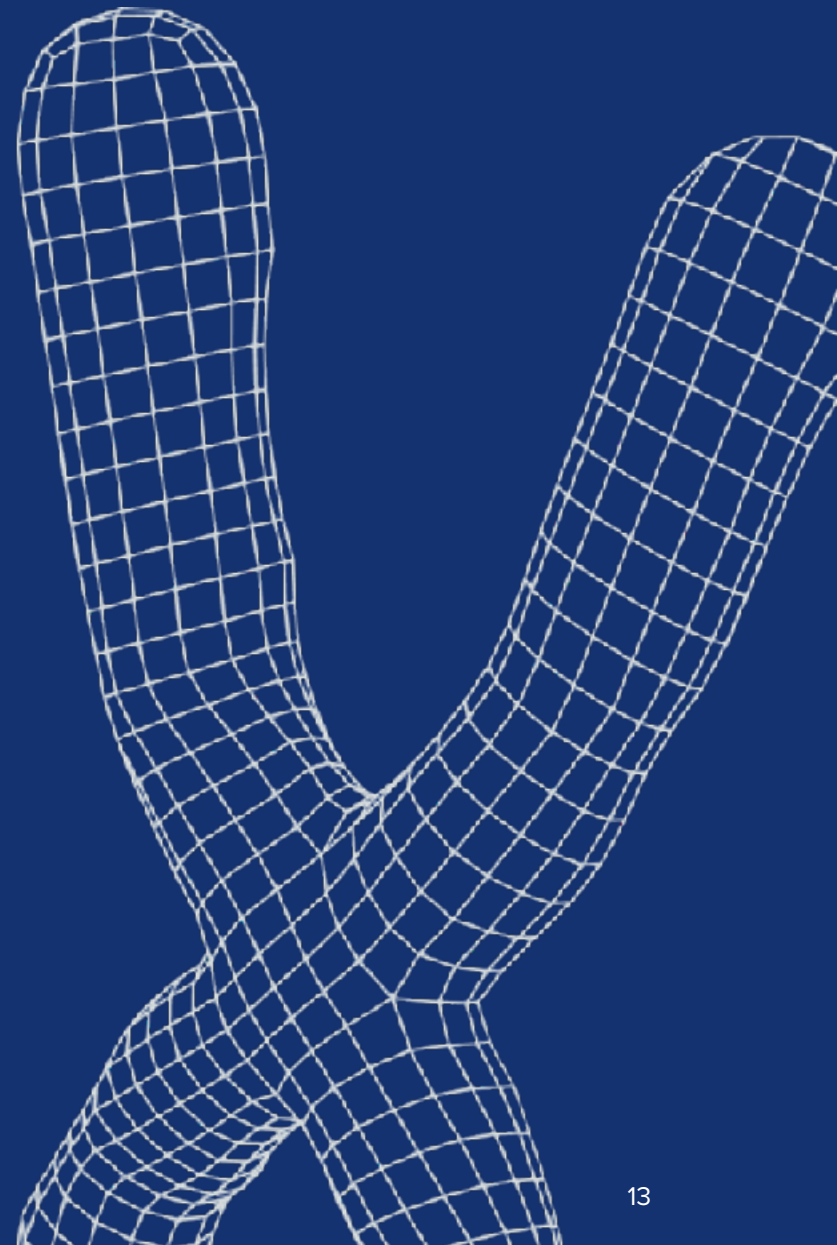


Fig. 4. A-C: Comparision of AMP gene expression between Control T_0 cohort (Control T0) and *N. perurans* Infected T1 cohort (AGD + T1) in swim bladder (3A), intestine (3B) and gill (3C). Expression of AMP genes was normalized to housekeeping gene expression in the selected organs.
*Statistical analisis of AMP gene expression was performed using a non-parametric Mann-Whitney test. Statistically significant p-values are denoted *:(p-value = < 0.05). Bars represent mean values ±standard deviation.*

McGrath, et al. "Antimicrobial peptide gene expression in Atlantic salmon (Salmo salar) seven days post-challenge with Neoparamoeba perurans". Developmental and Comparative Immunology (2022)

Gene Expression and Epidemiology



Gene Expression and Epidemiology

Any further questions?

Talk to us

SCIENCE ADVANCES | RESEARCH ARTICLE

ECOLOGY

Aquaculture mediates global transmission of a viral pathogen to wild salmon

Objective: To illuminate the epidemiology of Piscine orthoeovirus-1 (PRV-1) in wild fish populations, particularly in endangered wild Pacific salmon

Utilization of Standard BioTools products:

- Biomark HD System
- IFC controller HX
- 96.96 dynamic arrays

Conclusions:

- Atlantic salmon aquaculture may have facilitated PRV-1 spread from Europe to the North and Southeast Pacific
- PRV-1 in endangered wild Pacific salmon may be fueled by aquacultural transmission, based on phylogeographic analyses and rtPCR surveillance

Mordecai, et al. "Aquaculture mediates global transmission of a viral pathogen to wild salmon". Science Advances (2021)

Gene Expression and Epidemiology

Any further questions?

Talk to us

Background

- Piscine orthoreovirus (PRV) causes moderate to severe pathological changes in salmon, endangering wild populations and resulting in downstream effects in the ecosystem.
- The introduction and origin of PRV-1 into wild salmon populations is unclear, thought to potentially be from farmed fish/aquaculture.
- The authors analyzed viral genomes to help determine the evolutionary history of PRV and quantify transmission dynamics between farm and wild salmon populations.

Mordecai, et al. “Aquaculture mediates global transmission of a viral pathogen to wild salmon”. Science Advances (2021)

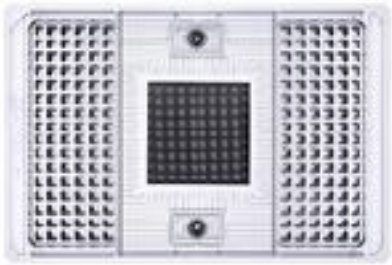
Gene Expression and Epidemiology

Any further questions?

Talk to us

Methods

- Data collected using the 96.96 GE IFC on the Biomark HD, to quantify the presence and relative load of viral PRV RNA. (Chinook n=6791, coho n=2165, sockeye n=4140)
- Samples were sequenced with NGS
- Phylogenetic analyses were performed to track the evolution of PRV-1 in wild and aquaculture groups
- PRV epidemiological modeling performed to track PRV prevalence in aquaculture and describe the distance between wild salmon vs aquaculture



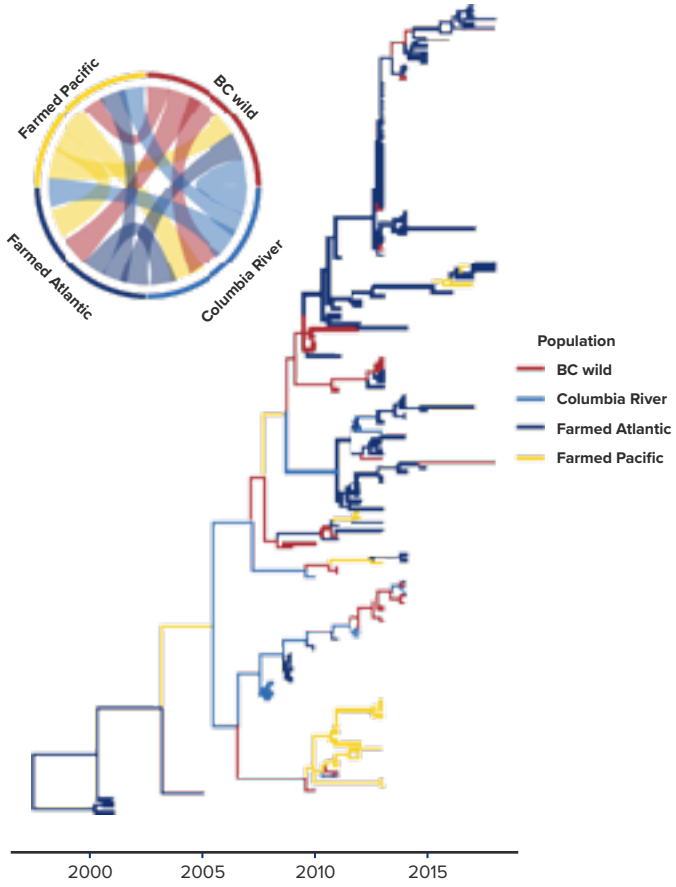


Fig.4. Phylogenetic evidence of transmission between populations. Maximum

Mordecai, et al. “Aquaculture mediates global transmission of a viral pathogen to wild salmon”. Science Advances (2021)

Gene Expression and Epidemiology

Any further questions?

Talk to us

Results and conclusions

Results:

- Origin of PRV-1 in the NE Pacific suggested to have diverged from a strain in the Atlantic in 1989
- PRV-1 prevalence in wild Chinook salmon was closely tied to farm proximity, suggesting transmission from farm to wild
- Phylogenetic reconstruction showed that wild and farmed salmon shared clades, indicating PRV-1 transmission

Conclusions:

- Freshwater hatcheries are a source of PRV transmission to wild salmon populations
- Standard BioTools IFC enabled high-throughput pathogen detection in thousands of samples, providing a fast, cost-effective solution over traditional qPCR and sequencing methods.

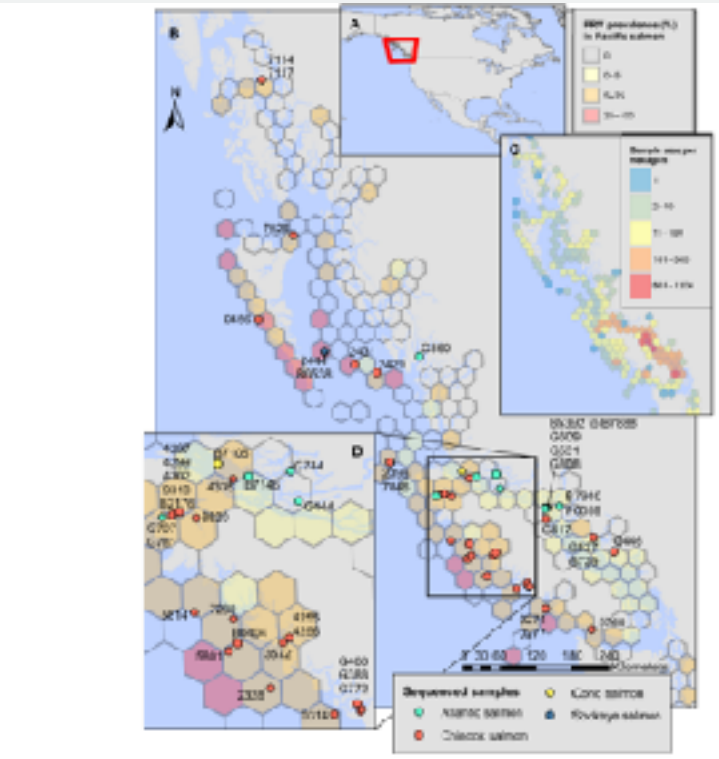


Fig. 3. Epidemiological map of PRV-1 distribution and prevalence. Prevalence ov PRV (hexagons) along the British Columbia coastline in three wild-sampled salmon spieces (Chinook, *n=6412*; coho, *n-2132*: sockeye, *n=3845*) and position of sequenced aquaculture and wild samples (points). (**A**) Locations of BC coast on map of North America. (**B**) PRV prevalence and sample sites along BC coastline. (**C**) Sample size of wild-sampled fish per hexagon. (**D**) Explanded region with high sequence sample density from (B).

Mordecai, et al. “Aquaculture mediates global transmission of a viral pathogen to wild salmon”. Science Advances (2021)

Modern aquaculture is powered by X9

Any questions?

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Trout Aquaculture - Case Studies

Using Standard BioTools Microfluidic Technology

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March 2023

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SNP genotyping for parentage

Any questions?

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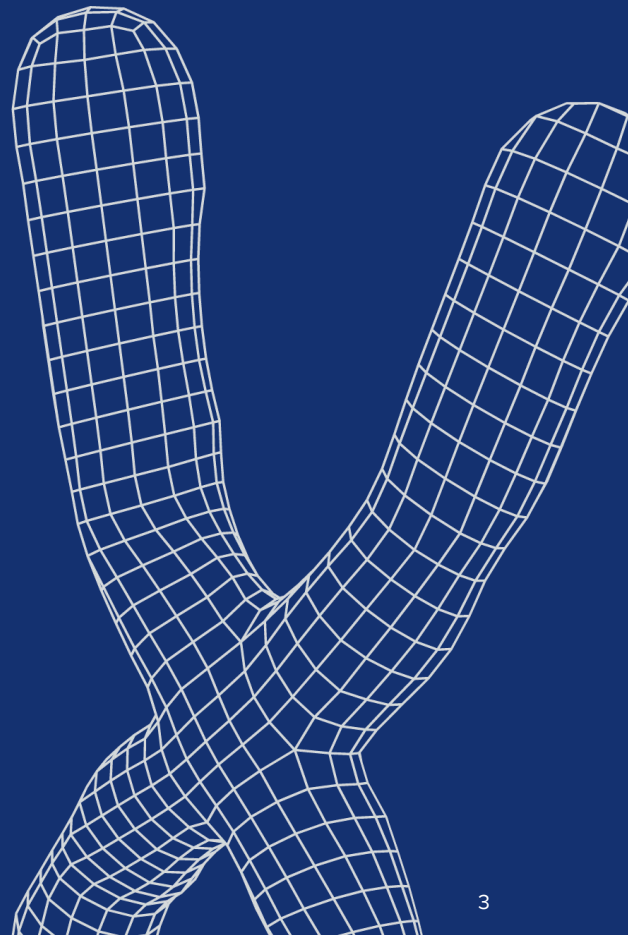
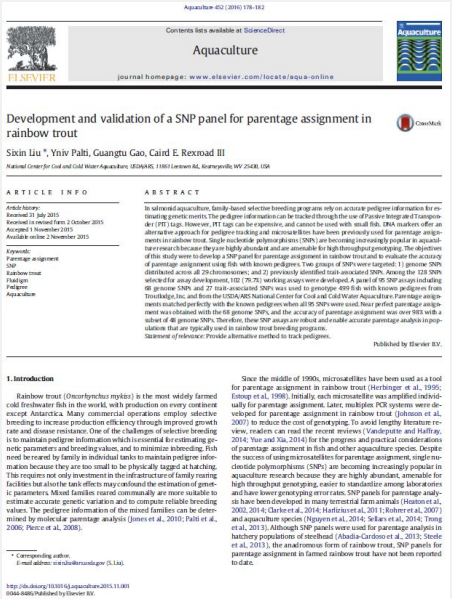


SNP Panel for Parentage of Rainbow Trout

Any further question?

Talk to us



Aquaculture 452 (2016) 178–182

Contents lists available at ScienceDirect

Aquaculture

journal homepage: www.elsevier.com/locate/aqua-online

Development and validation of a SNP panel for parentage assignment in rainbow trout

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ARTICLE INFO

Article history:
Received 31 July 2015
Received in revised form 2 October 2015
Accepted 1 November 2015
Available online 2 November 2015

Keywords:
Parentage assignment
SNP
Rainbow trout
Fluidigm
Pedigree
Aquaculture

ABSTRACT

In salmonid aquaculture, family-based selective breeding programs rely on accurate pedigree information for estimating genetic merits. The pedigree information can be tracked through the use of Passive Integrated Transponder (PIT) tags. However, PIT tags can be expensive, and cannot be used with small fish. DNA markers offer an alternative approach for pedigree tracking and microsatellites have been previously used for parentage assignments in rainbow trout. Single nucleotide polymorphisms (SNPs) are becoming increasingly popular in aquaculture research because they are highly abundant and are amenable for high throughput genotyping. The objectives of this study were to develop a SNP panel for parentage assignment in rainbow trout and to evaluate the accuracy of parentage assignment using fish with known pedigrees. Two groups of SNPs were targeted: 1) genome SNPs distributed across all 29 chromosomes; and 2) previously identified trait-associated SNPs. Among the 128 SNPs selected for assay development, 102 (79.7%) working assays were developed. A panel of 95 SNP assays including 68 genome SNPs and 27 trait-associated SNPs was used to genotype 499 fish with known pedigrees from Troutlodge, Inc. and from the USDA/ARS National Center for Cool and Cold Water Aquaculture. Parentage assignments matched perfectly with the known pedigrees when all 95 SNPs were used. Near perfect parentage assignment was obtained with the 68 genome SNPs, and the accuracy of parentage assignment was over 98% with a subset of 48 genome SNPs. Therefore, these SNP assays are robust and enable accurate parentage analysis in populations that are typically used in rainbow trout breeding programs.
Statement of relevance: Provide alternative method to track pedigrees.

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1. Introduction

Rainbow trout (*Oncorhynchus mykiss*) is the most widely farmed cold freshwater fish in the world, with production on every continent except Antarctica. Many commercial operations employ selective breeding to increase production efficiency through improved growth rate and disease resistance. One of the challenges of selective breeding is to maintain pedigree information which is essential for estimating genetic parameters and breeding values, and to minimize inbreeding. Fish need be reared by family in individual tanks to maintain pedigree information because they are too small to be physically tagged at hatching. This requires not only investment in the infrastructure of family rearing facilities but also the tank-effects may confound the estimation of genetic parameters. Mixed families reared communally are more suitable to estimate accurate genetic variation and to compute reliable breeding values. The pedigree information of the mixed families can be determined by molecular parentage analysis (Jones et al., 2010; Palti et al., 2008; Pierce et al., 2008).

Since the middle of 1990s, microsatellites have been used as a tool for parentage assignment in rainbow trout (Herbinger et al., 1995; Estoup et al., 1998). Initially, each microsatellite was amplified individually for parentage assignment. Later, multiplex PCR systems were developed for parentage assignment in rainbow trout (Johnson et al., 2007) to reduce the cost of genotyping. To avoid lengthy literature review, readers can read the recent reviews (Vandeputte and Haffray, 2014; Yue and Xia, 2014) for the progress and practical considerations of parentage assignment in fish and other aquaculture species. Despite the success of using microsatellites for parentage assignment, single nucleotide polymorphisms (SNPs) are becoming increasingly popular in aquaculture research because they are highly abundant, amenable for high throughput genotyping, easier to standardize among laboratories and have lower genotyping error rates. SNP panels for parentage analysis have been developed in many terrestrial farm animals (Heaton et al., 2002, 2014; Clarke et al., 2014; Harhinen et al., 2011; Rohrer et al., 2007) and aquaculture species (Nguyen et al., 2014; Sellars et al., 2014; Trong et al., 2013). Although SNP panels were used for parentage analysis in hatchery populations of steelhead (Abadia-Cardoso et al., 2013; Steele et al., 2013), the anadromous form of rainbow trout, SNP panels for parentage assignment in farmed rainbow trout have not been reported to date.

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http://dx.doi.org/10.1016/j.aquaculture.2015.11.001
0044-8486/Published by Elsevier B.V.

Objective: Develop and assess SNP genotyping panel for parentage assignment of rainbow trout.

Utilization of Standard BioTools products:

- EP1 System
- IFC Controller HX
- 96.96 dynamic arrays

Conclusion:

The SNP panel has sufficient power for genetic assignment of commercial rainbow trout strains used from Troutlodge in this study.

Liu, et al. Development and validation of a SNP panel for parentage assignment in rainbow trout Aquaculture (2016)

SNP Panel for Parentage of Rainbow Trout

Any further question?

Talk to us

Background

Selective breeding programs must maintain pedigree information to help increase production efficiency.

- Estimate genetic parameters & breeding values.
- Minimize inbreeding

Single Nucleotide Polymorphisms (SNPs) assays:

- High-throughput
- Easy to standardize
- Low error rates
- Proven in terrestrial animals for parentage assignment
- 60-100 SNPs adequate for accurate large scale parentage assignment

Liu, et al. Development and validation of a SNP panel for parentage assignment in rainbow trout Aquaculture (2016)

SNP Panel for Parentage of Rainbow Trout

Any further question?

Talk to us

Methods

Lab:

Fin clip samples

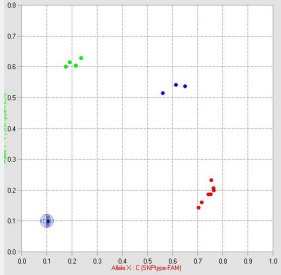
- Offspring previously genotyped on 57K array
- DNA concentration >30ng/uL

SNP Type assays

- SNPs across 29 chromosomes, MAF > 0.45
- Included additional trait-associated SNPs (stress, growth, disease resistance)
- 128 SNP assay designed, 95 selected for panel

Default SNP Type assay protocol in 96.96 GT Dynamic Array with STA

Data analysis:



Genotype calling

•SBIO software

Parentage analysis

•CERVUS

•SNPPIT

Table 1
Rainbow trout with known pedigrees used to evaluate the accuracy of parentage assignment.

Group	No. of families	No. of offspring	No. of dams	No. of sires
NCCCWA	10	60	17	13
Troutlodge	48	192	145	72
Total	58	252	162	85

Liu, et al. Development and validation of a SNP panel for parentage assignment in rainbow trout Aquaculture (2016)

Results and conclusions

Any further question?

Talk to us

Offspring to parent matching:

- All 95 SNPs = 100% accuracy
- 48 SNPs = 98% accuracy
- 36 SNPs = 92% accuracy
- Accuracy consistent with prior research

Conclusion

- SNP assays compatible for parentage assessment, low-cost, high-throughput, flexible assay choice to include trait-associated SNPs for rainbow trout populations studied.

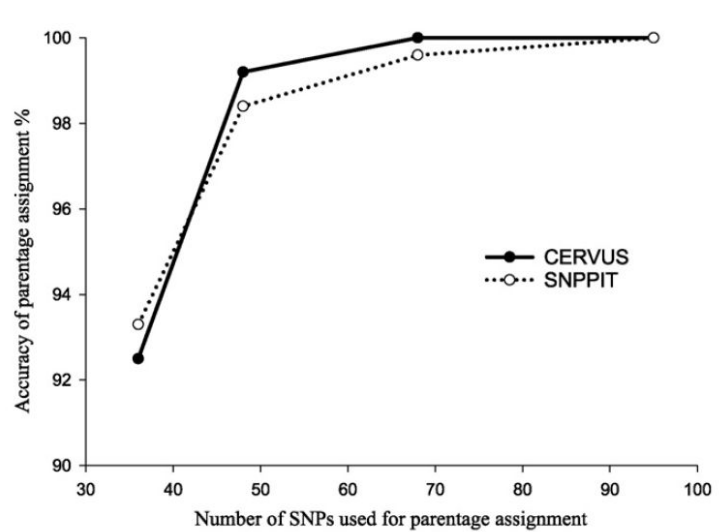


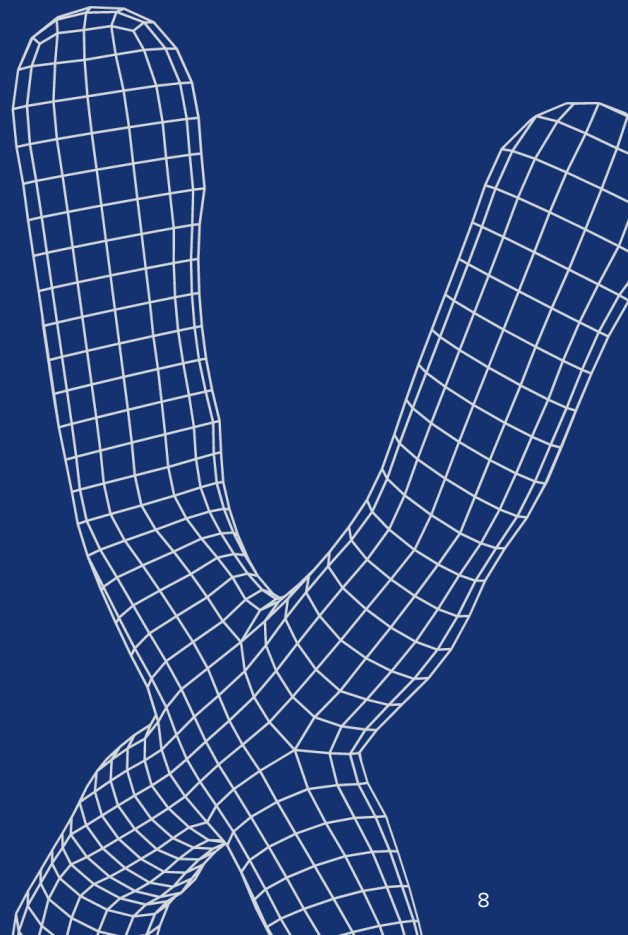
Fig. 1. Accuracy of parentage assignment with different numbers of SNPs.

Liu, et al. Development and validation of a SNP panel for parentage assignment in rainbow trout Aquaculture (2016)

Assessment of SNP genotyping for genetic differentiation

Any questions?

Talk to us



Assessment of SNP genotyping for genetic differentiation

Any further question?

Talk to us

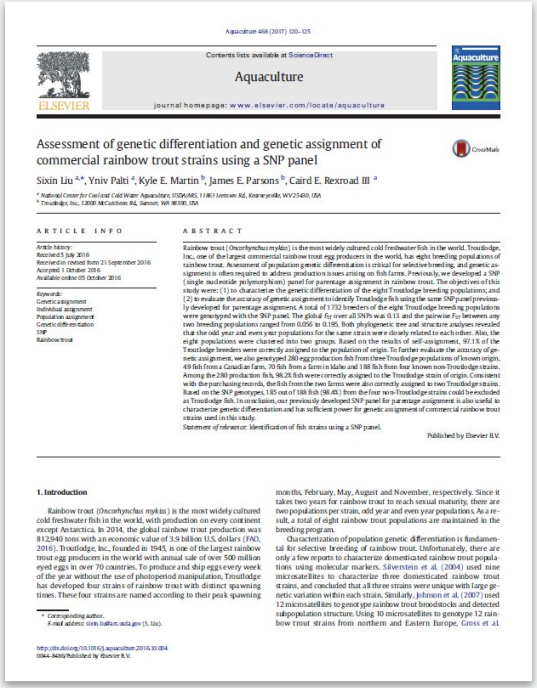
Objective: Characterize genetic differentiation of commercial rainbow trout strains in breeders and population fish.

Utilization of Standard BioTools products:

- EP1 System
- IFC Controller HX
- 96.96 dynamic arrays

Conclusions:

- 97.1% correct self-assignment to eight breeder populations.
- 98.2% correct assignment of production fish.



Aquaculture 468 (2017) 120–125

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journal homepage: www.elsevier.com/locate/aquaculture

Assessment of genetic differentiation and genetic assignment of commercial rainbow trout strains using a SNP panel

Sixin Liu [a,*], Yniv Palti [a], Kyle E. Martin [b], James E. Parsons [b], Caird E. Rexroad III [a]

ARTICLE INFO

ABSTRACT

Rainbow trout (Oncorhynchus mykiss) is the most widely cultured cold freshwater fish in the world. Troutdodge, Inc., one of the largest commercial rainbow trout egg producers in the world, has eight breeding populations of rainbow trout. Assessment of population genetic differentiation is critical for selective breeding, and genetic assignment is often required to address production issues arising on fish farms. Previously, we developed a SNP (single nucleotide polymorphism) panel for parentage assignment in rainbow trout. The objectives of this study were: (1) to characterize the genetic differentiation of the eight Troutdodge breeding populations; and (2) to evaluate the accuracy of genetic assignment to identify Troutdodge fish using the same SNP panel previously developed for parentage assignment. A total of 1732 breeders of the eight Troutdodge breeding populations were genotyped with the SNP panel. The global F_{ST} over all SNPs was 0.13 and the pairwise F_{ST} between any two breeding populations ranged from 0.056 to 0.195. Both phylogenetic tree and structure analyses revealed that the odd year and even year populations for the same strain were closely related to each other. Also, the eight populations were clustered into two groups. Based on the results of self-assignment, 97.1% of the Troutdodge breeders were correctly assigned to the population of origin. To further evaluate the accuracy of genetic assignment, we also genotyped 280 egg production fish from three Troutdodge populations of known origin, 49 fish from a Canadian farm, 70 fish from a farm in Idaho and 188 fish from four known non-Troutdodge strains. Among the 280 production fish, 98.2% fish were correctly assigned to the Troutdodge strain of origin. Consistent with the purchasing records, the fish from the two farms were also correctly assigned to two Troutdodge strains. Based on the SNP genotypes, 185 out of 188 fish (98.4%) from the four non-Troutdodge strains could be excluded as Troutdodge fish. In conclusion, our previously developed SNP panel for parentage assignment is also useful to characterize genetic differentiation and has sufficient power for genetic assignment of commercial rainbow trout strains used in this study.

Statement of relevance: Identification of fish strains using a SNP panel.

Published by Elsevier B.V.

1. Introduction

Rainbow trout (*Oncorhynchus mykiss*) is the most widely cultured cold freshwater fish in the world, with production on every continent except Antarctica. In 2014, the global rainbow trout production was 812,940 tons with an economic value of 3.9 billion U.S. dollars (FAO, 2016). Troutdodge, Inc., founded in 1945, is one of the largest rainbow trout egg producers in the world with annual sale of over 500 million eyed eggs in over 70 countries. To produce and ship eggs every week of the year without the use of photoperiod manipulation, Troutdodge has developed four strains of rainbow trout with distinct spawning times. These four strains are named according to their peak spawning months, February, May, August and November, respectively. Since it takes two years for rainbow trout to reach sexual maturity, there are two populations per strain, odd year and even year populations. As a result, a total of eight rainbow trout populations are maintained in the breeding program.

Characterization of population genetic differentiation is fundamental for selective breeding of rainbow trout. Unfortunately, there are only a few reports to characterize domesticated rainbow trout populations using molecular markers. Silverstein et al. (2004) used nine microsatellites to characterize three domesticated rainbow trout strains, and concluded that all three strains were unique with large genetic variation within each strain. Similarly, Johnson et al. (2007) used 12 microsatellites to genotype rainbow trout broodstocks and detected subpopulation structure. Using 10 microsatellites to genotype 12 rainbow trout strains from northern and Eastern Europe, Cross et al.

Liu, et al. Assessment of genetic differentiation and genetic assignment of commercial rainbow trout strains using a SNP panel Aquaculture (2017)

Assessment of SNP genotyping for genetic differentiation

Any further question?

Talk to us

Background and methods

Utilized rainbow trout SNP panel from Liu et al 2016 and EP1 System

Objectives of the study:

- Characterize eight Troutlodge breeding populations
- Evaluate accuracy of genetic assignment of the eight populations using the SNP panel

2012 Rainbow Trout

Table 1
Fish samples used in this study. The strains of Troutlodge breeders and production fish are coded by the last letter of the population names, which are prefixed with two-digit or four-digit of year-class of the populations.

Group	Population	Strain	No. of fish	Source
Breeders	10TLUA	August	216	Troutlodge
	10TLUN	November	234	Troutlodge
	11TLUF	February	216	Troutlodge
	11TLUM	May	217	Troutlodge
	11TLUA	August	213	Troutlodge
	11TLUN	November	234	Troutlodge
	12TLUF	February	196	Troutlodge
	12TLUM	May	206	Troutlodge
Production fish	2012TLUN	November	94	Troutlodge
	2013TLUN	November	92	Troutlodge
	2015TLUF	February	94	Troutlodge
Farmed fish	Farm 1		49	Canada
	Farm 2		70	Idaho, USA
Non-Troutlodge fish	UW		47	NCCCWA
	Shasta		47	NCCCWA
	European 1		47	Europe
	European 2		47	Europe

UW: University of Washington; NCCCWA: National Center for Cool and Cold Water Aquaculture.

Liu, et al. Assessment of genetic differentiation and genetic assignment of commercial rainbow trout strains using a SNP panel Aquaculture (2017)

Assessment of SNP genotyping for genetic differentiation

Any further question?

Talk to us

Table 3

Results of self-assignment of the eight Troutlodge breeding populations. Numbers in bold represent the number of fish assigned to the correct populations.

Population	11TLUF	12TLUF	11TLUM	12TLUM	10TLUA	11TLUA	10TLUN	11TLUN	Correctly assigned
11TLUF	**216**								100.0%
12TLUF	6	**188**	1	1					95.9%
11TLUM	3		**200**	14					92.2%
12TLUM			1	**205**					99.5%
10TLUA					**215**	1			99.5%
11TLUA					5	**207**	1		97.2%
10TLUN	1						**233**		99.6%
11TLUN	3				2		12	**217**	92.7%
Overall									97.1%

Results and conclusions

- 97.1% correct assignment of breeders to self-assigned populations.
- 98.2% of known origin production fish assigned to correct breeding populations.
- CN farm fish assigned to Troutlodge breeding populations which matched purchasing records.
- 98.4% of non-Troutlodge fish excluded as Troutlodge fish.

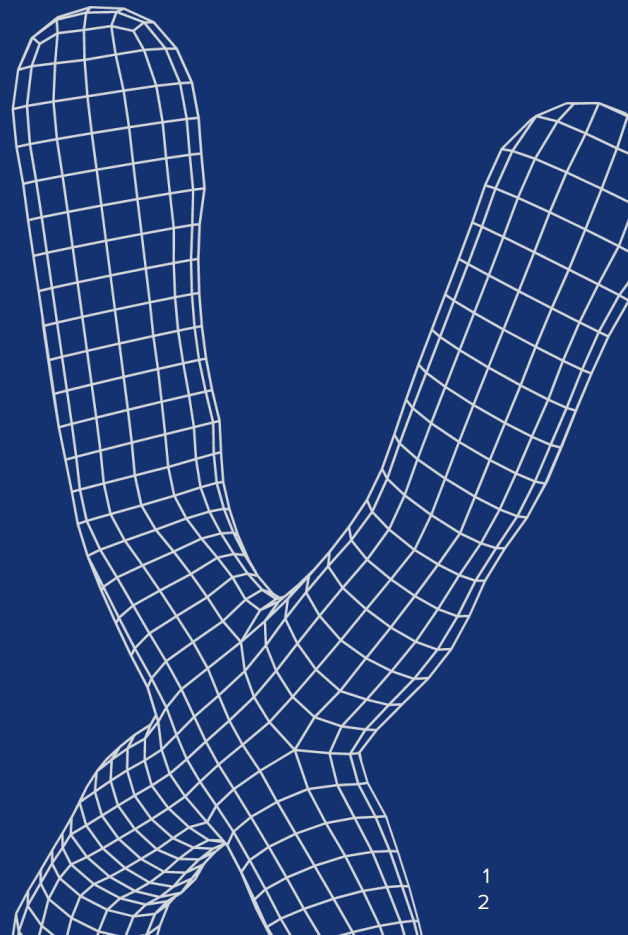
Confirmed SNP panel for parentage assignment and the panel has sufficient power for genetic assignment of commercial rainbow trait strains used.

Liu, et al. Assessment of genetic differentiation and genetic assignment of commercial rainbow trout strains using a SNP panel Aquaculture (2017)

Gene expression and fish welfare

Any questions?

Talk to us



Gene Expression Profiling And Fish Welfare

Any further question?

Talk to us

Objective: Deeper insight into stress and immune response influenced by different rearing conditions.

Utilization of Standard BioTools products:

- Biomark HD
- IFC Controller MX
- 48.48 dynamic arrays

Conclusion:

Stocking density and total water exchange has large impact on gene expression and welfare of fish.

Aquaculture 557 (2022) 738310

Contents lists available at ScienceDirect

Aquaculture

journal homepage: www.elsevier.com/locate/aquaculture

Gene expression profiling supports the welfare evaluation of rainbow trout (*Oncorhynchus mykiss*) reared under different environmental and management conditions in six commercial flow through systems

Lina Weirup [a,b,*], Alexander Rebl [c], Carsten Schulz [a,b], Henrike Seibel [a,b,*]

ARTICLE INFO

ABSTRACT

1. Introduction

Weirup, et al. “Gene expression profiling supports the welfare evaluation of rainbow trout (*Oncorhynchus mykiss*) reared under different environmental and management conditions in six commercial flow through systems” Aquaculture (2022)

Background

Any further question?

Talk to us

Species-appropriate treatment of fish is important for welfare of fish in farms.

Welfare measured by stressors in this study:

- Impact health, reproduction, and mortality.
- Elicit specific phenotypic responses and transcript level responses.
- Distinct transcriptional signatures exist for challenging conditions and stress.

Weirup, et al. “Gene expression profiling supports the welfare evaluation of rainbow trout (*Oncorhynchus mykiss*) reared under different environmental and management conditions in six commercial flow through systems” Aquaculture (2022)

Methods

Any further question?

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Many environmental and management conditions including:

- Water supply, exchange, temperature, oxygen, pH, bacterial load
- Minerals (ammonium, ammonia, nitrite, nitrate)
- Behavior & external morphological damage

Gene expression:

- Blood samples
- 3 HK genes + 91 target genes selected based on prior studies
- MX IFC controller and Biomark HD

Farms selected:

- Using flow through systems
- Characteristic differences in rearing conditions
- 10 fish per farm

Weirup, et al. “Gene expression profiling supports the welfare evaluation of rainbow trout (*Oncorhynchus mykiss*) reared under different environmental and management conditions in six commercial flow through systems” Aquaculture (2022)

Results And Conclusions

Any further question?

Talk to us

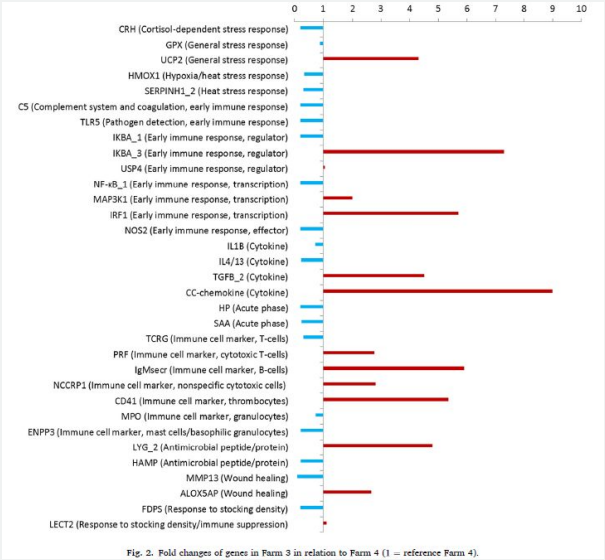

Fig. 2. Fold changes of genes in Farm 3 in relation to Farm 4 (1 = reference Farm 4).

Largest differences in fish welfare observed between Farm 3 and Farm 4 (reference) as evidenced by differentially expressed genes.

Significant differences were found in gene expression data between farms which complement the findings on:

- Histology
- Glucose and lactate concentrations
- Organ somatic indices
- External damage
- Water quality
- Environmental and management conditions

Weirup, et al. "Gene expression profiling supports the welfare evaluation of rainbow trout (Oncorhynchus mykiss) reared under different environmental and management conditions in a commercial flow-through system." Aquaculture (2022)

Modern aquaculture is powered by X9

Any questions?

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