

Aquaculture NRSP-8 Executive Summary: Annual Report 2020

Coordinator: Benjamin J. Reading, North Carolina State University

Co-coordinators: Steven Roberts, University of Washington
Moh Salem, University of Maryland
Eric Peatman, Auburn University

Species Leaders:

Catfish: Sylvie Quiniou, ARS Stoneville, Mississippi,

Oyster/shellfish: Dina Proestou, ARS University of Rhode Island, Rhode Island

Salmonids: Yniv Palti, ARS Leetown, West Virginia

Striped Bass: Benjamin J. Reading, North Carolina State University, North Carolina

Aquaculture Workshop:

Workshop Chair-elect 2021-2022: Rafet Al-Tobasei (Rafet.Al-tobasei@mtsu.edu)

Workshop Chair-elect 2020-2021: Moh Salem (mosalem@umd.edu)

Workshop Chair 2019-2020: Louis Plough (lplough@umces.edu)

Workshop Chair 2018-2019: Catherine Purcell (catherine.purcell@noaa.gov)

Aquaculture Workshop Report

The Aquaculture Workshop in 2021 was cancelled due to the COVID-19 pandemic and travel restrictions imposed by state and federal governments.

Leveraged funds:

Four (4) small research projects were funded at \$10,000 each in 2020 to provide preliminary data for grants: \$40,000 (2019-2020). Decisions regarding funding of these projects were made in 2020, just prior to COVID-19 pandemic closures (in many states “shelter in place” executive orders), which made disbursement of funds and execution of research challenging at best. These funds will officially be dispersed in the 2021 calendar year due to relaxation of research and other work-related restrictions that had been implemented by various state and federal agencies across the country.

Leveraged funds from diverse projects based on previously funded small research projects totaled over three million dollars from federal sources in 2020. This is in addition to over six million reported in 2019:

Total Leveraged Funding in 2020: \$ 3,419,110

This is about 1:53 return on investment for the aquaculture coordinator funds (\$65,000).

Total Leveraged Funding in 2019: \$ 6,340,999

This is 1:98 return on investment for the aquaculture coordinator funds (\$65,000).

Extramural funding agencies leveraged through collaborations and seed funding opportunities provided by this NRSP-8 program include NOAA, USDA NIFA, USDA AFRI, USDA Southern Regional Aquaculture Center, and the Ratcliffe Foundation (non-profit). In particular, the marine finfish and shellfish aquaculture initiatives of USDA and NOAA are to be recognized.

There were 30 publications from the NRSP-8 Aquaculture Community in 2020, including one research paper in the journal *Nature Scientific Reports* and two editorial features in *Science* magazine.

Specific major activities include:

Members of the NRSP-8 Aquaculture Group (among many others) played a role in contributing content matter expertise to advise NOAA and USDA on national marine aquaculture initiatives, which led to US Executive Order 13921: *Promoting American Seafood Competitiveness and Economic Growth* in May 2020. A review of this order was featured in *Science* magazine in May 2020 (doi:10.1126/science.abc7484) and the impacts of genetic tools to deliver improved farmed fishes also was featured in *Science* in November 2020 (doi:10.1126/science.abf7615).

Catfish

Channel catfish genome assembly refined with optical mapping; blue catfish genome assembly released. For the blue catfish, 469 NGS contigs (810 Mb) were integrated into 64 chromosomal scaffolds (N50 = 25 Mb) totaling 823 Mb, and an additional 25 Mb sequence was contained in 195 unaligned scaffolds. The blue catfish chromosome assembly currently contains only 334 gaps. The channel catfish genome assembly integrated 289 NGS scaffolds (826 Mb) into 79 chromosomal scaffolds (N50 = 20 Mb) totaling 833 Mb. An additional 20 Mb sequence was contained in 376 unaligned scaffolds. The channel catfish assembly was a significant improvement over the first channel catfish genome reference assembly produced from short-read sequencing. The effect of pond- or strip-spawning on growth and carcass yield of channel catfish progeny was published along with genomic predictions of columnaris disease resistance.

Shellfish and Crustaceans

Whiteleg shrimp genome sequencing is underway. Re-sequencing of wild and selected eastern oyster populations derived from multiple geographic regions along the US east Coast and Gulf of Mexico. Proteomic profiling was published showing developmental processes and temperature-influenced physiological responses in pacific oyster. Proteomic responses of larval geoduck to ciliates was published in *Scientific Reports*. Environmentally-induced differential DNA methylation and gene expression patterns were published for the eastern oyster, including responses to ocean acidification.

Trout and Salmon

The *de novo* genome assembly of the Arlee doubled-haploid rainbow trout was accepted by NCBI and annotated in RefSeq (accession GCF_013265735.2). A new linkage map is being developed for North American Atlantic salmon using genotype data from the new HD (50K) SNP chip that was developed this year in collaboration with Mowi North America and the Center for Aquaculture Technologies. The linkage map will be used for anchoring and ordering the sequence scaffolds from the new *de-novo* assembly in chromosome sequences. PacBio iso-seq was used improve the rainbow trout genome annotation and identifies alternative splicing associated with economically important phenotypes. More than 13,000 genome structural variants from whole genome resequencing of rainbow trout from two primary aquaculture

breeding programs were reported. Genome-wide association studies identified genomic loci affecting fish growth, fillet firmness and protein content, intramuscular fat, and moisture content in rainbow trout. A study identified distinct microbial assemblages associated with genetic selection for high- and low- muscle yield in rainbow trout.

Striped Bass

The second version of the striped bass genome draft was annotated through the NCBI Eukaryotic Genome Annotation Pipeline and is publicly available (GenBank accession GCA_004916995.1). A machine learning pipeline developed to analyze single nucleotide (SNP) markers (expressed quantitative trait loci, eQTL) related to growth in different strains of hybrid striped bass revealed 15,000 unique markers associated with growth traits. The white bass genome assembly was updated through the Dovetail™ Hi-C + HiRise™ scaffolding pipeline and short sequences (< 200 bp in length) are being filtered out of the assembly in preparation for submission to NCBI for annotation and public accessibility in 2021. Genotyping-by-sequencing panel was developed from diverse white bass populations for resistance to columnaris disease evaluated in striped bass, white bass, and hybrid striped bass. Genetically improved striped bass and white bass transferred to industry from *National Breeding Program for the Hybrid Striped Bass Industry*. Twenty (20) graduate and undergraduate students were trained in machine learning approaches in biological sciences including application of pattern recognition to evaluate gene and protein expression patterns related to predicting phenotypes in a variety of agriculturally important animals, including fishes and well as poultry; a CRISPR/Cas9 Guide to RNA design was published for student training.

The following pages include the full 2020 report for this NRSP-8 Aquaculture group.

NRSP-8 Aquaculture 2020 Full Annual Report

Leadership

Coordinator: Benjamin J. Reading, North Carolina State University

Co-coordinators: Steven Roberts, University of Washington
Moh Salem, University of Maryland
Eric Peatman, Auburn University

Species Leaders:

Catfish: Sylvie Quiniou, ARS Stoneville, Mississippi

Oyster/shellfish: Dina Proestou, ARS University of Rhode Island, Rhode Island

Salmonids: Yniv Palti, ARS Leetown, West Virginia

Striped Bass: Benjamin Reading, North Carolina State University, North Carolina

2020 Aquaculture Workshop Report:

Workshop Chair-elect 2020-2021: Moh Salem (mosalem@umd.edu)

Workshop Chair-elect 2021-2022: Rafet Al-Tobasei (Rafet.Al-tobasei@mtsu.edu)

Workshop Chair 2019-2020: Louis Plough (lplough@umces.edu)

Workshop Chair 2018-2019: Catherine Purcell (catherine.purcell@noaa.gov)

Theme

Aquaculture Genomics Workshop 2021: *This event was cancelled due to COVID-19 related travel restrictions for state and federal employees including academic and government participants. This group will resume a workshop at the International Plant and Animal Genome (PAG) Conference in 2022.*

Attendees 2021

Number: *Not applicable* (80 in 2020)

Number of institutes/organizations represented: *Not applicable* (49 in 2020)

Number of Countries represented: *Not applicable* (13 in 2020)

Invited Presentations (Plenary Speakers; \$1,000 travel awards) 2021

There were 3 awards in 2020; the 2021 Aquaculture Workshop was cancelled due to COVID-19 pandemic.

Other Contributed Presentations: 0 (14 in 2020)

Poster Session Participants: 0 (15 in 2020)

Aquaculture Reception Attendees: 0 (100 in 2020)

Business Meeting Minutes

Time: *Cancelled*

Place: *Cancelled*

Number of Attendees: *Cancelled* (19 in 2020)

Travel Support & Opportunities for Trainings

The 2021 PAG meeting and Aquaculture Workshop was cancelled due to the COVID-19 pandemic. The travel of five students/postdocs was funded to attend the Aquaculture Workshop at PAG 2020 (\$1,000 each). The purpose of the travel award program is to help graduate students and postdoctoral fellows to travel to the annual PAG meetings and present their research. We will resume this program at PAG in 2022.

Jorgenson Travel Award:

Not awarded. This workshop was cancelled in 2021 and will resume in 2022.

Plenary speaker travel awards (\$1,000 each)

Not awarded. This workshop was cancelled in 2021 and will resume in 2022.

NRSP-8 Aquaculture 2020 Progress: Species Leaders indicated in **BOLD.**

Members of the NRSP-8 Aquaculture Group contributed content matter expertise to advise NOAA and USDA on national marine aquaculture initiatives, which led to US Executive Order 13921: *Promoting American Seafood Competitiveness and Economic Growth* in 2020. A review of this order was featured in *Science* magazine in May 2020 (doi:10.1126/science.abc7484) and the impacts of genetic tools to deliver improved farmed fishes also was featured in *Science* in November 2020 (doi:10.1126/science.abf7615).

Objective 1: Advance the quality of reference genomes for all agri-animal species through providing high contiguity assemblies, deep functional annotations of these assemblies, and comparison across species to understand structure and function of animal genomes.

Catfish (Quiniou, Liu)

For the blue catfish, 469 NGS contigs (810 Mb) were integrated into 64 chromosomal scaffolds (N50 = 25 Mb) totaling 823 Mb, and an additional 25 Mb sequence was contained in 195 unaligned scaffolds. The blue catfish chromosome assembly currently contains only 334 gaps. The channel catfish genome assembly integrated 289 NGS scaffolds (826 Mb) into 79 chromosomal scaffolds (N50 = 20 Mb) totaling 833 Mb. An additional 20 Mb sequence was contained in 376 unaligned scaffolds. The channel catfish assembly was a significant improvement over the first channel catfish genome reference assembly produced from short-read sequencing of the same genome – 42 of 58 chromosome arms were assembled as single scaffolds while the remaining chromosome arms contained only two to four scaffolds each.

Shellfish and Crustaceans (Roberts, Gómez-Chiarri, Putnam, Guo, Warren, **Proestou**)
Whiteleg shrimp genome sequencing is underway. Re-sequencing of wild and selected eastern oyster populations derived from multiple geographic regions along the US east Coast and Gulf of Mexico.

Salmonids (Salem, **Palti**, Al-Tobasei)

The *de novo* genome assembly of the Arlee doubled-haploid line was accepted by NCBI and annotated in RefSeq (accession GCF_013265735.2); the accompanying manuscript was accepted for publication in the journal *G3*. A new linkage map is being developed for North American Atlantic salmon using genotype data from the new HD SNP chip that was developed this year for this economically important sub-species of Atlantic salmon. The linkage map will be used for anchoring and ordering the sequence scaffolds from the new *de-novo* assembly in chromosome sequences. PacBio iso-seq

was used improve the rainbow trout genome annotation and identifies alternative splicing associated with economically important phenotypes. The study identified 10,640 high-confidence transcripts not previously annotated, in addition to 1,479 isoforms not mapped to the current reference genome. Intron retention and exon skipping accounted for 56% of alternative splicing (AS) events. Iso-seq and RNA-Seq data integration identified characteristic alternative splicing associated with fish growth, muscle accretion, disease resistance, stress response, and fish migration.

Striped Bass (*National Breeding Program for the Hybrid Striped Bass Industry*, Fuller, Abernathy, Borski, Berlinsky, **Reading**)

The striped bass genome assembly version 2.0 (NCSU_SB_2.0) was annotated through the NCBI Eukaryotic Genome Annotation Pipeline and is publicly available (GenBank accession GCA_004916995.1). The white bass genome assembly was updated through the Dovetail™ Hi-C + HiRise™ scaffolding pipeline and short sequences (< 200 bp in length) are being filtered out of the assembly in preparation for submitting to NCBI for annotation and public release. The newly formed *StriperHub* will also begin to disseminate public notifications of genome resource releases to the public.

Objective 2: Advance genome-to-phenome prediction by implementing strategies to identify and validate genes and allelic variants predictive of biologically and economically important phenotypes and traits.

Catfish (**Quiniou**, Liu)

The effect of pond- or strip-spawning on growth and carcass yield of channel catfish progeny was published along with genomic predictions of columnaris disease resistance.

Oyster (*Eastern Oyster Breeding Consortium*, Roberts, Gomez-Chiarri, Putnam, Lotterhoos, Puritz, Johnson, Eirin-Lopez, Allen, Zhang, Plough, **Proestou**)

Proteomic profiling was published showing developmental processes and temperature-influenced physiological responses in pacific oyster. Proteomic responses of larval geoduck to ciliates was published in *Scientific Reports*. Environmentally-induced differential DNA methylation and gene expression patterns were published for the eastern oyster, including responses to ocean acidification.

Salmonids (Salem, **Palti**, Al-Tobasei)

The first public HD (50K) SNP chip for North American Atlantic salmon was developed by USDA-ARS in collaboration with Mowi North America and the Center for Aquaculture Technologies. It is currently being used by USDA-ARS for evaluating genomic selection for sea-lice resistance in Atlantic salmon. A discovery study identified more than 13,000

genome structural variants from whole genome resequencing of rainbow trout from two primary aquaculture breeding programs. This was the first SV discovery research in rainbow trout providing the foundation for research on the association between genome structural variants and economically relevant phenotypes in rainbow trout aquaculture. Genome-wide association studies identified genomic loci affecting fish growth, fillet firmness and protein content, intramuscular fat, and moisture content in rainbow trout. A study identified distinct microbial assemblages associated with genetic selection for high- and low- muscle yield in rainbow trout.

Striped Bass (*National Breeding Program for the Hybrid Striped Bass Industry*, Berlinsky, Fuller, Abernathy, Woods, McGinty, Borski, **Reading**)

A machine learning pipeline was developed to analyze 15,000 single nucleotide (SNP) markers (expressed quantitative trait loci, eQTL) that were identified among muscle transcriptome data from sunshine hybrid striped bass. The pipeline identified 500 SNPs that were considered most important to the predicting the growth phenotypes of hybrids. When orthologs and paralogs were removed, these 500 SNPs were annotated to 29 unigenes related to important growth regulatory pathways. Adult, male, F6 domestic striped bass (n=60) from our selective breeding program were disseminated to major aquaculture producers in the U.S. for hybrid striped bass fry and fingerling production (directly contributing to the \$50 million farm gate per year industry). Additionally, fingerlings (n=150,000) representing the first F7 generation captive bred striped bass in the United States were also disseminated to commercial aquaculture producers. Studies focused on characterizing variation related to disease resistance in white bass (most resistant), striped bass (most susceptible), and hybrid offspring were completed and published.

Objective 3: Advance analysis, curation, storage, application, and reuse of heterogeneous big data to facilitate genome-to-phenome research in agricultural animal species of agricultural interest.

Catfish (**Quiniou**, Liu)

None from catfish this year.

Oyster (*Eastern Oyster Breeding Consortium*, Gómez-Chiarri, Roberts, **Proestou**)

None from oyster this year.

Salmonids (Salem, **Palti**, Al-Tobasei)

None from salmonids this year.

Striped Bass (*National Breeding Program for the Hybrid Striped Bass Industry*, Abernathy, Borski, Reading)

Twenty (20) students (graduate and undergraduate) were trained in machine learning approaches in biological sciences including application of pattern recognition to evaluate gene and protein expression to predict traits and phenotypes in a variety of agriculturally important animals including fishes and well as poultry. Digitization of machine learning training modules are being produced for the public and a CRISPR/Cas9 Guide to RNA design was published for student training.

Follow Striped Bass Genome Community and *StriperHub* research on Facebook: <https://www.facebook.com/stripedbassgenome/>

Research support mini-grants (coordinator grants)

Four (4) mini-grants (\$10,000 each) supported projects that fall under all three primary NRSP-8 objectives and include a variety of species. Awards listed (2020-2021). Decisions regarding funding these projects were made in 2020, just prior to COVID-19 pandemic closures (in many states “shelter in place” executive orders), which made disbursement of funds challenging at best. These funds will be dispersed in the 2021 calendar year due to relaxation of research and other work-related restrictions that had been implemented by various state and federal agencies across the country. Once awarded, the investigators will be given 12 months to complete these projects. Another round of mini-grants will be offered later in 2021-2022:

1. Shelly Trigg and Steven Roberts “**Comparative Epigenomic Analyses Across Bivalve Genome Resources (CEABiGR)**”, University of Washington.
2. Russell Borski and Benjamin Reading “**From Genotype to Phenotype: A Gene Editing Tool for Any Life History Stage using Adeno-Associated Viral Vectors for Application of CRISPR/Cas9 in Farmed Finfishes**”, North Carolina State University.
3. Refet Al-Tobesi and Moh Salem “**FAASG Functional Annotation of the Rainbow Trout Genome: Role of DNA Methylation in Gene Expression**”, Middle Tennessee State.
4. Kevin Johnson, Morgan Kelly, and Jerome La Peyre “**Transcriptome sequencing to describe the genomic basis for hypoxia tolerance in the Eastern oyster**”, Louisiana State University.

Support of NRSP-8 Bioinformatics

A total of \$5,000 of these Aquaculture Coordinators funds were allocated to NRSP-8 Bioinformatics support (Coordinator Jim Reecy).

Leveraged Funds and Stakeholder Use of Project Outputs

NRSP-8 Seed Funding: **\$0** (\$40,000 in 2019-2020 delayed until 2020-2021 due to COVID-19; \$30,000 in 2018-2019)

Total Leveraged 2020 Funding: **\$ 3,419,110** (\$ 6,340,999 in 2019)

Leveraged funds from diverse projects exceed \$ 3.4 million from federal sources, which is about a 1:53 return on investment of the \$65,000 Aquaculture Coordinators funds for 2019-2020. Selected grants are highlighted below:

8. **US Department of Agriculture (USDA)**, USDA-NIFA special research grants program aquaculture research, GRANT # 2018-70007-28828, *Underlying mechanisms for selected disease resistance and enhanced non-specific resistance in rainbow trout*. (PI T. Welker) **\$309,489** (10/01/2018 through 09/30/2021).
7. **US Department of Agriculture (USDA)**, USDA-NIFA-AFRI Foundational, Diseases of Agricultural Animals program area, GRANT # 2020-06096, *Seed Grant: Phage endolysins, Alternative antimicrobials for Streptococcus iniae*. (PI G. Ramena) **\$200,000** (02/01/2021 through 01/31/2022).
6. **US Department of Agriculture (USDA)**, Agricultural and Food Research Initiative (AFRI), *FACT: AquaMine - A High Performance Genomic Data Mining System for Species of Importance to US Aquaculture*. (PI C. Elsik) **\$500,000** (4/1/2021-3/31/2025).
5. **NOAA**, *Leveraging transformative 'omics technologies to alleviate barriers to US shellfish production*. (PI S. Roberts) **\$233,135** (07/01/20 through 06/30/25).
4. **NOAA**, *Development of 'omics and bioinformatics approaches for marine organisms in support of research in aquaculture, ocean acidification, and fisheries assessments*. (PI S. Roberts) **\$285,153** (07/01/20 through 06/30/25).
3. **NOAA, Washington Sea Grant**, *Enhancing sustainability of shellfish aquaculture through streamlined maturation control*. (PI S. Roberts) **\$200,000** (02/01/20 through 01/31/23).
2. **US Department of Agriculture (USDA)**, National Institute of Food and Agriculture (NIFA) GRANT # 2021-67015-33388, *Whole-Genome Analyses/Selection to Increase Muscle Yield and Reduce Fillet Downgrading In Rainbow Trout*. (PIs M. Salem, Leeds, T.I., Kumar, V.I., Smith, B.R., Cleveland, B.E., and Al-Tobesi, R.A.) **\$500,000** (2021 through 2025).
1. **National Oceanic and Atmospheric Administration (NOAA)**, National Sea Grant Aquaculture Program, Advanced Aquaculture Collaborative Programs. *Establishing the Sea Grant Striped Bass Aquaculture Hub (StriperHub): Commercialization, Economics, and Marketing*. (PIs North Carolina Sea Grant, B.J. Reading--StriperHub Coordinator, R.J. Borski, D.L. Berlinsky) **\$1,191,333** (2/1/2020 through 01/30/2023).

Other Active Research Projects (Previously Reported in 2019)

Total Funding: **\$ 6,340,999** (2019 about 1:98 return on investment)

7. **Southern Regional Aquaculture Center**, US Department of Agriculture National Institute of Food and Agriculture (USDA NIFA). *Evaluation of Probiotics in Finfish Hatcheries to Improve Larval Production*. (PIs M.O. Frinsko, S.G. Hall, B.J. Reading) **\$150,000** (09/01/2018 through 08/31/2021).
6. **US Department of Agriculture (USDA)**, Agricultural and Food Research Initiative (AFRI), *Molecular basis of sex determination and differentiation in catfish*. (PIs Z.J. Liu, R. Dunham) **\$500,000** (6/1/2019 through 5/31/2022).
5. **NOAA**, *Developing new oyster sterilization technology to avoid triploid summer mortality*. (PI L. Plough) **\$100,000**.
4. **Ratcliffe Foundation**, *Shellfish Aquaculture Innovation Laboratory (SAIL): Using Science and New Technologies to Assist Shellfish Aquaculture Businesses in Maryland*. (PI L. Plough) **\$391,000**.
3. **NOAA Regional Shellfish Aquaculture Consortium Grants**, States Marine Fisheries Commissions, *From sequence to consequence: genomic selection to expand and improve selective breeding for the eastern oyster*. (PIs Eastern Oyster Breeding Consortium, X. Guo - Coordinator) **\$4,400,000** (8/1/2019 through 7/31/2024); similar grants were also awarded to the Gulf of Mexico and Pacific States.
2. **US Department of Agriculture (USDA)**, National Institute of Food and Agriculture (NIFA) Special Research Grants Program Aquaculture, *Modifying microbiomes to mitigate infectious diseases in aquaculture facilities*. (PI M. Gomez-Chiarri) **\$299,999** (10/1/2019 through 9/30/2021).
1. **US Department of Agriculture (USDA)**, National Institute of Food and Agriculture (NIFA) GRANT # 2018-06539, *High-Quality Reference Assembly and Annotation of the Rainbow Trout Genome*. (PIs M. Salem, Y. Palti, G. Gao, H. Zhou) **\$500,000** (2019 through 2022).

Publications (30 in 2020; 29 in 2019)

30. Lange, M.D., Abernathy, J., Shoemaker, C., Zhang, D., Kirby, A., Peatman, E., and Beck, B. 2020. Proteome analysis of virulent *Aeromonas hydrophila* reveals the upregulation of iron acquisition systems in the presence of a xenosiderophore. *FEMS Microbiology Letters* 367(20):fnaa169.
29. Lange, M.D., Farmer, B., and Abernathy, J. 2020. Vertebrate mucus stimulates biofilm development and upregulates iron acquisition genes in *Flavobacterium columnare*. *Journal of Fish Diseases* 43(1):101-110.
28. Trigg, S.A., Mitchell, K.R., Thompson, R.E., Eudeline, B., Vadopalas, B., Timmins-Schiffman, E.B., and Roberts, S.B. 2020. Temporal proteomic profiling reveals

- insight into critical developmental processes and temperature-influenced physiological response differences in a bivalve mollusc. *BMC Genomics* 21:723. doi:10.1186/s12864-020-07127-3
27. Downey-Wall, A.M., Cameron, L.P., Ford, B.M., McNally, E.M., Venkataraman, Y.R., Roberts, S.B., Ries, J.B., and Lotterhos, K.E. 2020. Ocean Acidification Induces Subtle Shifts in Gene Expression and DNA Methylation in Mantle Tissue of the Eastern Oyster (*Crassostrea virginica*). *Frontiers in Marine Science* 7:828. doi:10.3389/fmars.2020.56641
 26. Timmins-Schiffman, E., Guzmán, J.M., Thompson, R.E., Vadopalas, B., Eudeline, B., and Roberts, S.B. 2020. Larval Geoduck (*Panopea generosa*) Proteomic Response to Ciliates. *Scientific Reports* 10:6042. doi:10.1038/s41598-020-63218-x
 25. Venkataraman, Y.R., Downey-Wall, A.M., Ries, J., Westfield, I., White, S.J., Roberts, S.B., and Lotterhos, K.E. 2020. General DNA Methylation Patterns and Environmentally-Induced Differential Methylation in the Eastern Oyster (*Crassostrea virginica*). *Frontiers in Marine Science* 7:225. doi:10.3389/fmars.2020.00225.
 24. Vallejo, R.L., Fragomeni, B.O., Cheng, H., Gao, G., Long, R.L., Shewbridge, K.L., Macmillan, J.R., Towner, R., and Palti, Y. 2020. Assessing Accuracy of Genomic Predictions for Resistance to Infectious Hematopoietic Necrosis Virus With Progeny Testing of Selection Candidates in a Commercial Rainbow Trout Breeding Population. *Frontiers in Veterinary Science*, 7:939. DOI 10.3389/fvets.2020.590048.
 23. Ma, H., Han, Y.-C., Palti, Y., Gao, G., Liu, S., Palmquist, D.E., Wiens, G.D., and Shepherd, B.S. 2021. Structure and regulation of the NK-lysin (1–4) and NK-lysin like (a and b) antimicrobial genes in rainbow trout (*Oncorhynchus mykiss*). *Developmental & Comparative Immunology*, 116:103961. DOI <https://doi.org/10.1016/j.dci.2020.103961>.
 22. Magadan, S., Mondot, S., Palti, Y., Gao, G., Lefranc, M.P., and Boudinot, P. 2021. Genomic analysis of a second rainbow trout line (Arlee) leads to an extended description of the IGH VDJ gene repertoire. *Developmental & Comparative Immunology* 118:103998. DOI <https://doi.org/10.1016/j.dci.2021.103998>.
 21. Cleveland, B.M., Gao, G., and Leeds, T.D. 2020. Transcriptomic response to selective breeding for fast growth in rainbow trout (*Oncorhynchus mykiss*). *Marine Biotechnology*, 22:539-550.
 20. Cleveland, B.M., Gao, G., Radler, L.M., and Picklo, M.J. 2020. Hepatic Fatty Acid and Transcriptome Profiles during the Transition from Vegetable-to Fish Oil-Based Diets in Rainbow Trout (*Oncorhynchus mykiss*). *Lipids*. DOI <https://doi.org/10.1002/lipd.12287>.

19. Gao, G., Magadan, S., Waldbieser, G.C., Youngblood, R.C., Wheeler, P.A., Scheffler, B.E., Thorgaard, G.H., and Palti, Y. 2021. A long reads-based *de-novo* assembly of the genome of the Arlee homozygous line reveals chromosomal rearrangements in rainbow trout. *G3 Genes/Genomes/Genetics* jkab052. DOI 10.1093/g3journal/jkab052.
18. Ali, A., Al-Tobasei, R., Lourenco, D., Leeds, T., Kenney, B., Salem, M. 2020. Genome-wide scan for common variants associated with intramuscular fat and moisture content in rainbow trout. *BMC Genomics* 21(1):529.
17. Ali, A., Al-Tobasei, R., Lourenco, D., Leeds, T., Kenney, B., Salem, M. 2020. Genome-wide identification of loci associated with growth in rainbow trout. *BMC Genomics* 21(1):209.
16. Chapagain, P., Walker, D., Leeds, T., Cleveland, B.M., Salem, M. 2020. Distinct microbial assemblages associated with genetic selection for high- and low- muscle yield in rainbow trout. *BMC Genomics* 21(1):820.
15. Banczyk, W., Salem, M. 2020. Die Rolle der DNA-Extraktion bei der Mikrobiomforschung. *BIOspektrum* 26(5):518-519 DOI: 10.1007/s12268-020-1439-6
14. Samsa, L.A., Andersen, L.K., Groth, A.M., and Goller, C.C. 2020. CRISPR/Cas9 Guide RNA Design *In Silico* Activity. *CourseSource*. <https://doi.org/10.24918/cs.2020.46>.
13. Farmer, B.D., Fuller, S.A., Beck, B.H., Abernathy, J.W., Lange, M.D., and Webster, C.D. 2021. Differential susceptibility of white bass (*Morone chrysops*), striped bass (*Morone saxatilis*) and hybrid striped bass (*M. chrysops* × *M. saxatilis*) to *Flavobacterium columnare* and effects of mucus on bacterial growth and biofilm development. *J. Fish Dis.* 44:161-169.
12. Gibbens, S. 2020. Toxic 'forever chemicals' flow freely through this river—and now its fish. *National Geographic*, March 24, 2020 (*striped bass aquaculture* featuring S. Belcher from Guillette et al., 2020 below). <https://www.nationalgeographic.com/science/article/toxic-chemical-pfas-found-in-north-carolina-striped-bass>
11. Stokstad, E. 2020. New genetic tools will deliver improved farmed fish, oysters, and shrimp. Here's what to expect. *Science*, November 19, 2020 (*editorial* featuring B.J. Reading). doi:10.1126/science.abf7615
10. Andersen, L.K., Clark, R.W., Hopper, M.S., Hodson, R.G., Schilling, J., Kenter, L., Daniels, H.V., Woods III, L.C., Kovach, A., McGinty, A.S., Berlinksy, D.L., and Reading, B.J. 2021. Methods of domestic striped bass (*Morone saxatilis*) spawning that do not require the use of any hormone induction. *Aquaculture* 533:736025.
9. Andersen, L.K., Kenter, L.W., Clark, R.W., McGinty, A.S., Hopper, M.S., Salger, S.A., Schilling, J., Hodson, R.G., Kovach, A., Berlinksy, D.L., and Reading, B.J. 2021. Volitional tank spawning of domestic striped bass (*Morone saxatilis*) using human

- chorionic gonadotropin (hCG) and gonadotropin releasing hormone analogue (GnRHa) induced 'pace-setting' females. *Aquaculture* 532:735967.
8. Kenter, L.W., Kovach, A., Wojtusik, K.J., Reading, B.J., and Berlinsky, D.L. 2020. Paternal Strain Effects on Growth and Body Shape in Hybrid Striped Bass (White Bass female x Striped Bass male). *North American Journal of Aquaculture* 82:405-413.
 7. LeBlanc, N., Gahagan, B., Andrews, S., Avery, T., Puncher, G., Reading, B., Buhariwalla, C., Curry, R; Whitely, A., and Pavey, S. 2020. Genomic Population Structure of Striped Bass (*Morone saxatilis*) from the Gulf of St. Lawrence to Cape Fear River. *Evolutionary Applications* 13:1468-1486.
 6. Berlinsky, D.L., Goetz, F., Kenter, L., Reading, B.J. 2020. Regulating reproductive cycles for captive spawning. *In Fish Physiology Volume 38: Aquaculture* (Benfey, T.J., Farrell, A.P. and Brauner, C.J., Eds.).
 5. Phillips, C.A., Reading, B.J., Livingston, M., Livingston, K. and Ashwell, C.M. 2020. Evaluation via Supervised Machine Learning of the Broiler Pectoralis Major and Liver Transcriptome in Association with the Muscle Myopathy Wooden Breast. *Frontiers in Physiology* 11:1010.
 4. Bosworth, B., Waldbieser, G., Garcia, A., Lourenco, D. 2020. Effect of pond- or strip-spawning on growth and carcass yield of channel catfish progeny, *Ictalurus punctatus*. *J World Aquacult Soc.* 51:407-417.
 3. Proestou, D.A. and Sullivan, M.E. 2020. Variation in global transcriptomic response to *Perkinsus marinus* infection among eastern oyster families highlights potential mechanisms of disease resistance. *Fish and Shellfish Immunology* 96:141-151.
 2. Guillette, T.C., McCord, J., Guillette, M., Polera, M., Rachels, K.T., Morgeson, C., Kotlarz, N., Strynar, M., Knappe, D., Reading, B.J., and Belcher, S.M. 2020. Per and Polyfluoroalkyl Substance Exposure in Striped Bass (*Morone saxatilis*) of Cape Fear River is Associated with Biomarkers of Altered Immune and Liver Function. *Environmental Science and Technology*, 136:105358.
 1. Zhang, Y., Liu, Z.J., and Li, H. 2020. Genomic prediction of columnaris disease resistance in catfish. *Marine Biotechnology* 22:145-151.