NRSP-8 Aquaculture 2019 Annual Report

Leadership

Coordinator: Benjamin J. Reading, North Carolina State University
Co-coordinators: Steven Roberts, Washington State University
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

2019 Aquaculture Workshop Report

Workshop Chair 2019-2020: Louis Plough (lplough@umces.edu)
Chair-elect 2020-2021: Moh Salem (Mohamed.Salem@mtsu.edu)
Chair-elect 2021-2022: Rafet Al-Tobasei (Rafet.Al-tobasei@mtsu.edu)
Workshop Chair 2018-2019: Catherine Purcell (catherine.purcell@noaa.gov)

Theme

Aquaculture Genomics Workshop 2020

Attendees

Number: 80 *(80 in 2019)*
Number of institutes/organizations represented: 49 (*43 in 2019)*
Number of Countries represented: 13

Invited Presentations (3 Plenary Speakers; $1,000 travel awards)

1. **Applications of Genomics to Expedite Genetic Improvement in Aquaculture Species** Ross D. Houston, The Roslin Institute and R(D)SVS
2. **Genomic Selection in Aquaculture: From Wild Stock to Advanced Breeding Schemes in *Penaeus monodon*** Herman Raadsma, University of Sydney
3. **Genomic Selection: From SNP Chips to Whole-Genome Sequence Data** Daniela Lourenco, University of Georgia

Other Contributed Presentations: 14 *(15 in 2019)*
Poster Session Participants: 15 *(20 in 2019)*
Aquaculture Reception Attendees: 100 *(80 in 2019)*

Business Meeting Minutes

Time: Saturday January 11, 2020, 5:00-5:46 pm
Place: Pacific Salon 3/4, Town and Country Hotel, San Diego, CA
Number of Attendees: 19 (9 in 2019)

1. Louis Plough (Workshop Coordinator, University of Maryland Center for Environmental Science) Call to Order.

2. Jim Reecy (Bioinformatics Coordinator, Iowa State University) provided an update on bioinformatics funding support. The key points made were as follows:
    - **Maintaining data**
        - The federal government funding agencies are and will be requiring that we maintain our generated data.
        - Reecy suggests that data sharing should become a compliance part of our grant planning from this point forward.
    - **Database Curation**
        - As long as we have a genome assembly and stable coordinators then associations can be curated into databases (e.g., Animal QTL DB).
        - Nothing towards this has been done for catfish yet.
        - A problem with the QTL database is that USDA NIFA did not fund this as they historically have.
        - This means that the salary of its primary curator at Iowa State is not supported.
        - Reecy asked all coordinators for $5,000 each ($30k total), which in addition to
        $12,000 from Reecy directly, would allow for the salary of the database coordinator to be paid through September.
        - September was chosen because funding opportunities (e.g., NSF funding) will be available and/or awarded by then.
        - Reecy hopes to move the tasks of coordinating this away from himself and Iowa State.
        - Fiona McCarthy (Present Bioinformatics Co-Coordinator, University of Arizona) and James Koltes, (Present Bioinformatics Co-Coordinator, Iowa State University) will be taking this over. *McCarthy and Koltes may be coordinator elects (?)
    - **A project that is nearing completion under Jim Reecy & his group:**
        - The development of a pipeline that can assemble transcripts and some annotation data with a given Iso-Seq dataset (poster 336).

3. Ben Reading (Aquaculture Coordinator, North Carolina State University) followed up Reecy's Bioinformatics update:
    - We are able to contribute $5,000 to this Bioinformatics Plan.
    - The attendees of the business meeting do not express attitudes against this. [They] agree that if no dissents are among the other coordinators at the NRSP-8 meeting tomorrow 12 January 2020 then we will contribute $5,000 towards this as well.

4. Ben Reading provided information on the species reports.
    - 29 published papers were reported, including one in Nature.
    - ~ $700,000 funds garnered were reported, which is exceptional relative to our $60,000 of funding.

5. Ben Reading called for nominations for the Aquaculture workshop coordinator for 2021-2022. Moh Salem (University of Maryland) nominated Rafet Al-Tobasei of Middle Tennessee State University (Rafet.Al-tobasei@mtsu.edu). This was seconded by Yniv Palti (USDA ARS).

6. Ben Reading reviewed the small-funding opportunities.
    - There were four proposals that were clearly ranked above the rest and the group is able to fund these at $10,000 each.
    - No attendee expressed any arguments against funding these proposals. Ben will notify coordinators of which proposals were ranked the highest.

7. Ben Reading followed up with attendees and directly with Moh about reducing the student award monies (suggested during the Aquaculture business meeting in 2019). Ben Reading also suggested possibly submitting a consortium grant or something similar to better ensure that the species with less developed "omics" resources are not "left behind."
    - Moh commented that his idea behind this was in part to account for how things will change in the next five years.
    - In theory this would be just aquaculture species, but this is dependent on the results of the NRSP meeting tomorrow with all species coordinators.
    - Catherine Purcell (NOAA) asked if the student awards would be consolidated into more small funding opportunities.
    - Ben Reading responded by suggesting perhaps we select the species as a group that are in the most need of this support.
    - Moh called on Jim Reecy to provide his thoughts on the future after NRSP-8.

- Jim Reecy responded: The ARS directors have effectively said that they do not want to see another NRSP-8 -type proposal come forward. They are thinking perhaps the Bioinformatics part segways off.
- The response of all coordinators beyond aquaculture is important here. Perhaps they are looking to incorporate more phenotypic biology, predictive biology, nutrition, etc. (i.e., going beyond genetics). Jim Reecy believes this would be considered worthy of investment by the directors.
- A white paper is written by the Bioinformatics group asking about how funding can be found to take over the Bioinformatics database projects (the plant community has this without having to apply for competitive funding opportunities).
- However, this (going to ARS or ARS in collaboration with universities, for example, for monies to move into independent bioinformatics efforts) must be a collective effort.
- The industry wants:
    - A well-developed workforce
    - They know that the well-developed workforce requires funding. Especially towards workers in the US.
    - They want the workforce to be data-savvy (i.e., how do we handle great amounts of data).
    - New phenotypes, in particular those phenotypes associated with efficiency
- Caird Rexroad contributed: an industry partner like Smithfield has “genomics” as part of their operating budget. This demonstrates that the industry partners are certainly our advocates that we should call upon and collaborate more with.
- Moh replied asking for what we can do to be more connected to the industry. Reecy replied that they should be more included in our workshops, provide greater feedback, collaborate to solve questions, etc. Reecy added that industry folks have a decreased presence in the last twenty years, but this is a tie that we should be maintaining.
- John Buchannan added that a way to connect with industry should be simple outreach. Several people are simply not aware that meetings such as PAG exist. It would be worth looking through our sign-in sheets and other resources and reaching out to these people. John also suggested perhaps dividing the day clearly into two: industry and aquaculture. John said Aquatech will give a talk.
- Caird Rexroad noted that we should make sure that we attend [their] meetings, state aquaculture meetings, trade shows, etc.

8. Ben Reading suggests that we should consider having another workshop or consortium that we can organize for aquaculture only to be incorporated into the future of the NRSP plans with all coordinators.
    - Moh suggested that NIFA may be able to support the costs for a workshop.

9. Caird Rexroad created a sub-committee on aquaculture is re-writing the national strategic plan for aquaculture research. The previous plan was mostly supported by USDA and NOAA. At some point this draft will be open for public comment. Caird has called us to make sure that [we] review it. This document being open for comment will be announced by National Aquaculture Association, etc.

10. Meeting adjourned.

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)
Long-read DNA sequences were produced from homozygous, doubled haploid individuals and assembled using Canu. Nucleated red blood cells were also used to produce optical maps on the Bionano Saphyr instrument; the channel catfish genomic DNA was isolated from cells that had been embedded in agarose and stored for 11 years whereas the blue catfish DNA was isolated from fresh cells. 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. For example, while both channel catfish chromosome 1 assemblies spanned from telomere-to-telomere, the original chromosome 1 assembly contained 1,115 gaps in 13 scaffolds whereas the new chromosome 1 assembly contained only 2 gaps in 2 scaffolds. The new assembly also revealed mis-orientation of smaller scaffolds in the original assembly.

Oyster (Gómez-Chiarri, Putnam, Guo, Warren, **Proestou**)
Re-sequencing of wild and selected eastern oyster populations derived from multiple geographic regions along the US east Coast and Gulf of Mexico at 20X coverage.

Salmonids (Salem, **Palti**)
A *De-novo* genome assembly of the Arlee doubled-haploid line was generated towards generating a pan-genome reference for rainbow trout. The assembly is based on PacBio long reads sequencing and scaffolding with Bionnano optical map and Hi-C contact map. The contiguity of the Arlee genome assembly is much better than the current reference genome in GenBank from another genetic line, with contigs and scaffolds N50 of 9,835,815 and 47,542,702, respectively. A De-novo genome assembly for a widely used aquaculture strain of North American Atlantic salmon is in progress using the tri-binning approach. PacBio sequencing and initial contigs assembly were completed with contigs N50 of 796,316 and 765,732 for the male and female parental genomes, respectively. Genome resequencing is underway in Chinook salmon and steelhead for broad representation of genomic variation across populations of each of these species.

Striped Bass (*National Breeding Program for the Hybrid Striped Bass Industry*, Fuller, Abernathy, Kovach, Berlinsky, **Reading**)
A second, updated draft of the striped bass genome has been uploaded to GenBank and is available for download through the NCBI (NCSU_SB_2.0, GenBank Accession no. SSXF00000000.1). The Dovetail Genomics Hi-Rise pipeline was employed to create this version of the genome assembly by scaffolding the Illumina short read sequences and PacBio long read sequences used for the original draft genome with Illumina sequencing data generated by Chicago and Dovetail Hi-C pipelines. This version of the genome consists of 629 scaffolds with a final size of 598.11 Mb and striped bass transcriptome data is currently being processed by NCBI for annotation. A similar approach was taken to generate a white bass genome assembly, 645.14 Mb in size consisting of 46,120 scaffolds, although this has not yet been uploaded to GenBank. Third-generation, long-read sequencing technologies are currently being employed to recover a haplotype-resolved moronid genome through the re-sequencing and analyses of white bass / striped bass / hybrid striped bass trios.

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)

Channel catfish gonadal sex differentiation starts approximately 19 dpf. To provide information about DNA methylation before commitment of sex phenotypes during critical period of sex differentiation, genome-wide DNA methylation profiles of genital ridge samples from genetic female and male catfish were generated by bisulfite sequencing. At 9 and 12 dpf, between 77.1% and 78.4% of C's in the CpG sites were methylated in the females and males, respectively, and then some CpG sites were demethylated, approaching 75.7% and 74.5% methylated CpG sites at 16 dpf in females and males, respectively. The level of whole genome methylation in channel catfish is slightly higher than that of mouse, but slightly lower than that of zebrafish (80.3%).
Correlation matrix generated by male and female methylation profiles revealed subtle differential methylation between the two sexes. The overall methylation profiles in both sexes of catfish at 9 dpf and 12 dpf were more similar, whereas the methylation levels at 16 dpf were different from and lower than those at 9 dpf and 12 dpf.

Oyster (*Eastern Oyster Breeding Consortium*, Roberts, Gomez-Chiarri, Putnam, Lotterhoos, Puritz, Johnson, Eirin-Lopez, Allen, Zhang, Plough, **Proestou**)
Development of 600K and subsequent 50K SNP chips for Eastern oyster that can be applied to Canadian, East Coast, and Gulf oyster populations is in progress. Population genomic analysis of re-sequence data--Outlier analysis and environmental association analysis--are underway. RNA-seq analyses are ongoing to understand the genetic/genomic basis for Dermo-resistance in Eastern Oyster breeding populations and identify variants associated with Dermo resistance. Investigation of genetic basis for low-salinity tolerance in eastern oyster continues to quantify heritability for salinity tolerance and identify QTL underlying tolerant phenotypes. GWAS study to identify allelic variants associated with response to low CO2 in eastern oyster larvae initiated.

Salmonids (Salem, **Palti**)
Genome-wide association study identified genomic loci affecting fillet firmness and protein content in rainbow trout. Genome-wide association study identified genomic loci affecting egg quality traits in commercial rainbow trout breeding populations, including early embryonic survival to the eyeing eggs stage, fecundity and egg size. Those regions are being evaluated for annotated candidate genes and their potential impact on genomic selection accuracy. Diversity of the bacterial communities in rainbow trout gut showed significant variation between fish breeding families, but not between the fast- and slow-growing fish. However, some bacterial taxa with functional implications were indicative of fish growth rate. Allelic variation for candidate genes associated with migration timing was validated with markers in over 50,000 Chinook salmon and 20,000 steelhead. Candidate genes investigated for age/size at maturity in steelhead, and markers are being developed to quantify allelic variation of individuals.

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 produced from striped bass males of varying geographic strains (Texas, Florida, South Carolina, Virginia, and North Carolina aquaculture domestic strain). The pipeline identified 500 SNPs that were considered important to the classification of hybrids into groups based on size and sire strain. When orthologs and paralogs were removed, these 500 SNPs were annotated to 29 unigenes. The machine learning pipeline also enabled alleotyping of these genes. Specifically, we found that 7 of the 29 genes were inherited exclusively from the white bass maternal parent; the remaining 22 genes were potentially inherited from either the striped bass or white bass parent. Wild white bass gathered from Arkansas, Texas and Alabama along with available domesticated strains were used to establish a base breeding population for familywise evaluations of growth and nutrient utilization on alternative, sustainable diets. Genotyping-by-sequencing panel was developed from white bass populations, where identified SNPs can discriminate domestic stocks from wild-sourced individuals. Additional genetic markers are being developed to rapidly identify gender and parentage. Adult, male, domestic striped bass (n=60) and white bass broodstock from our selective breeding program (n=100) were disseminated to major aquaculture producers in the U.S. for hybrid striped bass fry and fingerling production (directly contributing to the $56 million farm gate per year industry). Studies focused on the characterization of variation behind disease resistance between parent white bass (most resistant), striped bass (most susceptible) and hybrid offspring are ongoing, including QTL mapping of backcross hybrids and gene expression analysis (RNA-seq) with common fish pathogens including.

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.

Oyster (*Eastern Oyster Breeding Consortium*, Gómez-Chiarri, Roberts, **Proestou**)
Eastern Oyster Epigenetics Workshop. Held at URI May 21-23, 2019. Organizer: Hollie Putnam. Funding from NRSP-8 aquaculture: $10,000. Eastern Oyster Genome Workshop. Held at URI May 23-24, 2019. Organizer: M. Gomez-Chiarri. Eastern Oyster Breeding Consortium Round Table. Held at VIMS October 7-8, 2019. Organizer: S.K. Allen Jr.

Salmonids (Salem, **Palti**)

The Narum laboratory has contributed to development of FishGen.net database for storage of large-scal
e genotypes for genetic tagging and monitoring studies.

Striped Bass (*National Breeding Program for the Hybrid Striped Bass Industry,* Abernathy, Borski, **Reading**)
Ongoing studies using different and novel machine learning-based analytical platforms are focused on small molecule (metabolomics), gene expression (RNA-Seq), and protein (proteomics) profiling to better understand hybrid striped bass growth performance (heterosis effects) and natural recruitment/reproductive success in several different wild stocks of striped bass in watersheds of the mid-Atlantic region. Transcript quantification pipelines from RNA-seq datasets are being built utilizing both alignment-based and alignment-free approaches. Performance metrics are being gathered and analyzed to assist in determining optimal approaches for transcript-level and gene-level quantitation in moronids. Similarly, these approaches are being coupled with various count-based techniques to explore accuracy of differential gene expression among real and simulated datasets. Follow Striped Bass Genome Community 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 (2019-2020):

1. Shelly Trigg and 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.

Travel Support & Opportunities for Trainings

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. The awardees of PAG 2020 are as follows:

1. Samuel Hart, University of Washington (WA, USA), "**Genome of the Soft-Shell Clam and Its Transmissible Cancer**".
2. Sarah Berry, James Cook University and CSIRO, "**Stress regulation and tolerance in shrimp: the transcriptomic response to ammonia exposure in the black tiger shrimp, *Penaeus monodon"***.
3. Jacob Bledsoe, University of Idaho, "**Impacts of Functional Feed Ingredients on Mucosal Immunity and Microbiota of Atlantic Salmon and Potential Implications for Sea Lice Resistance**".
4. Alexandra McCarty, University of Maryland, "**QTL and joint-association mapping reveal loci associated with acute low salinity tolerance in the Eastern oyster (*Crassostrea virginica*)**".
5. Anne Beemelmans, Memorial University, St. John's, NL, Canada, "**DNA Methylation Dynamics in Atlantic Salmon (*Salmo salar*) after Being Challenged with High Temperature and Moderate Hypoxia**".

Jorgenson Travel Award winner is: Alexandra McCarty (amccarty@umces.edu). QTL and joint-association mapping reveal loci associated with acute low salinity tolerance in the eastern oyster (*Crassostrea virginica*).

Plenary speaker travel awards ($1,000 each)

1. **Applications of Genomics to Expedite Genetic Improvement in Aquaculture Species** Ross D. Houston, The Roslin Institute and R(D)SVS
2. **Genomic Selection in Aquaculture: From Wild Stock to Advanced Breeding Schemes in *Penaeus monodon*** Herman Raadsma, University of Sydney
3. **Genomic Selection: From SNP Chips to Whole-Genome Sequence Data** Daniela Lourenco, University of Georgia

Leveraged funds and stakeholder use of project outputs

NRSP-8 Seed Funding: $40,000 (2019-2020); $30,000 (2018-2019)
Total Leveraged Funding: $ 7,532,332 (2019)

Leveraged funds from diverse projects totaling more than seven million dollars from federal sources. Selected grants are highlighted below:

8. **NOAA**, *Developing new oyster sterilization technology to avoid triploid summer mortality*. (PI L. Plough) **$100,000**.

7. **Ratcliffe Foundation**, *Shellfish Aquaculture Innovation Laboratory (SAIL): Using Science and New Technologies to Assist Shellfish Aquaculture Businesses in Maryland*. (PI L. Plough) **$391,000**.

6. **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** (8/1/209 through 7/31/2024); similar grants were also awarded to the Gulf of Mexico and Pacific States.

5. **US Department of Agriculture (USDA),** 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).

4. **US Department of Agriculture (USDA),** 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).

3. **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).

2. **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).

1. **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; Collaborator B.J. Reading) **$150,000** (09/01/2018 through 08/31/2020).

Major impact products (could be potential impact)

<u>Catfish</u>

Channel catfish genome assembly refined with optical mapping; blue catfish genome assembly released. DNA methylation profiles revealed subtle differential methylation patterns between the two genders that underlie sex determination.

Shellfish and Crustaceans

Pacific white shrimp genome published; initiate sequencing of whiteleg shrimp genome. Re-sequencing of wild and selected eastern oyster populations derived from multiple geographic regions along the US east Coast and Gulf of Mexico. 600K and 50K SNP chips developed for eastern oyster were applied to different populations and RNA-seq analyses are ongoing to understand the genomic basis for Dermo-resistance in Eastern Oyster. Three Eastern Oyster workshops were held: Epigenetics Workshop, Genome Workshop, Breeding Consortium Round Table.

Trout and Salmon

Genome assembly of doubled-haploid rainbow trout based on PacBio long read sequencing and scaffolding with Bionnano optical map and Hi-C contact map; genome assembly for Atlantic salmon is in progress using the tri-binning approach; Genome resequencing is underway in Chinook salmon and steelhead for broad representation of genomic variation across populations for each species. Genome-wide association studies identified genomic loci that affect fillet firmness, protein content, egg quality, fecundity, and egg size in rainbow trout. Allelic variation for candidate genes associated with migration timing/age at maturity was validated with markers in over 50,000 Chinook salmon and 20,000 steelhead. Contributions were made to development of FishGen.net database for storage of large-scale genotypes for genetic tagging and monitoring studies

Striped Bass

The second striped bass genome draft is uploaded to GenBank; transcriptome data is currently being processed by NCBI for annotation. 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. Different and novel machine learning-based analytical platforms are focused on small molecule (metabolomics), gene expression (RNA-Seq), and protein (proteomics) profiling to better understand hybrid striped bass growth performance (heterosis effects) and reproductive success in several different wild stocks of striped bass in watersheds of the mid-Atlantic region. Different strains of white bass from the midwest were assembled to establish a base breeding population for familywise evaluations of growth and nutrient utilization on alternative, sustainable diets; genotyping-by-sequencing panel was developed from white bass populations. Genetically improved striped bass and white

bass transferred to industry from *National Breeding Program for the Hybrid Striped Bass Industry*.

Publications (2019)

29. Phillips, C.A., Reading, B.J., Livingston, M., Livingston, K. and Ashwell, C.M. *Accepted*. Evaluation via Supervised Machine Learning of the Broiler Pectoralis Major and Liver Transcriptome in Association with the Muscle Myopathy Wooden Breast. *Frontiers in Physiology*, in press.

28. Hornick, K.M. and Plough, L.V., 2019. Tracking genetic diversity in a large-scale oyster restoration program: effects of hatchery propagation and initial characterization of diversity on restored vs. wild reefs. *Heredity* 123:92-105.

27. Hughes, A.R., Hanley, T.C., Byers, J.E., Grabowski, J.H., McCrudden, T., Piehler, M.F. and Kimbro, D.L. 2019. Genetic diversity and phenotypic variation within hatchery-produced oyster cohorts predict size and success in the field. *Ecological Applications* 29(6): e01940.

26. Jaris, H., Brown, D.S. and Proestou, D.A. 2019. Assessing the contribution of aquaculture and restoration to wild oyster populations in a Rhode Island coastal lagoon. *Conservation Genetics* 20(3):503-516.

25. 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.

24. Proestou, D.A., Corbett, R.J., Ben-Horin, T., Small, J.M. and Allen Jr, S.K., 2019. Defining *Dermo* resistance phenotypes in an eastern oyster breeding population. *Aquaculture Research* 50:2142-2154.

23. Ali A., Al-Tobasei R., Lourenco D., Leeds T., Kenney B. & Salem M. (2019) Genome-Wide Association Study Identifies Genomic Loci Affecting Filet Firmness and Protein Content in Rainbow Trout. *Frontiers in Genetics* 10: 386.

22. Chapagain P., Arivett B., Cleveland B.M., Walker D.M. & Salem M. (2019) Analysis of the fecal microbiota of fast- and slow-growing rainbow trout (*Oncorhynchus mykiss*). *BMC Genomics* 20: 788.

21. Grummer, J.A., L.B. Behergaray, L. Bernatchez, B.K. Hand, G. Luikart, S.R. Narum, and E.B. Taylor. 2019. Aquatic landscape genomics and environmental effects on genetic variation. *Trends in Ecology and Evolution* 34:641-654.

20. Janowitz-Koch, I., C. Rabe, R. Kinzer, D. Nelson, M.A. Hess, and S.R. Narum. 2019. Long-term evaluation of fitness and demographic effects of a Chinook salmon supplementation program. *Evolutionary Applications* 12:456-469.

19. Pearse, D.E., Barson, N.J., Nome, T., Gao, G., Campbell, M.A., Abadía-Cardoso, A., Anderson, E.C., Rundio, D.E., Williams, T.H., Naish, K.A., Moen, T., Liu, S., Kent, M., Moser, M., Minkley, D.R., Rondeau, E.B., Brieuc, M.S.O., Sandve, S.R., Miller, M.R., Cedillo, L., Baruch, K., Hernandez, A.G., Ben-Zvi, G., Shem-Tov, D., Barad, O., Kuzishchin, K., Garza, J.C., Lindley, S.T., Koop, B.F., Thorgaard, G.H., Palti, Y., Lien, S. 2019. Sex-dependent dominance maintains migration supergene in rainbow trout. *Nature Ecology and Evolution* 3: 1731-1742.

18. Silva, R.M.O., Evenhuis, J.P., Vallejo, R.L., Gao, G., Martin, K.E., Leeds, T.D., Palti, Y., Lourenco, D.a.L. 2019. Whole-genome mapping of quantitative trait loci and accuracy of genomic predictions for resistance to columnaris disease in two rainbow trout breeding populations. *Genetics Selection Evolution* 51: 42.

17. Steele, C.A., M.A. Hess, S.R. Narum, M.R. Campbell. 2019. Parentage-based tagging: reviewing the implementation of a new tool for an old problem. *Fisheries* 44:412-422.

16. Vallejo, R.L., Cheng, H., Fragomeni, B.O., Shewbridge, K.L., Gao, G., Macmillan, J.R., Towner, R. & Palti, Y. (2019). Genome-wide association analysis and accuracy of genome-enabled breeding value predictions for resistance to infectious hematopoietic necrosis virus in a commercial rainbow trout breeding population. *Genetics Selection Evolution* 51: 47.

15. Weigel, D., F. Monzyk, C. Sharpe, S.R. Narum, C.C. Caudill. 2019. Evaluation of a trap-and-transport program for a threatened population of steelhead (*Oncorhynchus mykiss*). *Conservation Genetics* 20:1195-1199.

14. 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. 2019. 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*, in press.

13. Abdelhamed, H., Ozdemir, O., Waldbieser, G**.**, Lawrence, M.L., Karsi, A. 2019. Effects of florfenicol feeding on diversity and composition of the intestinal microbiota of channel catfish (*Ictalurus punctatus*). *Aquaculture Research*, in press.

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