**NRSP-8 Salmonids Aquaculture Research Progress Report for 2014**

**Leadership**

Coordinator: John Liu, Auburn University, Alabama

Co-coordinator: Caird Rexroad, ARS Leetown, West Virginia

Species Leaders:

Catfish: Sylvie Quiniou, ARS Stoneville, Mississippi

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

Salmonids: Yniv Palti, ARS Leetown, West Virginia

Shrimp: Michael Criscitiello, Texas A&M University, Texas

Striped Bass: Craig Sullivan, Aquagyn, North Carolina

2015 Workshop Chair: Roger Vallejo, ARS Leetown, West Virginia

2015 Chair elect: Mohamed Salem, Middle Tennessee State University, Tennessee

2016 Chair elect: Nate Campbell, Columbia River Intertribal Fish Commission, Idaho

**Research Support Activities**

The Aquaculture Genome Co-Coordinators of USDA-NIFA National Research Support Project 8 (NRSP8) requested proposals for activities that support community research efforts for US Aquaculture species; primarily catfish, oyster, salmon, shrimp, striped bass and/or rainbow trout. Overall 11 projects were received from 10 PIs and 9 institutions covering catfish, oysters, rainbow trout, sablefish, shrimp, striped and white bass, and tilapia. All proposals were ranked, with the top three funded in FY14 and the next four prioritized for FY15 funding.

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| **PIs** | **Institutions** | **Title** | **Species** |
| Steven Roberts | University of Washington, WA | Resource coordination workshops focused on oysters and other shellfish | Oysters |
| Michael R. Garvin Gary H. Thorgaard | Washington State University, WA | Genomic Resources for Rainbow Trout Growth and Development | Rainbow trout |
| Benjamin J. Reading Charles H. Opperman | North Carolina State University, NC | Implementing Genome Resources for Temperate Basses (Genus *Morone*) | Striped bass White bass |
| Krista Nichols Rick Goetz Adam Luckenbach Ben Koop | NOAA, Seattle, WA | Improvement of the sablefish (*Anoplopoma fimbria*) genome sequence and assembly with long-read technology | Sablefish |
| Thomas D. Kocher | University of Maryland, MD | Proposal for PacBio sequencing to assemble LG3 of the Blue tilapia | Tilapia |
| Marine S. Brieuc  James E. Seeb Kenneth I. Warheit | USGS, Seattle, WA University of Washington, Seattle, WA Washington Dept Fish and Wildlife, Olympia, WA | Genotyping to enhance our knowledge of economically in domesticated Oncorhynchus mykiss using the O\_my\_50K SNP chip available from USDA | Rainbow trout |
| Acacia Alcivar-Warren | Environmental Genomics, MA | Community Research Efforts for Sequencing US farmed Pacific whiteleg shrimp (Litopenaeus vannamei) | Shrimp |

**Student Travel Awardees for PAG**

Coordinator’s funds were used to support student presentations at the Aquaculture Workshop. Award winners included:

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| --- | --- | --- | --- | --- |
| **NAME** | **Institution** | **Country** | **Advisor** | **Species** |
| Orly Eshel | The Hebrew University of Jerusalem | Israel | Berta Levavi-Sivan | Tilapia |
| Ailu Chen | Auburn University | USA | John Liu | Catfish |
| Xin Geng | Auburn University | USA | John Liu | Catfish |
| Carlos Rodriguez | The University of Adelaide | Australia | Mike Wilkinson | Kryptolebias marmoratus |
| Agnieszka Stadnik | Simon Fraser University | Canada | William Davidson | Atlantic Salmon |

**Progress towards NRSP8 Objectives**

**Objective 1: Advance the status of reference genomes for all species, including basic annotation of worldwide genetic variation, by broad sequencing among different lines and breeds of animals.**

**Catfish**

* Cooperative research between USDA-ARS Warmwater Aquaculture Research Unit and the School of Fisheries, Aquaculture and Aquatic Sciences at Auburn University has resulted in the first generation catfish genome sequence assembly. Next generation sequences from a doubled haploid channel catfish were error-corrected and assembled using the MaSuRCA/Whole Genome Shotgun Assembler pipeline. Mate pair reads from 3kb and 8kb length fragments, and paired end sequences from 34.4 kb fosmid clones were used to link contigs into scaffolds. Illumina and Pac Bio sequences were used to fill scaffold gaps, which improved the average contig lengths from 7.2 kb to 17.1 kb. Half the assembled bases were contained in 2,861 contigs of 76.7 kb or longer (up to 607 kb) and in 113 scaffolds of 1.88 Mb or longer (up to 11.5 Mb). 99% of the assembled bases were contained in 5,299 scaffolds of 1kb or longer. The kmer-based genome size estimate was 948 Mb, and the combined lengths of contigs and degenerates (sequences deemed as genomic repeats) was 934 Mb. 93.7% of assembled bases could be placed on the high density genetic map, and 95.6% could be placed on the BAC physical map. The catfish genome was annotated using transcriptome sequencing. Through transcriptome analysis of various tissues, a total of almost 28,000 genes were identified, and 23,000 complete cDNAs have been assembled and annotated. Gene families and gene duplication were analyzed.
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* Development and validation of SNP resources in different lines of blue catfish

***Oyster***

* Proposal to sequence and assemble the Eastern Oyster Genome was funded by the USDA NIFA Animal Breeding, Genetics, and Genomics program. PI: Marta Gómez-Chiarri.
* Draft genome of Pearl oyster (*Pinctada fucata*) is in progress (NCBI BioProject ID PRJDB2628).
* Mantle transcriptome of pearl oyster (*Pinctada maxima*) was sequenced, assembled and annotated. In addition, 1764 SSRs were identified.
* The Pacific Oyster methylome was characterized. Genes that are regulated by CpG methylation largely originate within the eukaryotic lineage suggesting that alternate methylation patterns contiribute to the radiation of eukaryotic taxa.

***Salmonids***

* The first rainbow trout reference genome was published (Berthelot et al., 2014) and the genome assembly was posted at the NCBI genome database.
* Thousands of SNP markers from RAD tags were identified and genotyped for various populations of *O. mykiss* (Matala et al. 2014)*, O. tshawytscha, O. nerka,* and *O. kisutch*.
* An effective method for custom amplicon sequencing (GT-seq) that allows thousands of fish to be genotyped for panels of 100-1000 SNPs was developed (Campbell et al. 2014, E-published).

***Shrimp***

* A high quality draft assembly of the *Litopenaeus vannamei* remains elusive. Several groups are working on this, including a teams led by Mike Criscitiello at Texas A&M and Rogerio Sotelo-Mundo at CIAD in Hermosillo Mexico, and one led by Jianguo He from Sun Yat-sen University in China. Efforts are currently focused upon assembly methods and inclusion of more PacBio data.

***Striped bass***

* The 585 Mb hybrid Illumina-PacBio striped bass genome sequence assembly was annotated and an jBrowse website is being designed for presenting access to it online with availability via the the NRSP8 website, URL: <http://stripedbass.animalgenome.org/> anticipated in 2016. A dedicated virtual machine platform has been setup to develop cyber resources for the Striped Bass Genome Database project at NC State University. Female and male white bass genomes also have been sequenced using Illumina and assembled using the striped bass genome as a reference. The female and male white bass genome assemblies consist of 57,533 contigs (643 Mb) and 56,818 contigs (644 Mb), respectively and partial Cegma scores indicate that both assemblies are 97.98% complete."

**Objective 2: Develop strategies to identify and exploit genes and allelic variation that contribute to economically relevant phenotypes and traits, in part through improving functional annotation of the genomes of our species.**

***Catfish***

* Bulked segregant RNA-seq (BSR-Seq) was used to analyze differentially expressed genes and associated SNPs with disease resistance against enteric septicemia of catfish (ESC). A total of 1,255 differentially expressed genes were found between resistant and susceptible fish. In addition, 56,419 SNPs were identified as significant SNPs between susceptible and resistant fish located on 4,304 unique genes. Detailed analysis of these significant SNPs allowed differentiation of significant SNPs caused by genetic segregation and those caused by allele-specific expression. Mapping of the significant SNPs, along with analysis of differentially expressed genes, allowed identification of candidate genes underlining disease resistance against ESC disease. Genomic sequencing of multiple individuals allowed identification of 8.4 millons of SNPs and analysis between the domestic and wild catfish allowed identification of selection sweeps.
* Continued characterization of immune responses and underlying gene actors in innate and specific immune responses in catfish

***Oyster***

* The transcriptomes of wild juvenile oysters from high and low salinity regimes were sequenced and compared to identify candidate genes for osmoregulation. High nucleotide sequence divergence between the Eastern Oyster and Pacific Oyster limits the extent to which the *C. gigas* genome can serve as a reference genome for *C. virginica*; however, purifying selection on protein sequences in this genus allowed for accurate functional annotation of *C. virginica* predicted protein sequences.
* The transcriptomes of juvenile Eastern Oysters from ROD (*Roseovarius* Oyster Disease) resistant and susceptible families were sequenced and compared to characterize the responses of different families to the disease as well as provide insight to mechanisms of disease resistance. Transcripts involved in immune recognition, signaling, protease inhibition, detoxification, and apoptosis were differentially expressed among the two families.
* Two Illumina GoldenGate genotyping arrays containing 384 SNP markers were designed for *Crassostrea gigas* and *Ostrea edulis* respectively and used to genotype 1000 individuals from wild and selected populations as well as families bred for commercially important traits. Overall success rate was 60%. These arrays provide adequate power for parentage assignment.
* Transcriptomes of Pacific Oysters from three wild populations were sequenced and aligned to the Pacific Oyster genome. 5.8 × 105 SNPs were identified and non-synonymous SNPs were enriched in genes involved in apoptosis and responses to biological stimuli. HRM genotyping assays have been developed for approximately 1300 SNP markers.

***Salmonids***

* The rainbow trout 57K SNP array is now commercially available from Affymetrix in two formats; for samples in 96-well plates and for samples in 384-well plates (more economical). For the 96 format the minimum order is 192 samples and for the 384 format the minimum order 1,920 samples. More ordering information on the array and a data sheet with technical information are available on the Affymetrix web site: <http://www.affymetrix.com/estore/catalog/prod900010/AFFY/Axiom%26%23174%3B+Trout+Genotyping+Array#1_1>
* GWAS studies were conducted for disease resistance in rainbow trout (Campbell et al. 2014, E-published), and tested natural populations of steelhead for genomic association with variable environments and landscapes (Matala et al. 2014).
* SNP markers were used to identify specific stocks of Chinook salmon and to identify run-timing, straying, and delayed mortality in natural populations (Hess et al. 2014; Rechisky et al. 2014).
* A total of 76 differentially expressed miRNAs including 10 miRNAs novel to rainbow trout were identified in skeletal muscle under the influence of estrogen. The known miRNAs include important myogenic miRNAs, such as miR-1, miR-133a, miR-126, miR-145, miR-499 and miR-206.
* A stringent set of 9,674 large intergenic noncoding RNAs (lncRNAs) were identified by RNA-Seq analysis of rainbow trout transcriptome. These lincRNAs in general are less conserved than protein-coding genes, and typically co-expressed with their neighboring genes. Many of them are tissue-specific and functionally associated with important biological processes.

***Shrimp***

* Several RNAseq projects have been completed in this species, including a refined transcriptome annotation from the Texas A&M/CIAD team late this year (*Scientific Reports* 4:7081 2014).

***Striped bass***

* Artificial neural networks and supervised machine learning were employed to further evaluate relationships between ovary transcriptome profiles and egg quality (fertility) in striped bass. Expression levels of as few as 250-1,000 ovary genes proved to be a robust predictor of egg quality (R2 always > 0.80) in separate studies involving analyses of gene expression by microarray or RNA-Seq in different groups of domesticated and wild striped bass. Egg transcriptome profiles were nearly as informative as ovary profiles from the same females, implicating maternal transcripts deposited in eggs in control of egg quality.

**Objective 3: Facilitate analysis, curation, storage, distribution and application of the enormous datasets now being generated by next-generation sequencing and related "omics" technologies with regard to animal species of agricultural interest.**

***Oyster***

* Proposal to hold resource coordination workshops focused on oysters and other shellfish funded through NRSP8 Aquaculture Program. PI: Steven Roberts.

***Salmonids***

* A bioinformatics pipeline was developed for genotyping SNPs from raw sequence data for the GT-seq method (Campbell et al. 2014, E-published).

***Shrimp***

* The shrimp community is slowly making data more accessible. Acacia Alcivar-Warren’s Environmental Genomics is moving on shrimp projects internationally in epigenomics and environmental toxicology, and had set up a One Health Genomics website that was unfortunately hacked. Most groups are still sharing data via small institution repositories (e.g. <http://repository.tamu.edu/handle/1969.1/152151>).

**PUBLICATIONS**

***Catfish***

1. Liu S, Yao J, Zhang J, and Liu ZJ. 2014. Next generation sequencing yields the complete mitochondrial genome of the striped raphael catfish, *Platydoras armatulus* (Siluriformes: Doradidae). Mitochondria DNA
2. Sun L, Liu S, Wang R, Jiang Y, Zhang Y, Zhang J, Bao L, Kaltenboeck L, Dunham R, Waldbieser G, Liu ZJ. 2014. Identification and analysis of genome-wide SNPs provide insight into signatures of selection and domestication in catfish. PLoS One 9(10): e109666.
3. Argue B, Kuhlers D, **Liu ZJ**, Dunham RA. 2014. Growth of channel catfish (*Ictalurus punctatus*), blue catfish (*I. furcatus*), and their F1, F2, F3, and F1 reciprocal backcross hybrids in earthen ponds. Journal of Animal Science 92(10):4297-305.
4. Sun L, Liu S, Wang R, Li C, Zhang J, Liu ZJ. 2014. Pathogen recognition receptors in channel catfish: IV. Identification, phylogeny and expression analysis of peptidoglycan recognition proteins. Developmental and Comparative Immunology 46:291-299.
5. Jiang Y, Xu P, Liu ZJ. 2014. Generation of physical map contig-specific sequences. Frontiers in Genetics 5: 243.
6. Dunham R, Taylor JF, Rise M, Liu ZJ, 2014. Development of strategies for integrated breeding, genetics and applied genomics for genetic improvement of aquatic organisms. Aquaculture 420-421:S121-S123.
7. Zhang J, Yao J, Wang R, Zhang Y, Liu S, Sun L, Jiang Y, Feng J, Liu N, Nelson D, Waldbieser G, **Liu ZJ.** 2014. The cytochrome P450 genes of channel catfish: their involvement in disease defense responses as revealed by meta-analysis of RNA-Seq datasets. Biochimica et Biophysica Acta-General Subjects 1840:2813-2828.
8. Yao J, Li C, Zhang J, Liu S, Feng J, Wang R, Li Y, Jiang C, Song L, Chen A, **Liu ZJ.** 2014. Expression of nitric oxide synthase (NOS) genes in channel catfish is highly regulated and time dependent after bacterial challenges. Developmental and Comparative Immunology 45:74-86.
9. Hutson AM, Liu ZJ., Kucuktas H, Umali-Maceina G, Su B, and Dunham RA. 2014. QTL map for growth and morphometric traits using a channel catfish x blue catfish interspecific hybrid system. Journal of Animal Science 92:1850-1865.
10. Wang R, Zhang Y, Liu S, Li C, Sun L, Bao L, Feng J, **Liu ZJ.** 2014. Analysis of 52 Rab GTPases from channel catfish and their involvement in immune responses after bacterial infections. Developmental and Comparative Immunology 45:21-34.
11. Liu S, Sun L, Li Y, Sun F, Jiang Y, Zhang Y, Zhang J, Feng J, Kaltenboeck L, Kucuktas H, and Liu ZJ. 2014. Development of the catfish 250K SNP array for genome-wide association studies. BMC Research Notes 7:135. DOI: 10.1186/1756-0500-7-135.
12. Geng X, Feng J, Liu S, Wang Y, 2, Arias C, Liu ZJ. 2014. Transcriptional regulation of hypoxia inducible factors alpha (HIF-alpha) and their inhibiting factor (FIH-1) of channel catfish (Ictalurus punctatus) under hypoxia. Comparative Biochemistry and Physiology, Part B, Biochemistry and Molecular Biology 169:38-50.
13. Feng J, Liu S, Wang X, Kaltenboeck L, Kucuktas H, Li J, **Liu ZJ** 2014. Hemoglobin genes are differentially regulated under heat stress conditions between sensitive and tolerant catfish in different tissues. Comparative Biochemistry and Physiology, Part D, Genomics and Proteomics 9:11-22.
14. Wong LL, Peatman E, Kelly L, Kucuktas H, Na-Nakorn U, and **Liu ZJ.** 2014. Catfish species identification using Lab-on-Chip PCR-RFLP. Journal of Aquatic Food Product Technology 23:2-13.
15. Li C, Waldbieser G, Bosworth B, Beck BH, Thongda W, Peatman E (2014) SNP Discovery in Wild and Domesticated Populations of Blue Catfish, *Ictalurus furcatus*, Using GBS and Subsequent SNP Validation.   *Molecular Ecology Resources*; 14: 1261-1270
16. Wang X, Li C, Thongda W, Luo Y, Beck BH, Peatman E (2014) Characterization and mucosal responses of interleukin 17 family ligand and receptor genes in channel catfish *Ictalurus punctatus*.  *Fish Shellfish Immunology* 38:47-55
17. Thongda W, Li C, Luo Y, Beck BH, Peatman E (2014) L-rhamnose-binding lectins (RBLs) in channel catfish, *Ictalurus punctatus*: characterization and expression profiling in mucosal tissues.  *Dev Comp Immunol* 44(2):320-331
18. Li C, Beck BH, Peatman E (2014) Nutritional impacts on gene expression in the surface mucosa of blue catfish (*Ictalurus furcatus*) *Dev Comp Immunol* 44(1):226-234
19. Moulana M., Taylor E.B., Edholm E.S., Quiniou S.M., Wilson M. and Bengten E. Identification and characterization of TCRγ and TCRδ chains in channel catfish, *Ictalurus punctatus*. Immunogenetics, 2014 Oct;66(9-10):545-61.
20. Rosser T.G., Griffin M.J., **Quiniou** S., Khoo L. and Pote L. 18S rRNA gene sequencing identifies a novel species of *Henneguya* parasiting the gills of the channel catfish (Ictaluridae). Parasitology Research. 2014 Dec;113(12):4651-8

***Oyster***

1. Deng, Y., Lei, Q., Tian, Q., Xie, S., Du, X., Li, J., Wang, L., Xiong, Y., 2014. De novo assembly, gene annotation, and simple sequence repeat marker development using Illumina paired-end transcriptome sequences in the pearl oyster Pinctada maxima. Bioscience, Biotechnology, and Biochemistry 78, 1685–1692. doi:10.1080/09168451.2014.936351
2. Eierman, L.E., Hare, M.P., 2014. Transcriptomic analysis of candidate osmoregulatory genes in the eastern oyster *Crassostrea virginica*. BMC Genomics, 15:503.
3. Lapègue, S., Harrang, E., Heurtebise, S., Flahauw, E., Donnadieu, C., Gayral, P., Ballenghien, M., Genestout, L., Barbotte, L., Mahla, R., Haffray, P., Klopp, C., 2014. Development of SNP-genotyping arrays in two shellfish species. Mol Ecol Resour 14, 820–830. doi:10.1111/1755-0998.12230
4. McDowell, I.C., Nikapitiya, C., Aguiar, D., Lane, C.E., Istrail, S., Gomez-Chiarri, M., 2014. Transcriptome of American Oysters, Crassostrea virginica, in Response to Bacterial Challenge: Insights into Potential Mechanisms of Disease Resistance. PLoS ONE 9, e105097. doi:10.1371/journal.pone.0105097
5. Wang, J., Qi, H., Li, L., Que, H., Wang, D., Zhang, G., 2015. Discovery and validation of genic single nucleotide polymorphisms in the Pacific oyster Crassostrea gigas. Mol Ecol Resour 15, 123–135. doi:10.1111/1755-0998.12278
6. Wang, X., Li, Q., Lian, J., Li, L., Jin, L., Cai, H., Xu, F., Qi, H., Zhang, L., Wu, F., Meng, J., Que, H., Fang, X., Guo, X., Zhang, G., 2014. Genome-wide and single-base resolution DNA methylomes of the Pacific oyster Crassostrea gigas provide insight into the evolution of invertebrate CpG methylation. BMC Genomics 15, 1119. doi:10.1186/1471-2164-15-1119

***Salmonids***

1. Ali, A., Rexroad, C., Thorgaard, G., Yao, J. & Salem, M. (2014). Characterization of the rainbow trout spleen transcriptome and identification of immune-related genes. *Frontiers in Genetics,* 5.
2. Berthelot, C., Brunet, F., Chalopin, D., Juanchich, A., Bernard, M., Noël, B., Bento, P., Da Silva, C., Labadie, K., Alberti, A., Aury, J.-M., Louis, A., Dehais, P., Bardou, P., Montfort, J., Klopp, C., Cabau, C., Gaspin, C., Thorgaard, G.H., Boussaha, M., Quillet, E., Guyomard, R., Galiana, D., Bobe, J., Volff, J.-N., Genêt, C., Wincker, P., Jaillon, O., Crollius, H.R. & Guiguen, Y. (2014). The rainbow trout genome provides novel insights into evolution after whole-genome duplication in vertebrates. *Nat Commun,* 5**:** 3657.
3. Fetherman, E.R., Winkelman, D.L., Baerwald, M.R. & Schisler, G.J. (2014). Survival and Reproduction of <italic>Myxobolus cerebralis</italic>-Resistant Rainbow Trout Introduced to the Colorado River and Increased Resistance of Age-0 Progeny. *PLoS ONE,* 9**:** e96954.
4. Hess, J.E., J.M. Whiteaker, J.K. Fryer, S.R. Narum. 2014. Monitoring stock specific abundance, run-timing, and straying of Chinook salmon in the Columbia River using genetic stock identification. North American Journal of Fisheries Management 34:184-201.
5. Liu, S., Gao, G., Palti, Y., Cleveland, B.M., Weber, G.M. & Rexroad, C.E., Iii (2014). RNA-seq Analysis of Early Hepatic Response to Handling and Confinement Stress in Rainbow Trout. *PLoS ONE,* 9**:** e88492.
6. Manor ML, Weber GM, Cleveland BM, Yao J, Kenney PB. 2014. Expression of genes associated with fatty acid metabolism during maturation in diploid and triploid female rainbow trout. Aquaculture. 435:178–186.
7. Matala, A.P., M.W. Ackerman, M.R. Campbell, and S.R. Narum. 2014. Relative contributions of neutral and non-neutral genetic differentiation to inform conservation of steelhead trout across highly variable landscapes. Evolutionary Applications, 7:682-701.
8. Meek, M.H., Stephens, M.R., Wong, A.K., Tomalty, K.M., May, B. & Baerwald, M.R. (2014). Genetic characterization of California's Central Valley chinook salmon. *Ecology,* 95**:** 1431-1431.
9. Palti, Y., Gao, G., Miller, M.R., Vallejo, R.L., Wheeler, P.A., Quillet, E., Yao, J., Thorgaard, G.H., Salem, M. & Rexroad Iii, C.E. (2014). A resource of single-nucleotide polymorphisms for rainbow trout generated by restriction-site associated DNA sequencing of doubled haploids. *Molecular Ecology Resources,* 14**:** 588-596.
10. Rechisky, E.L., D.W. Welch, A.D. Porter, J.E. Hess, S.R. Narum. 2014. Testing for delayed mortality effects in the early marine life history of Columbia River yearling Chinook salmon. Marine Ecology Progress Series 49:159-180.
11. Vallejo, R., Palti, Y., Liu, S., Evenhuis, J., Gao, G., Rexroad, C., Iii & Wiens, G. (2014a). Detection of QTL in Rainbow Trout Affecting Survival When Challenged with Flavobacterium psychrophilum. *Marine Biotechnology,* 16**:** 349-360.
12. Vallejo, R.L., Palti, Y., Liu, S., Marancik, D.P. & Wiens, G.D. (2014b). Validation of linked QTL for bacterial cold water disease resistance and spleen size on rainbow trout chromosome Omy19. *Aquaculture,* 432**:** 139-143.
13. Wang L, Ma H, Fu L and Yao J. 2014. Kpna7 interacts with egg-specific nuclear factors in rainbow trout (Oncorhynchus mykiss). Molecular Reproduction and Development. 81:1136–1145.

***Striped bass***

1. Chapman, R,W., Reading, B.J., Sullivan, C.V. 2014. Ovary transcriptome via artificial intelligence reveals a transcriptomic fingerprint predicting egg quality in striped bass, Morone saxatilis. PLoS ONE 435 9(5):e96818.
2. Schilling, J., Nepomuceno, A., Schaff, J.E., Muddiman, D.C., Daniels, H.V., and Reading, B.J. 2014. Compartment Proteomics Analysis of White Perch (Morone americana) Ovary Using Support Vector Machines. J. Proteome Res. 13(3):1515-1526.