

## 2009 Aquaculture Genome Report for NRSP8

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The 2010 NRSP8 Aquaculture Genome Workshop was held in conjunction with the International Plant and Animal Genome XVII Conference in San Diego, California. Dr. Krista Nichols (Purdue University) served as the Program Chair *in absentia*, and Dr. Matthew Rise (Memorial University of Newfoundland) served as the Aquaculture NRSP8 secretary and Program Chair-Elect. Yniv Palti (USDA/ARS National Center for Cool and Cold Water Aquaculture) assisted with the organization of the workshop. In attendance were approximately 100 during the course of the workshop, with 85 participants signed in from 13 countries: USA, Canada, Chile, China, France, Israel, Netherlands, Poland, Singapore, South Africa, South Korea, Slovenia, and UK. The workshop included 3 invited lectures (below), 22 contributed talks and poster presentations at the evening reception representing. The overall theme of the workshop was the use of next generation sequencing technologies to support mapping and functional genomics approaches to germplasm improvement. Invited lectures included:

Dr. Derek Stemple, Wellcome Trust Sanger Institute, presenting “RNAseq Annotation of the Expressed Zebrafish Protein-Coding Genome”

Dr. Scott LaPatra, Clear Springs Foods, presenting “Selective Breeding of Food Size Rainbow Trout: Current and Future Prospects;” and

Dr. Jerry Dodgson, Michigan State University, presenting “Comparative Genome Sequencing: Low Price, High Value”

The business meeting was convened at 5:00 pm January 9<sup>th</sup> for discussion on the budget and to elect new officers. For the 2011 Workshop, Dr. Rise will serve as Chair and Dr Sylvie Quiniou (ARS-CGRU) will serve as Chair-Elect. Changes in Officer Positions include:

Dr. Geoff Waldbieser was elected to represent Aquaculture as the NRSP8 Chair-Elect

Dr. John Benzie will serve as the Shrimp Coordinator instead of as an Industry Representative

Dr. Nagaraj Chatakondi will no longer serve as an Industry Representative as he has left industry to join ARS, Mitt Walker will replace him. Mitt is the Catfish Commodity Director of the Alabama Farmers Federation.

Dr. Tom Kocher will no longer serve as Tilapia Coordinator; this position will remain vacant for the foreseeable future.

In 2009, Coordinator's funds were used to support travel, the aquaculture genome workshop, and two community based projects (oyster genome workshop, rainbow trout PCR pool construction).

## Progress Towards Objectives

**Objective 1: Create shared genomic tools and reagents and sequence information to enhance the understanding and discovery of genetic mechanisms affecting traits of interest.**

### Catfish

Catfish Whole-genome sequencing: The USDA has funded a catfish whole-genome sequencing project through an AFRI grant awarded in 2009 entitled “Whole Genome Sequencing of Catfish”, John Liu and Geoff Waldbieser, co-PI’s, and Steven Salzberg (University of Maryland). Research includes production and assembly of sequence contigs from a homozygous channel catfish using single and paired reads (Illumina and 454 technologies). Paired reads from a homozygous blue catfish will be mapped to the channel catfish assembly. Existing genomic resources (physical maps, genetic maps, polymorphisms, BAC end sequences, cDNA sequences) will be incorporated into the assembly.

Physical map-linkage map integration: An effort to integrate the majority of the CHORI-212 catfish physical map contigs to an expanded catfish linkage map is nearing completion by Dr. Liu and Dr. Peatman’s at Auburn University. BAC-end associated microsatellites were identified from map contigs and genotyped on a mapping panel of backcross hybrid progeny.

New catfish microarray design and testing: A new Agilent catfish microarray including thousands of additional genes from channel catfish and blue catfish sequenced in the recent JGI EST projects is in final design and construction stages. The array will be constructed and tested using monies obtained through a competitive Alabama Agricultural Experiment Station grant for research into mucosal immune responses of blue, channel and hybrid catfish. Researchers interested in adding non-public features to the array or collaborating on microarray projects are encouraged to contact Dr. Eric Peatman at Auburn University ([peatmer@auburn.edu](mailto:peatmer@auburn.edu)). Pilot testing and protocol development will be conducted through the spring and details made publicly available on the web.

Catfish SNP chip: A large set of quality SNPs have been identified from ESTs at Auburn University. Additional SNPs have been identified from genome sequencing of reduced-representation libraries through collaborative efforts between ARS-Stoneville and Auburn University. These SNPs are to be used for the construction of the SNP chip of catfish.

An effort to integrate the majority of the CHORI-212 catfish physical map contigs to an expanded catfish linkage map is near completion in John Liu and Eric Peatman’s labs at Auburn University. BAC-end associated microsatellites were identified from map contigs and genotyped on a mapping panel of backcross hybrid progeny. The integrated linkage and physical map will support the whole genome sequencing project.

### Oyster

Whole genome sequencing of the Pacific oyster (*Crassostrea gigas*), a collaboration among the Institute of Oceanology of Chinese Academy of Sciences (IOCAS), the Beijing Genomics Institute (BGI), and international Oyster Genome Consortium (OGC), is in progress. The OGC is working to provide information from genetic and physical maps to BGI in order to assist the

assembly process. Contigs assembled to date by BGI will be useful in designing exon-based SNP assays, in order to provide Type I marker loci for the USDA-sponsored GigaSNP project.

Members of the Oyster Genome Consortium collaborated on the processing and annotation of EST sequences and 60 BAC clones produced by the JGI under a Community Sequencing Project. The BACs have been assembled into 16 contigs, with completion of annotation expected by March 2010. All BAC sequences have been deposited in GenBank, with a release date of 1 March 2010.

The Hedgecock lab published a gene-centromere map for the Pacific oyster. This map shows more recombination per chromosome than previously inferred and identifies markers that are very tightly linked to their respective centromeres. The latter will be useful in the current project to associate genetic, physical, and cytogenetic maps. The Gaffney lab published papers on Type I SNP markers in the Pacific and eastern oysters. These will be useful in the effort to integrate genetic and physical maps, and will allow preliminary cross-species comparison of two taxa that are estimated to have diverged ~40 mya. Gaffney and Jenny (University of Alabama) are coordinating the analysis of homologous BAC contigs from the eastern and Pacific oysters, for a first look at comparative genomics in this group. The Roberts lab identified a large number of novel transcripts that were annotated and submitted to GenBank. Implementing bioinformatic approaches, microsatellite markers were described and homologous genes in *Crassostrea virginica* were identified and published. Immune related genes were quantified in pathogen challenged oysters to better understand the oyster immune response. The Guo lab has developed EST-based SSR markers for several bivalve species, and annotated host-defense genes in ESTs from the zhikong scallop.

The Hedgecock and Gracey labs at USC clustered, aligned, and annotated the EST sequences produced by the JGI under a Community Sequencing Project. The raw and annotated data will be deposited in GenBank about March 1, 2010. The Hedgecock lab published an analysis of mitochondrial genome transcription, which shows that (1) mitochondrial genes are expressed at grossly different levels and must experience post-transcriptional modification to achieve stoichiometric balance in molecular complexes; (2) the antisense strand is transcribed and may play a regulatory role in modulating mitochondrial expression; and (3) expression depends on genotype and on maternal or nuclear-by-cytoplasmic factors. The Boudry lab has published the first use of RNA interference in the oyster, demonstrating the role of vasa in germ cell development. They have also identified QTL for resistance to summer mortality and OsHV-1 load in *C. gigas*, and QTL for resistance to bonamiosis in the European flat oyster *O. edulis*.

### **Salmonids**

A major accomplishment was the integration of the genetic and chromosome maps of rainbow trout and Atlantic salmon which was published this year (Phillips et al. 2009). This is especially timely because Sanger sequencing of the Atlantic salmon genome is beginning in 2010 and the French Genoscope group is planning to begin 454 sequencing of the rainbow trout genome. Both genomes are large and have many duplicate genes, so 454 sequencing would be impossible without a genome sequence of a related species to use as a scaffold. Although the Atlantic salmon chromosomes have been totally rearranged compared to Pacific salmon and trout, our work showed that large syntenic blocks of genes corresponding to chromosome arms in rainbow

trout have been conserved between the two species (Figures 1 and 2). We scored an average of 5 genetic markers that were conserved between the two species for each chromosome arm and they were usually found in the same order.

NCCCWA and collaborators from INRA and UC Davis are currently integrating the physical and genetic maps using microsatellites from BES of clones from the 180 largest contigs. Most of the markers were genotyped and the results will be published in 2010. In addition, we fingerprinted and generated end sequences of 10,000 clones from the new EcoRI and BamHI BAC libraries and identified 60 microsatellite markers from those clones. We also integrate the maps by screening PCR super-pools of the BAC library with over 300 markers that represent all the genetic linkage groups.

Characterization of Linkage Disequilibrium in Rainbow Trout: There are several genetic mapping approaches for identifying genes affecting production traits in populations of fish. Approaches which do not use pedigree information require the use of large numbers of genetic markers to identify chromosome segments which may contain genes of interest. An analysis of 49 genetic markers on 96 unrelated fish from the NCCCWA Broodstock population revealed that these approaches will require markers spaced every 2 centiMorgans, or approximately 1,500 markers. The current genetic map only has 1,200 markers. Therefore, these approaches will have significant limitations until new markers are developed.

Single Nucleotide Polymorphic Markers for Rainbow Trout: State of the art genome based technologies for managing breeding populations and identifying genes affecting production traits require large numbers of genetic markers. ARS developed a strategy for identifying single nucleotide polymorphic markers (SNPs) by repeated sequencing of 1% of the rainbow trout genome identified 47,128 potential new markers. An attempt to validate 384 of these markers produced 167 new markers which were placed on the genetic map and are available for genomic analyses. This approach revealed the degree of complexity that a recent genome duplication event places on genome analyses in salmonids and will serve as a model for future SNP discovery activities.

The U.S. salmonid aquaculture industry suffers severe economic loss to diseases. Every year, viral and bacterial epidemics in farmed Atlantic salmon and rainbow trout have resulted in production losses accounting for millions of dollars of lost revenue. The development of genetic markers for immune response genes is important for improving natural disease resistance in aquaculture fish populations. Toll-like receptors (TLRs) are a family of transmembrane proteins that recognize conserved pathogen structures to induce immune responses in human and in other vertebrates. In 2009 NCCCWA have completed the identification, annotation and genetic mapping of nine TLR genes in rainbow trout. Detailed mapping and annotation of TLR genes in rainbow trout and the development of genetic markers for the different TLR genes provide useful tools for genetic improvement of disease resistance in rainbow trout and other salmonids.

WVU and NCCCWA characterized the rainbow trout transcriptome using 454-Pyrosequencing. A total of ~1.3 million reads with an average length of 344 bp (447 million bases) were generated from a double-haploid individual. *De novo* assembly of the sequences yielded 151,847 Tentative Consensus sequences (TCs) and 224,391 singletons. A combination assembly of the

454-pyrosequencing data and the pre-existing EST sequences resulted in 161,818 TCs (average length 758 nt) and 261,071 singletons. The 454 library significantly increased the suite of annotated EST sequences available for rainbow trout.

To identify microRNAs from rainbow trout, WVU constructed a microRNA library from a pool of nine somatic tissues. Analysis of the library identified 210 unique sequences representing 54 distinct microRNAs. In addition, 13 microRNAs were computationally predicted from the rainbow trout transcriptome. The majority of the microRNAs showed characteristic tissue-specific expression patterns suggesting potential roles in maintaining tissue identity. Potential microRNA-target interactions were predicted and single nucleotide polymorphisms (SNPs) were identified in the microRNAs and their target binding sites.

WVU characterized the proteomic profile in degenerating muscle of rainbow trout in relation to the female reproductive cycle using a LC/MS-based label-free protein quantification method. A total of 146 significantly changed proteins in atrophying muscles (FDR <5%) was identified. Muscle atrophy was associated with decreased abundance in proteins of anaerobic respiration, protein biosynthesis, monooxygenases, follistatins, and myogenin, as well as growth hormone, interleukin-1 and estrogen receptors. In contrast, proteins of MAPK/ERK kinase, glutamine synthetase, transcription factors, Stat3, JunB, Id2, and NFkappaB inhibitor, were greater in atrophying muscle. These data will help identify genes associated with muscle degeneration and superior flesh quality in rainbow trout.

WVU identified a new isoform of the rainbow trout 14-3-3E1 gene. The new isoform contains an insertion of 48 nucleotides in the coding region of 14-3-3E1 which results in the introduction of a premature stop codon, producing a truncated protein lacking 17 amino acid residues at the C terminus. We show that the alternatively spliced isoform exhibits tissue and stage-specific expression and appears to have a different cellular function compared to the wild-type 14-3-3E1 protein.

This past year UC Davis conducted QTL mapping for whirling disease resistance in several rainbow trout families. Very strong linkage was detected for a single genomic region in all four mapping families, suggesting that this single region is capable of explaining a large percent of the phenotypic variance and almost all of the genetic variance contributing to the whirling disease phenotype (manuscript in prep). Additionally, gene expression studies comparing resistant and susceptible strains during early whirling disease progression have found several candidate genes with large expression profile differences between the strains (manuscript in prep) and future work will focus on mapping these candidates to determine if they lie within the identified QTL region and fine-mapping this region to obtain better resolution.

### **Shrimp**

A SNP-based linkage map has been constructed in Rothschild lab. International Shrimp Genome Consortium is organizing the initiation of whole genome sequencing project. The genome sequencing launch meeting is set to be in June of 2010. The major players of the consortium involve researchers from China, US, and Thailand.

## Striped Bass

Efforts continued to create a medium density linkage map for striped bass (*Morone saxatilis*) based on 498 microsatellite DNA markers developed by researchers in the N.C. State University (NCSU) Departments of Biology (C.V. Sullivan) and Genetics (C.R. Couch), at Kent SeaTech Corporation (M. Westerman and J. Stannard), and at the USDA/ARS National Center for Cool and Coldwater Aquaculture (NCCCWA) in Kearneysville, WV (C. Rexroad III). The mapping effort was funded by the NOAA Marine Aquaculture Initiative grant program. Our current objective is to obtain the genotypes of 143 fish (3 parents plus 70 progeny from each of two performance tested full-sib families of striped bass) at 325 marker loci. Genotyping in the project is being conducted at the Virginia Institute of Marine Science (VIMS) Marine and Aquaculture Molecular Genetics Laboratory. Based on progress to date, the VIMS researchers (K. Reece and J. Cordes) expect to complete the genotyping work in spring of 2010. We anticipate that the NCCCWA, NCSU and VIMS researchers will complete the linkage map in summer of 2010 and that the evaluation of fish performance data relative to genotype and discovery of any quantitative trait loci will be completed by the end of the year.

The NCSU researchers obtained funding from N.C. Sea Grant to utilize the panel of available microsatellite DNA markers to undertake a detailed genetic characterization of their special line of white bass, *M. chrysops* (NCSU-WB1), which has been domesticated over 8 generations in captivity, has been distributed to the ARS Stuttgart National Aquaculture Research Center (SNARC) and to members of the Striped Bass Growers Association (see below). One objective is to identify a minimum suite of markers that can be used to discriminate between NCSU-WB1 and other captive or wild strains of white bass so that unauthorized distribution or adulteration of the line can be detected (and prevented). The genotyping effort on the project is well underway at NCSU and should be completed in 2010. This effort should aid in application of the striped bass linkage map to selective breeding of white bass, the female parent of the hybrid striped bass (HSB) produced in commercial aquaculture.

A major impediment to selective breeding of superior striped bass and hybrid striped bass for farming is poor egg quality. Currently, only about half of the female striped bass selected for breeding can be successfully reproduced in a given year. The root causes of poor egg quality are largely unknown. In order to facilitate the identification of proteins and genes whose expression is linked to poor egg quality, N.C. State University scientists in the Department of Biology (B.J. Reading and C.V. Sullivan) and in the Genomic Science Laboratory (J. Schaff and N. Glassbrook) undertook the pyrosequencing of 230,151 expressed sequenced tags (ESTs) from ovarian tissue of striped bass pooled from fish at all stages of oocyte development, spawning and atresia generating 144,302 unique short read sequences. Subsequent analyses of the data were conducted in collaboration with R.W. Chapman at the S.C. Marine Resources Research Institute (MRRRI). The short read sequences were clustered with CAP3, resulting in 11,203 contigs and the high quality contig assemblies were subjected to BLAST (blastx) search of the National Center for Biotechnology Information (NCBI) database and annotated according to the criteria outlined by the Gene Ontology (GO) Consortium using the Blast2GO software suite. Of the total contigs, 4,120 (36.8%) could be fully annotated with GO terms and 5,726 (51.1%) remain unknown. We are working to deposit all of the high-quality EST sequences in the NCBI Short Read Archive for public use. This EST/contig collection also has been submitted to Agilent Technologies (Santa Clara, CA) for oligo cDNA microarray design. We anticipate a 60-mer oligo array with ~11,000 probes. This collection of ovarian ESTs represents the first

contribution of a large reference sequence database for species of the genus *Morone* and provides a basis for gene expression and proteomics studies in temperate basses.

The Mediterranean seabass, *Dicentrarchus labrax*, is a close relative of the striped bass that is farmed extensively in the European Union and elsewhere and is under intensive genomic investigations, which have included several studies investigating various physiological systems that have generated ESTs. We downloaded in FASTA format all of the EST sequences for this species that were available at the NCBI online database (N=54,200) and used CAP3 to assemble these sequences into 423 unique contigs and 1,018 singletons. These 1,441 unigenes were subjected to BLAST (blastx) search and annotation using Blast2GO. A total of 399 sequences were annotated with GO terms (27.7%). The number of unknown unique sequences was 866 (60.1%). The total number of contigs available for *D. labrax* (1,441) is only 12.9% of the number present in our online database for the striped bass ovary. We are currently comparing the contig sets for striped bass and seabass to determine whether any *D. labrax* sequences will be added to the Agilent microarray under development.

While our striped bass 'OvaryUniClone' array underdevelopment should permit more efficient analysis of the target organ due to higher coverage of its transcriptome than that offered by a general cDNA array, we also are working with R.W. Chapman from the MRRRI to develop a general cDNA microarray for the temperate basses (genus *Morone*) that could be used in studies of extra-ovarian reproductive processes, growth physiology, and other physiological phenomena. Ovarian tissues representing all stages of oocyte growth, ovulated eggs, and atretic follicles from one or more individual female white perch, *M. americana*, were collected by dissection or through ovarian biopsy. Testis undergoing spermatogenesis and early- and late-spermiation were also collected. Additionally, liver and muscle was collected from male fish during spermiation and spermatogenesis, and from females during atresia and early-, late-, and post-vitellogenesis. Other tissues (spleen, hindgut, foregut including pyloric caecae, skin, stomach, visceral fat, heart including the bulbous, atrium and ventricle, head kidney, gill filaments, brain excluding pituitary, and the pituitary) were collected from at least 6 fish of mixed sexes (N=3+ each). These tissues have been preserved in RNAlater<sup>®</sup> and will be used in 2010 to develop an organismal transcriptome and general cDNA microarray for the white perch, which is our major laboratory model for reproductive physiology in *Morone* species.

Several functional genomics projects also are being conducted by at NCSU investigators (R.J. Borski, C.V. Sullivan, E.J. Noga) and SNARC scientists (J.A. Fuller, M. McEntire) involving investigation of genes and proteins regulating growth, reproduction and immunity in striped bass, white bass and HSB, or in the white perch (*M. americana*), which is a laboratory model for *Morone* reproduction.. Examples include growth regulating hormones and their receptors ( e.g., growth hormone [GH], GH receptor [GHR], IGF-I, IGFR), egg yolk precursor proteins (vitellogenins [Vtgs]), and anti-microbial peptides. The NCSU studies also involve the three doctoral students (A. Baltzegar, S. Salger, and V.N. Williams) in the NCSU inter-disciplinary program of graduate education and research in Aquaculture Genomics established in the Biology Department with support from the USDA-CSREES Food and Agricultural Sciences National Needs Graduate and Postgraduate Fellowship (NNF) Grants Program. These functional genomics studies are being integrated with the microsatellite DNA marker discovery and linkage mapping project discussed above in investigations of the disparate expression of candidate genes and proteins among families of striped bass and hybrid striped bass. These lines of investigation will greatly benefit from the development and availability of the transcriptome information and cDNA microarrays discussed above.

During 2009, Stuttgart National Aquaculture Research Center researchers performed nearly 80 crosses using NCSU founder stocks of white bass for performance testing and trait evaluation for growth related traits. A portion of this effort was used to establish the first baseline heritabilities for white bass published in the literature. SNARC researchers also worked with industry HSB hatcheries and distributed thousands of F<sub>8</sub>-generation advanced fingerlings for industry testing and use. Also in 2009, the SNARC researchers began evaluating differential relative gene expression of growth and disease-related genes within and among families of white bass and HSB. Also, with funding support from the Southern Regional Aquaculture Center and CSREES, SNARC in collaboration with the University of Arkansas at Pine Bluff, began evaluating genetic and phenotypic influence on white bass and HSB larval size and quality, and the influence of genetic factors on metabolic and stress-related traits.

### **Tilapia**

While the whole genome sequencing project has been slowly progressing in the Broad Institute, a large number of BAC end sequences (110,880) have been generated at Genoscope. The BAC end sequences have been comparatively mapped in silico by Kocher's lab to stickleback genome sequence assembly. Working with Co-Factor Genomics, Kocher's lab is also generating the whole genome sequences of the tilapia genome using the next generation sequencing.

A total of 116,889 ESTs have been generated in Kocher's lab from 17 normalized libraries. These ESTs were assembled into 24,363 contigs.

### **Objective 2: Facilitate the development and sharing of animal populations and the collection and analysis of new, unique and interesting phenotypes.**

#### **Catfish**

Establishment of microsatellite pedigrees for individual identification: Microsatellite were genotyped on a resource population of channel catfish to establish pedigrees from families produced in the 2008 and 2009 spawning seasons. Only 21% of male and 26% of female broodstock spawned as 2 yr olds, while 40% of males and 49% of females spawned as 3 yr olds. This analysis confirmed prior research that showed multiple spawning by males in one season (up to 9 spawns). For the first time, we demonstrated that catfish females could spawn more than once per season in earthen ponds, and the spawns were usually separated by 1 month. Along with these paternal and maternal half-sib families, there were also 11 full-sib families produced by multiple same-pair matings separated by 28-65 days.

Channel catfish (female) X Blue catfish (male) hybrid catfish have superior production traits compared to the channel catfish, however inherent reproduction problems to produce in commercial quantities was a major bottleneck to adopt this genotype in the last 40 years. In the last 5 years, several hybrid catfish production problems have been overcome by the efforts of researchers at the university, USDA and industry and production has been rising steadily ever since. In 2009, about 60 million hybrid fry were produced (twice as much as in 2008). The hybrid catfish has recently been introduced to the commercial catfish farms and presently 47 farms have hybrid catfish in 1-10 ponds in their farms. In general, growth, feed conversion efficiency, survival, seinability and processing yield were superior to channel catfish. Producing

hybrid catfish rather than channel catfish has resulted in an increase of income of \$390 to \$5,340 per acre depending on the management of the catfish farm.

Oyster

Salmonids

Fish response to stress is an important factor in aquaculture production, having impacts on growth, feed efficiency, immune response, and reproductive characteristics. In 2009 we determined that major QTL loci are segregating in the NCCCWA broodstock which impacts response to handling stress as measured by cortisol concentrations in the blood. Efforts to identify the genes responsible for this effect include cortisol measurements for three generations of a broodstock pedigree combined with genetic marker analyses.

Bacterial cold water disease caused by *Flavobacterium psychrophilum* is a major concern for trout aquaculture. In 2009 we determined that major QTL loci are segregating in the NCCCWA broodstock which impacts resistance to *F. psychrophilum* as measured by 21-day survival post exposure to the pathogen. To identify genes affecting this trait we measured post exposure survival in three generations of a broodstock pedigree and identified informative families for conducting genetic marker analyses.

Shrimp

Striped Bass

Tilapia

**Objective 3: Develop, integrate and implement bioinformatics resources to support the discovery of genetic mechanisms that underlie traits of interest.**

A Teleost Alternative Splicing database has been developed at Auburn. A oyster database was developed at USC to house the clustered, aligned, and annotated oyster EST sequences. This database will be made public when the sequences are deposited and the MS submitted about March 1, 2010. The Gaffney lab is coordinating the annotation of the oyster BAC contigs. Preliminary annotations will be reviewed by the Oyster Genome Consortium prior to submission to GenBank. A comparison of aligned haplotypes is underway, and will contribute to the assembly of whole genome sequence data being collected at the Beijing Genomics Institute. The Boudry group in France has established a public web database containing ~30,000 Pacific oyster ESTs.

Catfish

Oyster

## Salmonids

The rainbow trout genetic map can be viewed and searched online through using a GMOD Browser on the Animal Genome databases web pages (<http://www.animalgenome.org/cgi-bin/host/rainbow/viewmap>).

## Shrimp

### Striped Bass

In collaboration with Z. Hu at Iowa State University, the 11,208 annotated striped bass ovarian contigs were assembled into a searchable database, which has been posted on the National Aquaculture Genomics website (part of the National Animal Genome Research Program (<http://www.animalgenome.org/cgi-bin/host/ncsu/seqdbinfo>)). In 2010, we anticipate a similar posting of contigs resulting from our ongoing effort to develop a whole organism (multiple tissues and gonad maturation stages) transcriptome of white perch.

### Tilapia

## Publications

### Catfish

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## Oyster

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