

ANNUAL REPORT OF MULTI-STATE RESEARCH ACTIVITY

PROJECT: NRSP-8
PROJECT TITLE: Aquaculture
PERIOD COVERED: January 1 to December 31, 2010
ANNUAL MEETING DATE: January 15-16, 2011

PARTICIPANTS: This list of participants was retrieved from the NIMMS System entirely based on subject of investigation (SOI) as listed below. However, we are aware that many contribute to aquaculture genomics without declaring their SOI for cultured aquatic species. One good example is Dr. Max Rothschild whose laboratory also studies the shrimp genome in addition to porcine genome.

3710 Catfish
3711 Trout
3712 Salmon
3713 Striped bass
3714 Tilapia
3715 Baitfish (minnows and shiners)
3716 Ornamental finfish
3719 Other cultured finfish
3720 Crawfish
3721 Marine shrimp
3722 Freshwater shrimp
3723 Oysters
3724 Clams and mussels
3725 Ornamental shellfish
3729 Other cultured shellfish
3799 Cultured aquatic animals, general/other

Participant	Station/Institution and Department
Gomez-Chiari, Marta	Rhode Island - University of Rhode Island
Guo, Ximing	New Jersey - Rutgers University
Kueltz, Dietmar	California -Davis : University of California, Davis
Liu, Zhanjiang (John)	Alabama - Auburn University
Nichols, Krista M	Indiana - Purdue University
Palti, Yniv	ARS, North Atlantic Area
Rexroad III, Caird	ARS, North Atlantic Area
Vallejo, Roger	ARS, North Atlantic Area
Yang, Jinzeng	ARS, Hawaii - University of Hawaii
Sullivan, Craig V.	ARS, North Carolina - North Carolina State University

BRIEF SUMMARY OF MINUTES OF ANNUAL MEETING:

PAG XIX Aquaculture Workshop Report, January 15-16, 2011

The 2011 NRSP8 Aquaculture Genome Workshop was held in conjunction with the International Plant and Animal Genome XIX Conference in San Diego, California. Dr Matthew Rise (Memorial University of Newfoundland) served as the Program Chair, and Dr. Sylvie Quiniou (USDA/ARS –CGRU) served as the

Aquaculture NRSP8 secretary and Program Chair-Elect. In attendance were approximately 100 during the course of the workshop, with 34 participants signed in from 11 countries besides the US: Canada, Norway, Japan, Netherlands, UK, France, Chile, New Zealand, China, Germany and Australia.

The NRSP8 Aquaculture Executive Committee received 14 applications for the \$1,000 Travel Awards. Eleven of the applicants were students or post-docs from US institutions and the rest were international applicants (1 from Spain, 2 from Chile). Ten travel awards were attributed. After a few years where the number of applicants decreased (2010, 11; 2009, 15; 2008, 21), this year seems to mark a halt to the trend. We also saw an increase of applicants from US institutions. The presentations covered a diverse range of fields (reproduction, growth, immunity) showing the input of Aquaculture Genomics to all physiological fields of research.

Five plenary speakers were invited to the 2011 Aquaculture Workshop: 1) Dr. William S. Davidson (Professor at Simon Fraser University with expertise in molecular evolution); 2) Dr. Ben F. Koop (Professor at the University of Victoria and Canada Research Chair in the Departments of Biology, and Division of Medical Sciences with expertise in molecular evolution and genetic variation; Dr. Davidson and Dr. Koop shared the Life Sciences Genome BC Award for Scientific Excellence for their contributions to salmonid genomics); 3) Dr. John T. Buchanan (as Director of Research and Development for Aqua Bounty Technologies); 4) Dr. John Liu (Distinguished Alumni Professor and Associate Dean for Research in the College of Agriculture, Auburn University); and 5) Dr. Geoffrey C. Waldbieser (Research molecular biologist for USDA-ARS and Leader of the Genetics, Physiology, and Health Research to Improve Catfish Production project). On Saturday morning, Dr. Davidson and Dr. Koop presented the history behind the salmon genome sequencing project as well as the status of the assembly. On Saturday afternoon, Dr. Buchanan spoke about the development of a genetically altered salmon for growth as well as the process needed to have such an animal authorized for commercial production. On Sunday, Dr. Liu and Dr. Waldbieser discussed the strategy behind the sequencing of the catfish genome as well as the present status of the assembly.

Several of the workshop's contributed talks focused on the development of new genomic resources for Aquaculture species (e.g. genome sequence for Pacific white shrimp, oyster, bluefin tuna and trout; physical map for Zhikong scallop; SNPs for salmon and catfish, repeat database from BES for tilapia) as well as strategies for sequencing genome de novo for non-traditional models. In addition, several contributed talks focused on the use of genomic tools (microarray, RNAseq, SNPs) to identify genes and markers associated with traits of interest (e.g. egg quality, growth rate, disease resistance, stress, muscle quality) for various aquaculture species. One contributed talk also discussed the development of a publicly available database. In total, besides the plenary lectures, 22 contributed presentations were given during the Saturday and Sunday sessions of the workshop.

On Sunday morning, the NRSP8 species progress reports were presented. The species reports are detailed in the annual report.

Officers:

2010 Species Coordinators Dr. John Liu, Auburn University and Dr. Caird Rexroad, USDA/ARS/NCCCWA

2010 Species Leaders

Catfish – Dr. Sylvie Quiniou, USDA/ARS/CGRU

Oyster – Dr. Patrick Gaffney, University of Delaware

Salmonids – Dr. Yniv Palti, USDA/ARS/CGRU

Shrimp – Dr. John Benzie, University College Cork
Striped Bass – Dr. Craig Sullivan, North Carolina State University
2011 Workshop Chair – Dr. Matthew Rise, Memorial University of Newfoundland
2011 Workshop Secretary – Dr. Sylvie Quiniou, USDA/ARS/CGRU
2011 NRSP8 Committee Chair-elect (Aquaculture), Dr. Geoff Waldbieser, USDA/ARS/CGRU

Future Officers:

2012 NRSP8 Committee Chair (Aquaculture), Dr. Geoff Waldbieser, USDA/ARS/CGRU
2012 Workshop Chair – Dr. Sylvie Quiniou, USDA/ARS/CGRU
2012 Workshop Secretary – Dr. Eric Peatman
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Minutes of Annual Business Meeting and Sign-in Sheets are attached.

ACCOMPLISHMENTS AND IMPACTS:

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: Genomic Reference contigs have been produced using Illumina-based high throughput (CGRU, BFGL, University of British Columbia, Auburn). The assembly of the first 22.5Gb (Q30) gave 279,054 contigs > 400bp (12.5% in contigs >10kb, 50.0% in contigs >4 kb and 91.7% in contigs > 1kb). Subsequently 49.4 Gb have been sequenced and are being integrated to the assembly. Gene transcripts from various tissues of multiple individuals with diverse genetic background were sequenced with Illumina GAllx giving 35.2Gb of data (Auburn, CGRU, BFGL). A set of filtered SNPs were identified including 446,169 intra-specific SNPs for channel catfish, 555,175 intra-specific SNPs for blue catfish, and 322,006 inter-specific SNPs between channel catfish and blue catfish. These filtered SNPs are distributed within 17,806 unique genes in channel catfish and 18,887 unique genes in blue catfish. In parallel, more than 100k genomic SNPs that could be matched with a zebrafish chromosome have been identified of which about 10,000 matched BAC end sequences. 2,000 BAC end-associated microsatellites have been mapped to the F1 backcross hybrid Linkage Map (Auburn). Finally, the DNA of 12 strains of *Aeromonas hydrophila* has been sequenced on Illumina GAllx giving an average Avg. 7M sequences per strain (~100X coverage) with average N50 contigs number and length of 16 and 110Mb respectively. Those 12 assemblies are currently being compared to *Aeromonas hydrophila* GenBank reference genome (Consortium of 18+ scientists from Mississippi State, Auburn, U. Arkansas at Pine Bluff, Louisiana State, Industry, and USDA-ARS).

Oyster: In 2010 the Oyster Genome Consortium was successful, after several years of effort, in establishing a whole genome sequencing project for the Pacific oyster (*Crassostrea gigas*). Sequencing was begun in 2010 as a joint effort of the Institute of Oceanology, Chinese Academy of Sciences and the Beijing Genomics Institute-Shenzhen at the Beijing Genome Institute. To date, BGI has obtained more than 200X coverage with Illumina sequencing and end-sequences of 450,000 fosmid clones. Genome assembly is difficult because of the very high polymorphism compared to other cultured species. The current assembly has a N50 contig size of 19 kb and scaffold size of 150 kb. The OGC was also successful in securing commitment from Genoscope (France) to sequence BAC ends from the oyster genomic library developed under USDA support. The library was shipped in late 2010 and sequencing is expected to be complete in 2011.

Rainbow Trout: The USDA-NCCCWA map was used for producing a first generation integrated physical and genetic map where more than 200 microsatellites isolated from BAC end sequences were genotyped and added onto the genetic map linkage groups. A high density RAD (restricted site associated DNA) genetic map of Swanson x Whale Rock recombinant double haploids is being constructed using approximately 7,600 SNPs to aid in future assembly of a reference genome sequence. A pooling and tagging scheme is used for sequencing of the ~15,000 clones of the BAC fingerprinting physical map minimal tiling path (MTP). This is a modification of the classic clone-by-clone approach. The source of DNA for the de-novo assembly projects is the Swanson DH homozygous line. The same source of genomic DNA was also used for producing the BAC libraries, BAC end sequences and fingerprinting physical map. Concurrent efforts are underway for high density sequencing of the Swanson-line transcriptome to facilitate annotation of protein-coding genes and all other transcribed sequences in the genome assembly. A panel of tissues was sequenced using Roche-454 pyrosequencing (1.3 million reads; 447 Mb) and assembled and annotated in combination with the large Sanger-based ESTs database of approximately 260,000 sequences. Gene Expression Atlas using Illumina sequencing of RNA from the same tissues was recently completed (520M reads; 130 Gb) and bioinformatic analysis is currently underway.

Shrimp: Pacific white shrimp (*Litopenaeus vannamei*) are of particular economic importance to the global shrimp aquaculture industry. A first SNP genetic map for Pacific white shrimp was built with 418 SNP markers from 347 contigs mapped onto 45 sex-averaged linkage groups. The approximate coverage for the female and male maps were 2071 and 2130 cM, respectively. This SNP genetic map lays the foundation for future shrimp genomics studies, especially the identification of genetic markers or regions for economically important traits (Du et al., 2010). A useful application based on EST sequences from Pacific white shrimp and other shrimp species was to predict SNPs that may distinguish shrimp species, locate SNPs that may segregate in multiple species, and determine the genetic similarities between different species. Overall, 4,597 SNPs were predicted from 4,600 contigs with 703 of them being interspecies SNPs, 735 of them possibly predicting species' differences, and 18 of them appearing to segregate in multiple species. While sequences appear relatively well conserved, SNPs do not appear to be well conserved across shrimp species (Gorbach et al., 2010). Candidate gene analysis for shrimp growth rate revealed that allele C of two SNPs, C109T and C395G in 5HT1R, tended to be associated with increased body weight, however, further studies need to be conducted using a large and diverse population sample (Marti et al., 2010).

Striped Bass: Scientists from the USDA-ARS National Center for Cool & Cold Water Aquaculture (NCCCWA), VIMS and NCSU genotyped two half-sib families of striped bass at 289 microsatellite DNA markers and assembled 26 linkage groups (only 2 markers remained unlinked). The resulting sex-averaged genetic linkage map, which spans 1701.6 cM with an average marker density of 5.99 cM per marker, was compared to the sequenced genome of a model teleost, the three-spined stickleback (*Gasterosteus aculeatus*), which revealed conserved synteny between the two species. The NCSU scientists developed a transcriptome for all stages of striped bass ovary development based on 230,151 ESTs assembled into 11,208 high-quality contigs of which BLASTx comparisons revealed 5,482 gene orthologues, most of which could be annotated with Gene Ontology terms. Based on this transcriptome, an open source, 60-mer oligo cDNA Agilent Technologies microarray spotted with 14,690 probes representing 11,313 striped bass unigenes was developed and deployed in studies of poor egg quality, a major problem in striped bass breeding. Preliminary analyses of the data via novel bioinformatics approach based on artificial neural network (ANN) and machine learning procedures revealed that over 90% of the variation between females in egg quality (e.g. percent of eggs yielding 4 h embryos) can be explained by the level of

transcription of only 250 genes in oocytes biopsied at the start of breeding activities. Several functional genomics projects also were conducted by NCSU investigators and scientists at the USDA-ARS Stuttgart National Aquaculture Research Center (SNARC) involving investigation of genes and proteins regulating growth, muscle regulation, metabolic function and regulation, reproduction and immunity in striped bass and its relatives (genus *Morone*).

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

Oyster: Currently, Pacific oysters are cultured on every continent except Antarctica, with development of selected resource families taking place in several countries (e.g., United States, France, Australia). Sharing of populations is limited by barriers to transport of broodstock. However, selection programs for improved growth and disease resistance have developed phenotypes of commercial interest, which are the subject of continuing genetic analyses (Dégremont et al 2010a,b; Fleury et al. 2010; Huvet et al. 2010; Lallias et al. 2010; Sauvage et al. 2010).

Rainbow Trout: Three multi-year pedigreed rainbow trout populations phenotyped for plasma cortisol in response to stress, resistance to bacterial cold water disease (BCWD) and spleen size have been characterized and propagated at the NCCCWA. To date we have detected QTL with major effects for the stress response and spleen size traits and genome scans to detect BCWD resistance QTL is currently underway. We identified 218 putative type-I SNPs markers associated with growth-rate by RNA-seq analysis of cDNA samples from the NCCCWA rainbow trout families. Genotyping individuals from the SNP discovery panel using the Sequenom iPLEX Genotyping platform validated association of 104 markers with the growth trait ($p < 0.01$).

The Nichols lab has completed a pyrosequencing run of brain transcriptome for brook trout that will contribute to the growing EST resources for this species, and have completed a study on the heritability of morphology and size in hatchery strains of this species. They continue to finalize a microarray analysis of the effects of QTL genotype and sex during embryonic development rate in rainbow trout. One paper on the QTL genotype effects on gene expression during embryonic development is published in Marine Biotechnology, and the manuscript on gene expression differences between the sexes during embryonic development is in preparation. QTL analyses of traits associated with smoltification and migration in *O. mykiss* are ongoing, and they have begun to identify SNP markers by RAD tag sequencing to further facilitate these efforts.

The Thorgaard and Phillips labs have completed and published a study of variation in Y chromosome sequences among rainbow trout populations. They are engaged in collaborative research to try to identify additional Y chromosome-specific sequences with the goal of identifying the sex-determining locus. They are also characterizing differences in morphology and behavior between clonal rainbow trout lines with varying levels of domestication with the goal of conducting QTL studies to characterize the genetic basis of any differences identified.

Striped Bass: The USDA-ARS SNARC generated 192 crosses of *Morone* using National Breeding Program foundation stocks and completed studies evaluating heritability of phenotypic variation growth of hybrid striped bass (HSB) as tank-reared fingerlings (42 dph) ($h^2_{\text{Dam}} > 0.67$ and $h^2_{\text{Sire}} > 0.44$ for length and weight) and in replicated communal production ponds (> 5,000 individually tagged fish) for ~120 days of growth ($h^2_{\text{Dam}} > 0.74$ and $h^2_{\text{Sire}} > 0.52$ for both traits). Twenty individuals from among the best and worst performing families were sampled and sent for transcript pyro-sequencing to produce transcriptome profiles

for superior and inferior phenotypes, and to identify associated SNPs for use in future selective improvement. Scientists from SNARC and the Univ. Arkansas at Pine Bluff evaluated the genetic and phenotypic influence of parental traits on HSB larval size and quality, and the influence of genetic factors on metabolic and stress-related traits, discovering that female phenotype does not significantly affect larval traits (e.g. growth) but that genotype does have a significant affect. This finding is significant because any increase in larval size at hatch resulting from selection would reduce the need for live feeds, which could make year-round tank production of fry and fingerlings economically viable for industry. Significant differences also were found in the rate of recovery for oxygen consumption in families of HSB following exposure to stress. SNARC and NCSU researchers also distributed advanced fingerlings and mature broodfish from National Breeding Program stocks to HSB producers engaged in propagation of commercial domesticated broodstocks..

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

Catfish: The Catfish Genome Database cBARBEL (abbreviated from catfish Breeder and Researcher Bioinformatics Entry Location) has been developed and publicly available. It is an online open-access database for genome biology of ictalurid catfish (*Ictalurus* spp.). It serves as a comprehensive, integrative platform for all aspects of catfish genetics, genomics and related data resources. cBARBEL provides BLAST-based, fuzzy, and specific search functions, visualization of catfish linkage, physical, and integrated maps, a catfish EST contig viewer with SNP information overlay, and GBrowse-based organization of catfish genomic data based on sequence similarity to the zebrafish chromosomes. Subsections of the database are tightly-related, allowing a user with a sequence or search string of interest to navigate seamlessly from one area to another. As catfish genome sequencing proceeds and ongoing quantitative trait loci (QTL) projects bear fruit, cBARBEL will allow rapid data integration and dissemination within the catfish research community and to interested stakeholders. cBARBEL can be accessed at <http://catfishgenome.org>.

Oyster: Complete sequences for 58 Pacific oyster BAC clones submitted to GenBank in November 2009 were annotated by Oyster Genome Consortium members (Gaffney et al. in prep) for eventual publication on an OGC web site in the planning stages. A large-scale EST sequencing project carried out by the US DoE Joint Genome Institute under their community sequencing project program has provided 52,000 EST contigs currently being mined for SNP development (Gracey and Hedgecock, pers. comm.). In November 2010, four members of the OGC steering committee (Boudry, Gaffney, Guo, Hedgecock) met with researchers at Beijing Genomics Institute at the 5th International Conference on Genomics to discuss progress in the Pacific oyster whole genome sequencing project, and to develop plans for data-sharing.

Salmonids:

Genome Map Data Mining Tool: The current rainbow trout WebFPC physical map on the Clemson University Genome Institute web site is continually updated with genetic markers and BACs sequence data that are being integrated onto the BAC contigs.

Genetic Map: The 2nd generation NCCCWA rainbow trout genetic map is now available through G-browser at the Animal Genome website of the NRSP-8 bioinformatics group (<http://www.animalgenome.org/cgi-bin/host/rainbow/viewmap>).

Sex Chromosomes in Salmonids: We are preparing a resource on sex chromosomes, conserved male-specific genes and sex linkage groups in salmonid fishes which will be on the Ruth Phillips faculty research web site: <http://directory.vancouver.wsu.edu/people/ruth-phillips>.

Striped bass: The 230,151 ESTs derived from striped bass ovary were posted to the National Center for Biotechnology Information (NCBI) Short Read Archive (GenBank: SRX007394) and the resulting 11,208 annotated contigs were assembled into a searchable database posted on the National Aquaculture Genomics website (<http://www.animalgenome.org/cgi-bin/host/ncsu/seqdbinfo>). Novel artificial neural network/machine learning algorithms for analysis of cDNA microarray data were developed and deployed in the study of the transcriptomics of egg quality in striped bass and will be published shortly.

PUBLICATIONS:

Refereed Manuscripts Published:

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51. Marti, S. M., S. K. Onteru, Z.-Q. Du, M. F. Rothschild. 2010. SNP analyses of the 5HT1R and STAT genes in Pacific white shrimp, *Litopenaeus vannamei*. *Spanish J. Agri. Res.* 8: 53-55.

Dissertations and Theses:

Name	Institution	Degree	Dissertation/thesis title
Brittany Kammerer	UC-Davis	Ph.D., completed	Short-term mechanisms of seawater acclimation in tilapia (<i>Oreochromis mossambicus</i>)
Pawapol Kongchum	Virginia Polytechnic Institute and State University	Ph.D., completed	Isolation of innate immune response genes, expression analysis, polymorphism identification and development of genetic markers for linkage analysis in common carp (<i>Cyprinus carpio</i>).
Jason Abernathy	Auburn University	Ph.D., completed	Genomic characterization of expressed sequence tags and gene expression profiling of the three life-cycle stages of <i>Ichthyophthirius multifiliis</i> .
Shaolin Wang	Auburn University	Ph.D., completed	Assembly of 500,000 inter-specific catfish expressed sequence tags and large scale gene-associated marker development for genome selection studies.
Valerie N.	North Carolina State	Doctoral	

Williams,	University	student, ongoing	
Justin Schilling,	North Carolina State University	Doctoral student, ongoing	
Scott A. Salger,	North Carolina State University	Doctoral student, ongoing	
Amanda L. Boury,	North Carolina State University	Doctoral student, ongoing	
Benjamin J. Reading	North Carolina State University	Postdoctoral Research Associate	
Jessica Piesz	University of Rhode Island	MS in Aquatic Pathology	Matrix metalloproteinases and hemocyte migration in the eastern oyster, <i>Crassostrea virginica</i> .
Shizu Watanabein	University of Hawaii at Manoa	Master, completed	Pacific threadfin skeletal muscle cDNA library construction and EST identification
Gavin Iwai	University of Hawaii at Manoa	Master, completed	Identification of Mitochondrial ATP-synthase 8/6 gene DNA sequence and Single Nucleotide Polymorphisms (SNPs) in wild and cultured Pacific Threadfin (<i>Polydactylus sexfilis</i>)
Annie Cox, Oceanography	University of Rhode Island	Ph.D, completed	Diversity and distribution of <i>Vibrio parahaemolyticus</i> , a bacterioplankton species of concern for human health, in Rhode Island.
Dina Proestou,	University of Rhode Island	Postdoctoral fellow, now a postdoctoral fellow at US EPA	
Chamilani Nikapitiya	University of Rhode Island	Postdoctoral fellow currently in training	
Peng Xu	Purdue University	Postdoctoral fellow.	

Minutes for NRSP-8 Aquaculture Genome Business Meeting

Co-coordinators: Dr. John Liu; Dr. Caird Rexroad;
Administrative Supervisor: Dr. Michael E. Vayda,
National Program Leader: Dr. Muquarrab Qureshi
Industry Representatives: Mitt Walker, Dr. Scott LaPatra,
Chair: Dr. Matt Rise
Secretary (Chair-elect): Dr. Sylvie Quiniou

Time: Saturday January 15, 2011, 5:00-6:00 p.m.

Place: Royal Palm Salon 3 & 4, Town & Country Hotel, San Diego, CA.

I. Call to order: Dr John Liu called the meeting to order at 5:00 pm, following the Saturday afternoon session of the Aquaculture Workshop.

II. Old Business

1. Species Coordinators' Reports: All coordinator's reports except Bioinformatics report will be deferred to 8:00 a.m.-9:00a.m. Sunday morning.

- a. Catfish Sylvie Quiniou, (Presented a species report on Sunday morning)
- b. Oysters Patrick Gaffney, (Did not present a species report)
- c. Salmonids Yniv Palti, (Presented a species report on Sunday morning)
- d. Shrimps John Benzie, (Did not present a species report)
- e. Striped bass Craig Sullivan, (Presented a species report on Sunday morning)

2. Bioinformatics report:

Dr James Reecy gave an overview of the NRSP-8 Bioinformatics Coordination Program and examples of type of support they can provide: 1) Facilitation of data transfer through the "File Sharing Platform"; 2) Hosting of data for public availability; 3) Creation of Host-relational database; 4) Genome Annotation; 5) GBrowse; 6) Creation of Virtual comparative map. Dr Reecy mentioned that any suggestions or inquiry can be sent to the helpdesk. He mentioned that they also provide on-site training sessions.

3. Administrator and Industry Rep Reports

- a. Dr. Muquarrab Qureshi, National Program Leader: No report given.
- b. Industry reps: No report given.
- c. Dr. Thomas Burr, Administrative Advisor. Dr Burr presented himself and expressed his interest in meeting with NRSP-8 members. He also suggested that it was time to start thinking about the follow-up to NRSP-8 2009-2013.

4. Future Workshop:

- a. Dr. Matt Rise was commended for his outstanding efforts on organizing this year's Workshop.

- b. Dr. Sylvie Quiniou will be our next workshop organizer. Format of next Workshop: Dr. Sylvie Quiniou will lead the discussion. All suggestions for the next Aquaculture Workshop including invited speakers should be sent to Dr. Sylvie Quiniou (Sylvie.quiniou@ars.usda.gov).

5. Other

Dr. John Liu mentioned that official participants are a part of the NRSP-8 report. Dr. Liu made a call to the participants to officially join NRSP-8 and explained how to join.

III. New Business

1. Recognition of Travel Awards recipients: Dr. Rise will mail the certificates.
2. AFRI and NRSP-8 update: Dr. Muquarrab Qureshi not present at the business meeting but will be present during the rest of the Conference.
3. Nomination and election for Secretary (Chair-elect) for 2011: Dr Eric Peatman was nominated as the Chair-Elect for 2011. Dr. Peatman accepted the nomination, and no other nominations were made. Dr Peatman was voted Chair-Elect for 2011.

4. Other

4.1 The budget is now \$65,000/year. About \$38,000 was spent before the meeting. The travel awards, invited speakers, poster exhibition and the reception will cost around \$20,000. The few thousand dollars left will be carried over to next year. Dr. Liu explained that part of the budget is used to sponsor some projects. This year 2 projects were sponsored.

4.2 Dr. Liu and Dr. Rexroad were commended for their work.

IV. Adjourn. Dr. Liu adjourned the business meeting at about 5:30 p.m.