

Minutes
NSRP-8 Swine Sub-committee
January 15, 2005
Town and Country Hotel
San Diego, CA

Joan Lunney, NSRP-8 Swine sub-committee chair, welcomed everyone and then presided over the session. The morning session included 4 invited speakers.

Hirohide Uenishi (huenishi@affrc.go.jp) Animal Genome Research Program, Natl. Inst. Agrobiological Sciences, Tsukuba, Japan, spoke on "Swine Immunogenomics: Resource Of Genomic Data And Its Application To Immunological Research In Pigs." He described several tools for analyzing gene expression data including his Pig EST Data Explorer (PEDE). He reviewed his group's progress with analyzing swine immune genes and their importance in predicting disease responses.

Randall S. Prather (PratherR@Missouri.Edu) University of Missouri-Columbia (MU), Columbia, MO USA spoke on "Gene Expression During Pig Embryogenesis as Determined by Using a Pig Reproductive Tissue-Specific Microarray." He noted that there is a 30% loss of conceptuses during the first month of gestation. In his lab cell function was studied by focusing on RNA. 10,848 attempts resulted in 8,661 ESTs for a 79% success rate. 1,115 of these had a score of < 200. Information can be accessed through the MU Swine Genome Website which includes 27 libraries, 38,334 ESTs, 14,970 unigenes, and 10,862 cDNAs with annotation. Dr. Prather warned that you must confirm that B-actin expression does not change if you are going to use it as a standard. He mentioned the Expression Analysis Systemic Explorer (EASE) program. Their microarray results were confirmed by agreement with RT-PCR results.

Lucina Galina (Lucina.Galina@PIC.com) from Sygen International, Franklin, KY USA spoke about "PathoCHIP - A genomics approach to understanding *Haemophilus parasuis* infection." Their studies of 200 colostrum deprived pigs from 6 sires were used in the experiment. Pigs were collected from the birth canal, disinfected and moved to disinfected units. Bovine colostrum was provided during the first 3 to 4 days. Pigs were then inoculated with *Haemophilus parasuis*. Clinical signs and lesions were recorded. There was an 80% survival rate. All control pigs were negative for *Haemophilus parasuis*. Among inoculated pigs 11% were fully resistant, 47% fully susceptible, 8% experienced septic shock, 9% were partially resistant, and 25% were less susceptible. Fully resistant pigs came from 5 of 6 sires.

Scott Fahrenkrug (fahre001@tc.umn.edu) from University of Minnesota, St. Paul MN USA spoke on "Microarray Profiling for Quality Control of Porcine Islet Isolation." Diabetes mellitus is a disease affecting millions of Americans. Porcine islet may provide a source of replacement islets for humans. A pig microarray with 13,297, 70 mer oligonucleotides was used. 40% redundancy was reported. A RNA 6000 Nano LabChip kit was used. The QuantArray and Genepix data imaging programs were both tested. Genepix was favored. Genespring and R/maanova were both used to analyze the data and they provided different results.

Dr. Fahrenkrug then led a discussion of plans of the joint NRSP8/NC1004 committee on future swine microarray options. Max Rothschild indicated that \$35 - \$40K was available for creating new microarrays. The group voted unanimously not to purchase Affymatrix chips. Dr. Tuggle asked if we would use information for the first chip or start completely over in designing the new chips. Qiagen/Oragen representatives indicated that their oligo sequences would like become available. [A letter will be sent to Dr. Rothschild confirming this.] Dr. Prather indicated that he preferred the oligo platform because it was more flexible and would allow individual PIs to add on oligos as needed. Dr. Moody expressed concern about the bioinformatics. Dr. Chris Elsik offered to provide bioinformatic support. The group vote to create a microarray sub-committee (Scott Fahrenkrug, Chair, Joan Lunney, CoChair, Chris Elsik, and Cathy Ernst; Jim Reecy, NRSP8 Bioinformatics Coordinator, was added later). This committee must provide a response to Dr. Rothschild by April.

Larry Schook (schook@uiuc.edu) University of Illinois at Urbana-Champaign, Illinois, USA started the afternoon with his talk on “Swine Genome Sequencing Consortium - Progress and Plans.” He provided an update on the swine genome sequencing consortium’s progress. There were 5 original focus points: 1) Focus on an integrated and universally accepted plan. (DONE); 2) Capture cost savings. (On-going); [\$30 million dollars needed for a 6X draft sequence of the pig genome; The Sanger Institute has offered \$15 million in matching funds.] 3) Garner industry support. (On-going); 4) Identify matching funds. (On-going); and 5) Assist a USDA led global initiative. The FPC (fingerprinted contigs) database can be accessed at http://www.sanger.ac.uk/Projects/S_scrofa/. Help is needed to reduce the # of contigs/chromosome. There are now 2041 radiation hybrid markers in FPC; > 95% are concordant with fingerprints in the human. There are 454,880 non-repetitive BES used to compare to human. The FPC database includes 423 contigs representing > 96% coverage. The timeline: Year 1 \$5-7 million = 3 fold coverage; Year 2 \$5-7 million for whole genome shotgun sequencing. The sequence will be released to the public as soon as it is generated.

Ronald D Green (rdg@ars.usda.gov), the USDA ARS, National Program Leader for Animal Production, Beltsville, MD USA spoke about the “USDA Animal Genomics Workshop.” He noted the progress from the Allerton I, II, and III meetings. He emphasized that interagency coordination is essential. He reported on the Program on Domestic Animal Genomics and the NIH Roadmap.

Margaret Dentine, NRSP8 Swine Technical Committee Advisor explained the new process for project reviews. NRSP8 received very favorable responses. She reminded us of the upcoming midterm review. She encouraged everyone to communicate with their experiment station director regarding the value of NSRP-8. She also reminded us to use the NIMS system to communicate to the group.

Muquarrab Qureshi, USDA CSREES National Program Leader discussed performance based budgeting. He mentioned program areas 303 and 304, discussed genome project updates and the NRI budget increase.

Max Rothschild, Swine Genome Coordinator, gave his update. 1500 microarrays were sent out to US and overseas labs. Those who have requested the arrays and not received them need to communicate a delivery date to Dr. Rothschild. There are no more microsatellite markers available. He encouraged everyone to go back to their institutions and ask for funds to support the pig sequencing project. He thanked those from commercial industry for their support. Jim Reecy, NRSP8 Bioinformatics Coordinator, described the Pig QTLdb, Expeditor and NAGRP Blast server.

The afternoon session was then devoted to NRSP-8 Station Reports presented by Joe Cassady (North Carolina State University), Cathy Ernst (Michigan State University), Max Rothschild and Chris Tuggle (Iowa State University), Gary Rohrer (USDA ARS MARC), Joan Lunney (USDA ARS BARC), Zhihua Jiang (Washington State University) and Craig Beattie (University of Nevada). Joe Cassady (North Carolina State University) discussed results for a mouse microarray study. A nutriogenomics approach was used to identify genes affecting adipocyte metabolism. M16 mice were fed a diet with 1% LA or 1% CLA for 0, 5, or 14 days. Several genes were differentially expressed including some which have not been previously associated with adipocyte metabolism.

Cathy Ernst (Michigan State University) reported on microarray work profiling pig muscle at various ages and transcriptional profiling of fat tissue.

Max Rothschild (Iowa State University) reported that they have placed 15 markers in a small region of chromosome 15 to identify QTL for meat quality and growth. Three regions have been associated with meat quality. They have also identified 3 genes with a strong association with sow longevity. An additional study by Benny Mote looked at polydactyl pigs. Several genes associated with the polydactyl condition are believed to be on SSC 18. He also described a project to determine the correlation among SNP density in the pig and human. The correlation between the incidence of SNPs at homologous locations in the pig and human was 0.77. Chris Tuggle (Iowa State University) reported that his group has used the pig microarray on lung, liver, muscle, and small intestine. Clustering has been done to find co-expressed genes. GeneCluster 2.0 correctly clustered 424 genes using a Bonferroni pair-wise test. He

also discussed transcriptional profiling in a study of lung tissue from *Salmonella cholerasuis* infected pigs. 57 genes were differentially expressed.

Gary Rohrer (USDA ARS MARC) noted that 129,000 ESTs have been deposited in genbank another 50,000 should be deposited soon. 1500 SNPs have been mapped and a manuscript is in development. A QTL scan for pork quality resulted in QTL for tenderness on SSC 2 and marbling and growth on SSC 17. Joan Lunney (USDA ARS BARC) discussed immune gene activation and the panel of ~200 immune genes that the BARC group is assaying for disease and vaccine research. She mentioned the USDA NRI Immune Toolkit Initiative. A NPB Ig Toolkit grant has also been submitted. She is collaborating with Dr. Johnson at the University of Nebraska on his large PRRS resistance studies. Zhihua Jiang (Washington State University) has been doing comparative mapping. He has developed what he calls a "Happy Panel". He is working on whole genome amplification and microarray genotyping. Craig Beattie (University of Nevada) gave an update on his work with the IMNpRH_{12,000 rad} panel. He reported 791 ms, 2774 ESTs and 677 BAC end primer pairs.

At the end there was a short NRSP8 swine business meeting. Dr. Zhihua Jiang was elected Swine NRSP8 secretary for the next year. A discussion of whether NC1006 and NRSP8 would hold a joint meeting in 2005/2006 was left for Dr. Cassady, 2005 Chair for both groups, to poll members for their preferences.