

ANNUAL PROGRESS REPORT
NATIONAL RESEARCH SUPPORT PROJECT – NRSP008
Year Ending 2004
Preliminary Information-Not for Publication
University of Nebraska, Lincoln

I. PROJECT TITLE:

NRSP008: National Animal Genome Research Program

II. COOPERATING AGENCIES AND PRINCIPAL LEADERS:

- Nebraska Agriculture Experiment Station and Department of Animal Science, UN-L.
- P.I. Daniel Pomp

Collaborators: Rodger Johnson, Jack Weber, Dale Van Vleck – Nebraska; Max Rothschild, Chris Tuggle - Iowa; Joe Ford – USDA-MARC; Alex Caetano – Embrapa (Brazil).

III. NATURE OF WORK AND PRINCIPAL RESULTS OF YEAR:

Objective 1: *Enhance and integrate genetic and physical maps of agriculturally important animals for cross species comparisons and sequence annotation.*

- Completed physical mapping (SCHP, RHP) of reproduction-relevant expressed genes (n = ~750 EST).

Objective 2: *Facilitate integration of genomic, transcriptional, proteomic and metabolomic approaches toward better understanding of biological mechanisms underlying economically important traits.*

- An ovarian follicle normalized library was created using tissue from the UN-L reproduction selection lines. Sequences for 7,000 clones were obtained, and ~4,000 clones were organized representing unique clusters. Clones representing the ~4,000 clusters from the normalized ovarian follicle library were spotted in duplicate onto 120 glass slide arrays. All arrays were hybridized with follicle and/or ovary RNA from the high Index and Control selection lines (representing 2.5M data points). Data were analyzed, resulting in a list of over 100 significantly differentially expressed genes. SNP detection is in progress within ~50 of these differentially expressed genes, with a goal of 3-5 SNPs per locus.

IV. APPLICATION OF FINDINGS:

- The Pig Reproduction EST Consortium project has significantly increased the density of Type I markers on the pig physical map, focusing on genes relevant to economically important traits. This project has enhanced the comparative maps between pig and human/mouse, which will be facilitative for porcine gene discovery. Sequencing and mapping of ESTs, together with resource development such as normalized libraries and microarrays, will be useful for positional cloning efforts and characterizing important biological/physiological events controlling economically relevant traits.
- Integration of genomics/proteomics/metabolomics approaches may be a mechanism to successfully bridge the gap between predisposition and physiology and enable more accurate selection of candidate genes underlying a QTL peak. By identifying SNPs within differentially expressed genes, we are testing the hypothesis that a subset of genes regulating reproduction at the physiological level will harbor genetic variation controlling genetic predisposition to reproductive phenotypes.

V. WORK PLANNED FOR NEXT YEAR:

- Continuing (Pomp and Johnson): Complete SNP discovery in the ovarian follicle differentially expressed genes (n=50), and use those SNPs for large-scale (n=1600 pigs) association studies in commercially relevant maternal lines of pigs.
- New (Jack Weber): Using a comparative genomics approach, regulatory regions will be identified for 12 genes important in controlling the immune response in pigs. These regions will then be analyzed for differences between strains of pigs that are being used in disease resistance studies.

VI. PUBLICATIONS in REFEREED JOURNALS:

- Caetano AC, JB Edeal, K Burns, RK Johnson, C Tuggle, D Pomp (2005) Physical mapping of the differentially expressed porcine ovarian transcriptome. *Animal Genetics* (Accepted).
- Bertani G, Gladney C, Johnson RK, Pomp D (2004) Evaluation of gene expression in pigs selected for enhanced reproduction. II: Anterior Pituitary. *J Anim Sci* 82:32-40.
- Caetano A, J Ford, RK Johnson, D Pomp (2004) Microarray profiling for differential gene expression in ovaries and ovarian follicles of pigs selected for increased ovulation rate. *Genetics* 168: 1529-37.
- Churchill GA and 101 others including D Pomp (2004) The Collaborative Cross: A community resource for the genetic analysis of complex traits. *Nature Genetics* 36:1133-1137.
- Gladney C, G Bertani, MK Nielsen, D Pomp (2004) Evaluation of gene expression in pigs selected for enhanced reproduction. I: Ovarian Follicles. *J Anim Sci* 82:17-31.
- Holl JW, JP Cassady, D Pomp, RK Johnson (2004) A genome scan for QTL and imprinted regions affecting reproduction in pigs. *J Anim Sci* 82:3421-3429.
- Moller M, Berg F, Riquet J, Pomp D, Archibald A, Anderson S, Feve K, Zhang Y, Rothschild MF, Milan D, Andersson L, Tuggle C (2004) High-resolution comparative mapping across pig chromosome 4 (SSC4), emphasizing the *FAT1* region. *Mammalian Genome* 15:771-31.

FUNDING ACKNOWLEDGMENTS:

This research is a contribution of the University of Nebraska Agricultural Research Division (Lincoln, NE) and was supported in part by funds provided through the Hatch Act. Parts of this research were conducted with funds from the Biotechnology Research Development Corporation (BRDC).