

**ANNUAL PROGRESS REPORT  
NATIONAL RESEARCH SUPPORT PROJECT – NRSP008  
Year Ending 2004**

**Joan K. Lunney  
Animal Parasitic Diseases Laboratory (APDL), ANRI  
BARC, ARS, USDA**

**I. PROJECT TITLE:**

NRSP008: National Animal Genome Research Program

**II. COOPERATING AGENCIES AND PRINCIPAL LEADERS:**

USDA BARC Personnel

Harry Dawson, Joseph F. Urban, Jr.

Nutrient Requirements & Functions Lab, Beltsville Human Nutrition Research Center

Collaborators at other Institutions

Douglas M Smith and Sam Ho, Pathology Department, Transplant  
Immunology Lab, Baylor University Medical Center

**III. Objectives**

Objective 1: Develop high resolution comparative genome maps aligned across species that link agricultural animal maps.

Objective 2: Increase the marker density of existing linkage maps used in QTL mapping and integrate them with physical maps of animal chromosomes.

Objective 3: Expand and enhance internationally shared species genome databases and provide other common resources that facilitate genome mapping.

**III. NATURE OF WORK AND PRINCIPAL RESULTS OF YEAR:**

**A. Objective 1:** Develop high resolution comparative genome maps aligned across species that link agricultural animal maps.

BARC scientists and members of the international SLA nomenclature committee developed new molecular nomenclature and phylogenies for swine Major Histocompatibility Complex (MHC) or Swine Leukocyte Antigen (SLA) class I and class II genes and haplotypes. Data is now displayed on the international IPD-MHC Sequence Database website: [www.ebi.ac.uk/ipd/mhc/sla/nomenclature.html](http://www.ebi.ac.uk/ipd/mhc/sla/nomenclature.html)

**B. Objective 2:** Increase marker density of existing linkage maps used in QTL mapping and integrate them with physical maps of animal chromosomes.

Expand real-time expression assays for panels of immune markers known to control vaccine and disease immunity (>350 genes targeted; real-time assays now available for >200 genes). Dr. Dawson has developed a database that can be accessed at [www.ba.ars.usda.gov/nrfl/nutri-immun-db/nrfl\\_query1new.html](http://www.ba.ars.usda.gov/nrfl/nutri-immun-db/nrfl_query1new.html)

Our infectious disease work has been aimed at determining effector mechanisms which lead to protective responses against infection. We have used real time gene expression assays to monitor immune gene activation during innate and adaptive [T helper 1 (Th1) and Th2] immune responses. We tested swine responses to infections with the intracellular protozoan parasite, *Toxoplasma gondii* or to vaccination for porcine reproductive and respiratory syndrome virus (PRRSV). We have confirmed Th1 immunity patterns with RNA collected from tissues of parasite infected pigs, using intracellular protozoan parasite, *Toxoplasma gondii* and compared that data to Th2 immunity resulting from infection with helminth parasite, *Ascaris suum*.

More recent data in collaboration with Federico Zuckermann's lab at Univ. Illinois has targeted gene expression patterns for understanding protective immunity for respiratory infections, particularly PRRSV. Our data indicated that the slow and weak development of innate immunity may help set the tone for a weak interferon-gamma (IFNG) response, thus enabling this virus to persist in infected pigs.

Genetic studies, to determine whether pigs which are genetically resistant to PRRSV infection are currently underway with scientists at Univ. Nebraska-Lincoln (R. Johnson, D. Petry, J. Weber and F. Osorio). They have identified lines of pigs which when infected at 21 days of age differ in their viral burden and clinical signs at necropsy 14 days later. Tests are underway to determine differences in immune gene expression with lung and bronchial lymph node samples from these pigs.

**C. Objective 3:** Expand and enhance internationally shared species genome databases and provide other common resources that facilitate genome mapping.

No research

#### **IV. APPLICATION OF FINDINGS:**

##### **A. Objective 1**

Establish internationally recognized nomenclature to identify and classify SLA class I and SLA class II gene polymorphisms. This will serve as a basis for determining critical genetic effects on infectious disease and vaccine responses. Have data fully accessible at an international website, the IPD-MHC Sequence Database website: [www.ebi.ac.uk/ipd/mhc/sla/nomenclature.html](http://www.ebi.ac.uk/ipd/mhc/sla/nomenclature.html)

##### **B. Objective 2**

Provides means to study expression and function of additional immune genes in normal breeding populations to identify early responders which might be more disease resistant/susceptible. New work in PRRSV resistance may help identify pigs which are more disease resistant and the protective mechanisms they employ to induce resistance.

#### **V. WORK PLANNED FOR NEXT YEAR:**

##### **A. Objective 1**

Complete SLA class II gene polymorphisms. Utilize SLA class I genes for preparing tetramers to understand peptide binding motifs of SLA class I molecules.

## B. Objective 2

The BARC team of scientists will be developing a broader panel of real-time PCR assays for immune and nutrition markers to track swine immune response gene expression. The Lunney lab in collaboration with NC229 scientists will continue research on PRRSV infection and vaccination to understand protective mechanisms and the genetic basis of PRRSV resistance.

## VI. PUBLICATIONS:

1. Galina-Pantoja L, Solano-Aguilar GI, Mellencamp MA, Bastiaansen J, Lunney JK. 2004. Relationship between immune cells and pig growth on a commercial farm. Proc. 18th IPVS Congress, Hamburg, Germany, 2004, Vol. I. p.381.
2. Dawson HD, Royae AR, Nishi S, Kuhar D, Schnitzlein WM, Zuckermann F, Urban JF, Lunney JK. 2004. Identification of Key Immune Mediators Regulating T helper 1 Responses in Swine. Vet. Immunol. Immunopathol. 100: 105-111.
3. Royae AR, Husmann R, Dawson HD, Calzada-Nova G, Schnitzlein WM, Zuckermann F, Lunney JK. 2004. Deciphering the involvement of innate immune factors in the development of the host responses to PRRSV vaccination. Vet. Immunol. Immunopathol. 102: 199-216.
4. Dawson HD, Beshah E, Nishii S, Solano-Aguilar G, Morimoto M, Zhao A, Madden KB, Ledbetter TK, Dubey JP, Shea-Donohue T, Lunney JK, Urban, JF Jr. Localized multi-gene expression patterns support an evolving Th1/Th2-like paradigm in response to infections with *Toxoplasma gondii* and *Ascaris suum* in pigs. Infection and Immunity. In Press.
5. Lunney, J.K. 2003. Are there immune gene alleles that determine whether a pig will be healthy? Genetics of Pig Health Symposium, Des Moines, IA. M. Boggess, Ed.; National Pork Board Press, DesMoines, IA. p.63-72.
6. Smith DM, Martens GW, Lunney JK, Ando A, Lee J-H, Ho C-S, Schook L, Renard C, Chardon P. 2004. Nomenclature for Factors of the SLA Class I System, 2004. Tissue Antigens. In Press.