

ABSTRACTS
2006 Poultry Science Association
Annual Meeting

July 16–19, 2006
Edmonton, Canada

*Author Presenting Paper

Sunday, July 16, 2006
SYMPOSIA AND ORAL SESSIONS

Ancillary Scientists Symposium: Functional Genomics: Building the Bridge Between the Genome and Phenome

1 Analysis of global gene expression in the avian neuroendocrine system. T. E. Porter*, L. E. Ellestad, M. Muchow, S. A. Jenkins, and M. S. Byerly, *University of Maryland, College Park*.

The pituitary gland and hypothalamus of the brain comprise the central components of the neuroendocrine system. This system plays an important role in the control of growth and metabolism. Traditionally, regulation of gene expression within the neuroendocrine system has been studied one gene at a time. In recent years, we have developed and used chicken cDNA microarrays to study gene expression profiles for thousands of genes simultaneously. This review will summarize our use of microarrays for expression profiling in the chicken pituitary and hypothalamus. We have studied ontogenic changes in global gene expression within the neuroendocrine system during late embryonic and early posthatch development. We have analyzed effects of treatments on gene expression in cultured pituitary cells. We have identified differentially expressed genes in the neuroendocrine system of chicken lines genetically selected for body composition (high versus low body fat) or size (high versus low body weight). Our findings have allowed us to focus our research on numerous candidate genes that might function within the neuroendocrine system to control growth and metabolism in chickens and other vertebrates.

Key Words: microarray, hypothalamus, pituitary

2 Functional mapping of gene networks controlling growth and metabolism. L. A. Cogburn*, *University of Delaware, Newark*.

The chicken has now reached model organism status with the recent completion of the genome sequence, a comprehensive catalog of expressed genes and genome-wide microarrays. We have developed an integrated systems cDNA microarray for transcriptional profiling across metabolic and somatic tissues. Temporal gene expression scans have been taken in divergently selected broiler lines (i.e., fat vs. lean and high vs. low growth) and in perturbation models (i.e., embryo-to-hatching transition and during fasting and re-feeding). One of the greatest challenges in understanding these vast volumes of microarray data is development of models to reconstruct functional gene networks and regulatory pathways. Using gene clustering and computational analyses of time series transcriptional profiles, we have identified a number of functional genes in key metabolic pathways that could control important phenotypes in the chicken. Several clusters of functionally related genes (i.e., metabolic enzymes, transcription factors, nuclear receptors, adipokines, transport proteins, signal transducers, etc.) have been identified that control major metabolic pathways. Furthermore, a number of these differentially expressed genes map to quantitative trait loci identified in our novel resource populations. These studies have given us the first picture of the transcriptional landscape of the chicken and some insight into the gene networks and regulatory pathways that control somatic growth and body composition. The discovery of a large number of obesity-related genes and adipokines could provide a better understanding of genes that contribute to excessive fatness in chickens and promote the use of this new model organism for study of human metabolic disorders (i.e., diabetes and metabolic syndrome).

Key Words: microarray, gene networks, transcriptome

3 Genetic mechanisms regulating feed intake, energy balance and body weight in poultry. M. P. Richards*, *USDA, ARS, ANRI, Growth Biology Laboratory, Beltsville, Maryland.*

In order to maintain a constant body weight, feed intake and energy expenditure must be coordinated and tightly regulated. This may not hold true for some poultry species intensively selected for such economically important traits as growth and meat production. For example, the modern commercial broiler does not adequately control voluntary feed intake to meet its energy requirements and maintain energy balance. As a consequence, feeding must be limited in these birds to avoid over consumption and excessive fattening during production. It is important to determine a genetic basis to help explain this situation and to offer potential strategies for producing more efficient poultry. This review summarizes what is currently known about the control of feed intake and energy balance at the gene level in birds. Highly integrated regulatory systems have been identified that link the control of feeding with energy status. How such systems function in poultry is currently being studied. One example recently identified in chickens is the AMP-activated protein kinase pathway that links energy sensing with modulation of metabolic activity to maintain energy homeostasis at the cellular level. In the hypothalamus, this same pathway may also play an important role in regulating feed intake and energy expenditure commensurate with perceived energy needs. Genes encoding key regulatory factors such as hormones, neuropeptides, receptors, enzymes, and transcription factors are some of the types of molecular components that comprise intricate networks of signaling, sensing, and metabolic pathways linking peripheral tissues with the central nervous system. Moreover, coordinate expression of specific gene groups can establish functional pathways that respond to and are regulated by such factors as hormones, nutrients, and metabolites. Thus, with a better understanding of the genetic basis for regulating feed intake and energy balance in birds important progress can be made in developing, evaluating, and managing new and more efficient commercial poultry lines.

Key Words: feed intake, energy balance, gene expression

4 Application of macrophage and intestinal cDNA microarrays to study innate mucosal immunity in avian coccidiosis. H. Lillehoj*, *United States Department of Agriculture, Animal and Parasitic Diseases Laboratory, Beltsville, Maryland.*

Coccidiosis is recognized as the major parasitic disease of poultry and is caused by the apicomplexan protozoa *Eimeria*. Coccidiosis seriously impairs the growth and feed utilization of infected animals resulting in loss of productivity. Conventional disease control strategies rely heavily on chemoprophylaxis and to a certain extent on live vaccines. These factors combined inflict tremendous economic losses to the world poultry industry in excess of \$3 billion annually. Increasing regulations and bans on the use of anticoccidial drugs coupled with the associated costs in developing new drugs and live vaccines urges the need for developing novel approaches and alternative control strategies for coccidiosis. Recent technological advances in high-throughput molecular approaches to identify disease resistance genes and molecular/cell biological pathways associated with complex biological phenomenon now enable the development of an alternative strategy to combat these diseases. Recently, application of functional genomics has led to the identification of avian genes associated with resistance to coccidiosis. In this report, I will describe new findings using the chicken macrophage and intestinal cDNA microarrays that

led to the identification of host genes which influence innate immune responses to *Eimeria* in the gut. Enhanced understanding of how *Eimeria* interact with host macrophages and intestinal immune system at the molecular and cellular levels will contribute to novel control strategies against coccidia. These EST sequences from *Eimeria*-stimulated intestinal IEL transcripts will be used to study global gene expression profiling and to identify novel immune-related genes during avian coccidiosis and in other enteric diseases of poultry. Those genes with significant differences can also be used as potential candidate genes influencing disease susceptibility traits.

Key Words: coccidiosis, global gene expression, innate mucosal immunity

5 Analysis of quantitative disease-resistance traits. S. J. Lamont*, *Iowa State University, Ames.*

Most of the important economic traits in poultry, including genetic resistance and immunity to disease, are quantitative traits. Thus, the genetic architecture of these traits is complex and difficult to elucidate. To enhance poultry welfare and food safety, however, improvement in host genetic resistance to disease is desirable. Understanding the functional genomics of host resistance to pathogens will enable poultry breeders to develop populations that are more innately resistant to disease. To accomplish this goal, the genes and chromosomal regions associated with disease resistance must be identified and characterized. In some instances, sufficient is known about the mechanisms of resistance from comparative studies to enable a targeted approach of analyzing specific biological candidate genes in poultry, such as the major histocompatibility complex. In other instances, the discovery process is better served by screening the genome comprehensively for genes or chromosomal regions associated with disease-resistance traits. The broad QTL scans may be based on structural variation such as microsatellites or single-nucleotide polymorphisms (SNP). Analysis of associations of structural variation with disease-resistance traits can be complemented by functional genomics studies that evaluate differential gene expression among groups. Similar to studies of structural variation, gene-expression analysis can be conducted in a targeted fashion on a small number of candidate genes, such as cytokines, or in a global fashion by using microarrays. In addition to the use of complementary genetic analysis approaches, the generation of novel resource populations for evaluation can greatly facilitate the process of discovering associations between disease-resistance traits and genes or markers. The use of these genetic analysis approaches will be presented via examples of their successful application in elucidating the genetic basis of resistance to Marek's Disease and Salmonellosis.

Key Words: disease resistance, QTL, genome

6 Genetical genomics: Combining gene expression with marker genotypes. D. De Koning*, C. Cabrera, and C. Haley, *The Roslin Institute, Roslin, United Kingdom.*

Microarrays have been widely implemented across the life sciences although there is still debate on the most effective uses of such transcriptomic approaches. In genetical genomics, gene expression measurements are treated as quantitative traits and genome regions affecting expression levels are denoted as expression quantitative trait loci or eQTL. The detected eQTL can either represent a locus that lies

close to the gene that is being controlled (cis-acting) or one or more loci that are unlinked to the gene that is being controlled (trans-acting). One powerful outcome of genetical genomics is the reconstruction of genetic pathways underlying complex trait variation. The potential of pathway reconstruction has now been demonstrated in some model species despite the small sample size in eQTL experiments to date.

In order to maximise the efficiency of future eQTL studies, we outline an experimental strategy that is particularly suitable for poultry. The improved efficiency is achieved by targeting the eQTL study at a functional trait for which QTL have been detected and combining this with a fine mapping study for the functional QTL. The proposed strategy has three components: 1) from a resource population, individuals that are non-recombinant for markers flanking the QTL region, are selected for the eQTL experiment. 2) Individuals that are recombinant for the QTL region are utilised for further fine mapping of the QTL. 3) Additional expression studies are carried out for some of the recombinant individuals to confirm or evaluate positional candidate genes underlying the QTL. The underlying assumption of the proposed strategy is that QTL with major effects on the phenotype for a functional trait will often have major effects on expression of one or more genes. In the build-up towards full-blown eQTL studies, we can study the effects of known candidate genes or marked QTL at the gene expression level in more focussed studies. To demonstrate the potential of genetical genomics, we have identified the cis and trans effects for a functional body weight QTL on GGA4 in breast tissue samples of chicken with opposite QTL genotypes.

Key Words: gene expression, QTL, transcriptomics

7 Functional annotation of genomic data with metabolic inference. R. L. Walzem*, *Texas A & M University, College Station.*

Metabolomics is emerging as a post genomic science with applications to production agriculture. The metabolome is the quantitative complement of all low molecular weight molecules present in cells or body fluids in a particular physiologic or developmental state. Although the tools of metabolomics are not fully developed, they have already proved insightful to gene function identification, description of the metabolic sequelae of toxicological, pharmaceutical, nutritional and environmental interventions.

Lipids are important metabolites essential for the function of both cells and the whole bird. The structural and energetic lipids present in blood and tissues are a particularly informative class of metabolites for diagnosing and understanding changes in energy balance and transport caused by different selection strategies or feeding regimens.

A key advantage of quantitative lipid metabolomics is the prior knowledge of most of the biochemical pathways responsible for lipid

synthesis, metabolism and catabolism. High precision measurements of the concentration of individual lipid metabolites, including oxylipids such as eicosanoids, allow estimation of steady-state metabolite profiles. Once developed, profiles are mapped using pathway knowledge for use alone or for the functional annotation of changes in gene expression. In this way a detailed understanding of both selection and environmentally imposed impacts on poultry production is developed. Such a deep understanding of the metabolic inference arising from specific selection strategies provides predictive capabilities to prevent or minimize unintended outcomes or identify appropriate diets or environmental conditions to optimize production outputs. Examples will be provided, including outcomes for selected samples from an ongoing discovery project that employs microarrays and gene expression profiling of chickens selected for extremes in growth rate (fast and slow) and abdominal adiposity (high and low).

Key Words: metabolomics, lipids, poultry

8 Using proteomics to understand avian systems biology and infectious disease. H. Liu*, *North Carolina State University, Raleigh.*

In an effort to understand the cellular systems and the roles of their constituents in different physiological states, proteomic studies have provided a greater understanding of the function of proteins within a global, cellular context, along with the more conventionally delineated molecular functions. In this presentation, we will focus on using Marek's disease as an example to demonstrate how we implement proteomics to understand avian infectious disease. Some of the mechanisms that govern the response of chicken cells to viral infection function by altering protein abundance levels and/or by inducing changes in protein modulation via post-translational modifications. Consequently, it is very important to be able to measure these fluctuating changes using proteomics. We have utilized mass spectrometry in protein mining experiments to evaluate protein expression in chicken embryo fibroblast cells infected with Marek's disease virus (MDV). As it is very likely that MDV proteins must interact with specific host proteins for pathogenesis to progress and for the virus to evade the host immune responses, it is thus also crucial to identify host proteins that interact with MDV proteins. We have used yeast two-hybrid assays to screen chicken spleen libraries and have identified chicken cDNA-encoded prey proteins that interact with virus-encoded bait proteins. The combination of mass spectrometry and yeast-two hybrid assays provides a powerful proteomic approach for understanding systems biology and infectious disease.

Key Words: proteomics, mass spectrometry, yeast two-hybrid

National Extension Workshop: National Poultry Extension Workshop

9 Washington update. R. D. Reynnells*, *USDA, Washington, DC.*

The 2006 Annual Extension Special Recognition Award is presented to Dr. Theresia Lavergne, (LA), who has made many significant leadership contributions in the areas of environmental protection and extension programming. I encourage you to participate in multi-state research committees, which will increase in importance with the

ever-reducing number of poultry faculty. For example, the WERA-204/ temp1361, (Animal Bioethics), and the NCR-131, temp 1981 (Applied Animal Behavior and Welfare) are important committees that complement other activities at Land Grant Universities. The Southern Region Poultry Extension Workshop (Triennial) committee is more national in character and will meet next in 2009. Ken Anderson, is Chair of that committee and they request you provide comments, and volunteer. The 2006 National Poultry Waste Management Symposium