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 metablome 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

is in Springdale, AR, and is coordinated by Susan Watkins (AR); with Casey Ritz (GA) Coordinator for 2008. The 2006 Future Trends in Animal Agriculture (FTAA) symposium is the sixth since 2001. The FTAA creates opportunities for positive dialogue between industry and animal activists. Proceedings are available. The 2005 Food and Biobased Cafeteriaware Composting for Federal Facilities in Washington, DC round table will be followed with a more in-depth symposium in 2006, and continued the theme of composting and biobased materials from the workshop, Biobased Plant Nutrient Products: Quality Assurance, Marketing, and Regulations, held in 2004. Proceedings are available for both workshops.

Key Words: recognition award, animal welfare, National Poultry Waste Management Symposium

10 Professional certification in the animal sciences. R. Frahm*, *American Registry of Professional Animal Scientists*, *Savoy, Illinois*.

A program to certify expertise in designated areas of specialization for professionals in the animal sciences will be presented. The American Registry of Professional Animal Scientists (ARPAS) was established in 1984 to certify expertise in various areas of specialization for qualified professionals in the animal sciences. ARPAS was founded with the support and affiliation of the Poultry Science Association, American Society of Animal Science, American Dairy Science Association, American Meat Science Association, and the Equine Science Society. To qualify as a Professional Animal Scientist, and be authorized to use the designation PAS, requires a minimum of a B. S. degree in one of the animal sciences or closely related field, passing a comprehensive exam in at least one of the 12 areas of specialization, one to four years of appropriate experience in the animal sciences depending on level of education, completion of at least 16 hours of approved continuing education each year, and following a stringent code of professional ethics. ARPAS members that have completed at least a M. S. degree in the appropriate discipline may apply to be Board Certified in one of five disciplines. Board Certification requires a M. S. degree in the discipline and passing a comprehensive examination in that discipline. Board Certification is offered in Animal Behavior, Animal Food Science, Animal Genetics, Animal Nutrition, and Animal Physiology. Successful applicants are authorized to use the designation of Board Certified in that discipline. ARPAS also publishes a peer reviewed journal bi-monthly titled: The Professional Animal Scientist.

Key Words: certification, professional, ethics