

efficacy of nine media for recovery and enumerative purposes: Brilliant Green with Novobiocin and Nalidixic acid (BGN+NA) agar, Brilliant Green Sulfa (BGS) agar, Campy Line Agar (CLA), CHROM (*Salmonella*) agar, Hektoen Enteric (HE) agar, Modified Brilliant Green Agar (MBGA), MacConkey Sorbitol (MacS) agar, Modified Lysine Iron Agar (MLIA), and Rainbow agar. Brilliant Green Sulfa (for *Salmonella*), CLA (for *Campylobacter*), and Rainbow (for *E. coli* O157:H7) agar were shown to have the greatest percent recovery of all the media tested (97%, 97%, and 100%, respectively) and gave accurate colony counts, while the other media tested were unreadable due to contaminant growth. Confirmation of positive colonies was performed by PCR. Results support the utility of these methods to detect possible pathogens in water runoff after poultry litter application.

Key Words: water runoff, poultry litter, *Salmonella*, *Campylobacter*, *E. coli* O157:H7

278P House characteristics and energy utilization in poultry houses raising large broilers. D. G. Overhults¹, A. J. Pescatore^{*2}, R. S. Gates³, J. P. Jacob², M. Miller⁴, and J. Earnest¹, ¹*Biosystems & Agricultural Engineering, University of Kentucky, Lexington, KY*, ²*University of Kentucky, Animal & Food Science, Lexington*, ³*University of Illinois, Agricultural & Biological Engineering, Urbana*, ⁴*Kentucky Poultry Federation, Winchester, KY*.

An energy efficiency assessment was conducted on 7 farms (with a total of 37 houses) growing 2.8-kg broilers with a 51-d growout. All

houses were 12.8-m x 128-m and were equipped with tunnel ventilation and evaporative cooling systems. All houses had 8-9 120-cm or 130-cm tunnel ventilation fans. Houses on all but 1 of the farms had dropped ceilings. All houses originally had sidewall curtains. Some curtains were either lightly insulated or fully insulated and covered. All houses used ½ house brooding with 24 pancake brooders (9.1 kW each) and 4 forced-air heaters (65.9 kW each). Propane was used on all farms. Annual propane use ranged from 10,603 to 22,194 L/house and electricity from 24,157 to 37,337 kWh/house. The average propane and electricity use were 14,308 L/house and 31,236 kWh/house, respectively. On a live wt basis, propane use was 31.4 to 75.2 L/1000 kg with an average of 44.7 L/1000 kg. Electricity use was 71.6 to 126.5 kWh/1000 kg with an average of 96.9 kWh/1000 kg.

Airspeeds during full tunnel ventilation were measured at broiler level in 12 houses about 23 m upstream from the tunnel fans at four equally spaced locations across the house. Mean airspeeds were 2.05 to 2.82 m/s with an average of 2.42 m/s for all houses. At each farm, a closed-house static pressure test was conducted in at least one house to evaluate house tightness. When operating 1 tunnel fan with the house closed, static pressure ranged from 14.7 Pa to 54.9 Pa, with an average pressure of 35.3 Pa. Fans for which in-situ performance data had been obtained were selected for this test, thus providing an estimate of the actual air leakage rate at the various static pressures recorded during the test. Sufficient data were available from 5 farms to estimate air leakage rate. At a static pressure of 24.9 Pa, estimated air leakage rates were 19,501 to 34,457 m³/h.

Key Words: broiler houses, energy efficiency

Poster Session: Extension and Instruction

279P Incorporating “problem-based learning” into an undergraduate introductory poultry science course. J. B. Hoffman*, *North Carolina State University, Raleigh*.

The standard instructional paradigm utilized in most introductory undergraduate courses consists of students learning identified content and processes through lecture, direct instruction, and guided discovery. Students then apply this new learning in well-structured situations or problem sets to see if they have “mastered” the lesson. The roles are quite clear in a standard instructional paradigm: teachers teach and students learn. However, poultry science instructors are not preparing students for “real-life” problems that they will have to solve as they enter the workforce by only utilizing this paradigm for teaching. In order to improve students’ problem-solving skills and analytical thinking, 27 students enrolled in Introductory Poultry Science (PO 201) at North Carolina State University were given a topic relating to poultry production, management, physiology, or nutrition and created their own problem-based case for their peers to solve. Students performed independent research in order to create their problem-based case studies and then presented these case studies to their classmates who investigated the problem and created problem resolutions. By incorporating problem-based learning into an introductory poultry science course instructors may put learning into context, teach students how to deal with real-life problems, promote higher order thinking, and improve students’ oral and written communication skills. This instructional methodology may meet the needs of pre-veterinary students, students interested in entering the poultry industry, and students pursuing graduate studies. Pre-veterinary students may improve their diagnostic and reference seeking skills while students interested in entering the poultry industry will learn how to trouble-shoot effectively. Lastly, students interested in

pursuing graduate studies will develop critical thinking and analytical skills necessary to be successful in scientific research.

Key Words: problem-based learning, introductory, poultry science

280P Survey of poultry nutrition and disease knowledge in exhibition poultry and small flock owners of the Mid-Atlantic States. B. A. McCrea^{*1}, T. Y. Morishita², and J. D. Latshaw³, ¹*Delaware State University, Dover*, ²*Western University of Health Sciences, Pomona, CA*, ³*The Ohio State University, Columbus*.

Survey responses from exhibition poultry and backyard flock owners from the Mid-Atlantic region were collected using a set of questions developed in a previous study at Ohio State University. Our objective was to determine the perception and level of knowledge in this group with regard to poultry health management and nutrition topics. Surveys were given to adult and youth poultry owners and exhibitors. Surveys were handed out at exhibition poultry shows and the Delaware Small Flock Education Series between March 2008 and February 2009. Shows locations were in Kent County, Delaware and Cecil County, Maryland. The Small Flock Education Series was held three times in each of Delaware’s three counties (New Castle, Kent, and Sussex) and provided the backyard poultry flock perspective.

In general, survey participants were equally knowledgeable about poultry health management and nutrition topics. Both groups, backyard poultry and exhibition poultry owners, indicated that there remains a lack of knowledge regarding antibiotic use and vaccination in the health management section. However, both groups were very knowledgeable

about medicated feeds. Participants were least knowledgeable about poultry feed composition and consumption in the nutrition section.

An understanding of these topics may be more effectively communicated to exhibitors, and the increasing population of backyard poultry owners, if it is known where poultry extension specialists should begin the edu-

cation process. The information discovered in the course of this survey will be used to develop extension materials and continuing education symposiums that incorporate poultry health and nutrition topics.

Key Words: extension, health, nutrition, exhibition poultry, backyard flock

Poster Session: Genetics

281P Quantitative trait loci for eggshell-related traits in the F₂ families from the Oh-Shamo (Japanese Large Game) and White Leghorn. T. Goto*¹, A. Ishikawa², S. Onitsuka¹, N. Goto¹, Y. Fujikawa¹, T. Umino¹, M. Nishibori¹, and M. Tsudzuki¹, ¹Hiroshima University, Higashi-Hiroshima, Japan, ²Nagoya University, Nagoya, Japan.

Recently, a great number of quantitative trait loci (QTLs) has been detected in experimental animals and livestock. In the chicken also, over 1,200 QTLs have been discovered for growth, meat, egg, behavior, and disease resistance traits. However, for eggshell-related traits, a considerably small number of QTLs have been reported. In the present study, we performed QTL analysis of eggshell-related traits with the Map Manager QTX b20 software in a unique chicken resource population of the 421 F₂ hens from intercrosses of an Oh-Shamo (Japanese Large Game) male and three White Leghorn females. The traits analyzed were eggshell size (the length of long and short axes of the egg: LLA and LSA), eggshell weight (EW), eggshell strength (ES), and eggshell thickness (ET), and they were measured at 300 and 400 days of hen ages. 118 microsatellite markers were genotyped. Interval mapping revealed nine significant QTLs with main effects on 300 d LLA (on chromosomes 8 and 11), 400 d LLA (chr. 8), 300 d LSA (chr. 8), 400 d LSA (chr. 8), 300 d EW (chr. 8), and 300 d ET (chrs. 1 and 9), and 400 d ET (chr. 1). The identified QTLs explained 6-14 % of the total phenotypic variance. The 300 d LLA QTL on chromosome 11 and 300 d ET QTLs on chromosomes 1 and 9 appeared to be new loci based on their map locations.

Key Words: chicken, eggshell, quantitative trait loci, mapping, microsatellite marker

282P The mitochondrial genome sequence and molecular phylogeny of the budgerigar, *Melopsittacus undulatus*. X. Guan*¹, D. Samuels², Z. Tu³, and E. Smith¹, ¹Virginia Polytechnic Institute and State University, Department of Animal and Poultry Sciences, Blacksburg, ²Vanderbilt University, School of Medicine, Nashville, TN, ³Virginia Polytechnic Institute and State University, Department of Biochemistry, Blacksburg.

The budgerigar, more commonly known as budgie, *Melopsittacus undulatus*, is a bird widely used as a pet and as a model for biomedical research into auditory and oxidative stress questions. Despite this significance, there is very little published genetic information about the budgie. Here, we describe the budgie's mitochondrial genome (mtGenome) sequence, a resource that could facilitate not only investigation into the budgie's extraordinary ability to deal with relatively higher levels of oxidative stress, but its relationship to parrots and other birds. The potential utility of the sequence, developed using PCR, was carried out by screening the D-loop and 16S rRNA for single nucleotide polymorphisms (SNPs) and using these to evaluate the phylogenetic relationship between the budgie and other avian species. The estimated total length of the mtGenome sequence was 18,193 bp, which includes a duplicated hyper variable region, a feature unique to only a few birds,

13 protein coding genes, and 24 RNAs (22 tRNA and 2 rRNA). The duplicated non-coding regions showed 86% sequence similarity. The coding region structure implicates gene conversion in the budgie mtGenome. Further, mtGenome-based phylogenetic analysis suggests that the budgerigar is most closely related to kakapo (*Strigops habroptilus*). The mitochondrial sequence of the budgie described here will form a useful resource for both parrot phylogeny and the role of the mtGenome in budgie longevity.

Key Words: budgerigar, mtGenome, rearrangement, control region, phylogenetics

283P Genetic diversity of *Campylobacter* populations in chicken ceca. P. Singh* and Y. M. Kwon, University of Arkansas, Fayetteville.

Campylobacter species is the most common human pathogen causing gastrointestinal infections and poultry is a major source of this pathogen. In this project, we aim to study the genetic diversity of *Campylobacter* strains within individual chickens using cecal samples to understand the nature of intestinal colonization by *Campylobacter* species. Genotyping was conducted based on the DNA sequence of Short Variable Regions (SVR) in the flaA gene. Cecal samples collected from ten market age chickens were used for isolation of *Campylobacter* genomic DNA and SVR was amplified with flaA gene-specific primers, cloned and sequenced. Sequencing results obtained from 85 clones (~10 clones/bird) showed that on an average 24.3 % of clones had mutations within individuals. When translated SVR sequences were analyzed, there was on an average 20.6 % of sequences carrying altered amino acids within individuals. The mutation did not show any consistent pattern, suggesting a random nature of the mutations. Four translated sequences had nonsense mutations to produce truncated proteins. These results suggest that there are multiple genotypes colonizing in a cecum and the occurrence of truncated FlaA protein may represent a novel mechanism for evasion of adaptive immune responses.

Key Words: *Campylobacter*, chicken, short variable region, cecum, genetic diversity

284P Association of single nucleotide polymorphisms in candidate genes with phenotypic traits in fat or lean chicken lines. X. Liu*¹, L. Cogburn², M. Muchow¹, E. Le Bihan-Duval³, J. Simon³, and T. E. Porter¹, ¹University of Maryland, Department of Animal and Avian Science, College Park, ²University of Delaware, Department of Animal and Food Science, Newark, ³Station de Recherches Avicoles-INRA, Nouzilly, France.

As a result of selection for rapid growth, excess fat accumulation in broiler chickens is a problem in the poultry industry. The current study investigated associations between single nucleotide polymorphisms