Data were collected from 381 birds of Norfa pullets produced by pedigreed mating between 30 sires and 90 dams. These data were utilized to construct and evaluate multisource multitrait selection indices and sub-indices depending on more than one source of information for each trait. The studied traits were antibody titers to SRBCs antigen (Ab), body weight at sexual maturity (BW) and egg number till 42-wk of age. The sources of information considered were individual’s own phenotype value (OP), its full (FS) and half sister’s (HS) averages. Three sub-indices (IS) were developed from the main multisource index. It was observed that, weighting factors of all traits in the main multisource index (Ab, BWsm and EN42) had the highest values. The variances of sub-indices (IS,Ab, IS,BWsm and IS,EN42) developed from the main multisource index were 2.576, 5513.06 and 62.35, respectively. Genetic progress achieved was also maximum in most traits. It was concluded that an index based on 3 sources of information was the most efficient index to improve the studied traits and could be applied to improve egg production and immune response traits.

**Key Words:** genetic improvement, selection index, antibody response, Norfa chickens

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**182 Genetic improvement achieved in immune response and some egg production traits using multi-source multi-trait selection indices in laying hens.** A. A. Enab,* G. M. Gebriel, F. H. Abdou, and E. M. Abou-Elewa, Menoufiya University, Shebin El-Kom, Menoufiya, Egypt.

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Nineteen generations of divergent selection for ascites susceptibility has resulted in a shift in hatch window. In fact, ascites susceptible (SUS) chicks hatch 4 h earlier than resistant (RES). The reasons for this hatch window change are unclear but could be associated with correlated responses in egg composition and shell characteristics. The current study was conducted to evaluate the ascites lines for egg traits measured at lay through 3 weeks storage. To accomplish this, Generation 19 breeders from Lines RES, SUS and the unselected base population REL were sampled. At 38 wk of age, a single day’s eggs production from 72 hens per line (n > 50 per line) were subjected to analysis using Dual Energy X-Ray Absorptiometry (DEXA). DEXA scans allow for a noninvasive measure of total egg, shell, albumen and yolk weight and shell calcium and thickness. Individual egg scans were taken on d 0 and after 1, 2 and 3 wk storage in an egg cooler maintained at 22 °C and 60% humidity. Since egg size differs between lines, data were also expressed relative to egg weight. Main effects, line and storage time, were analyzed using GLM procedure in SAS. Line differences were present with SUS line having lowest egg weight. Line differences were present with RES being the highest and SUS being the lowest for shell calcium and relative albumen, RES was the highest and REL lowest for shell thickness. SUS line had significantly higher relative yolk weight compared with REL and RES lines. Relative shell weight for SUS and RES lines were higher than REL. Concerning storage time, egg weight and relative yolk weight were lower for measurements taken at 2 and 3 weeks when compared with day of lay and wk 1 measurements. Storage time had no effect on shell weight or shell calcium; however shell thickness was lower at wk 3 of storage compared with the other storage times. Relative albumen weight decreased after each week of storage. Additional data will be collected to evaluate breeder age related changes in egg characteristics.

**Key Words:** broilers, ascites, DEXA, egg, storage

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cTHY28 is a highly conserved nuclear protein that was isolated in an in vitro screening procedure designed to identify cellular proteins that mediate apoptosis in avian lymphocytes. Structural analysis of cTHY28 revealed that it is a phosphoprotein, with a nuclear localization signal, as well as a putative glycosylation and myristolation site. However, the cellular function of cTHY28 has yet to be elucidated. In an attempt to gain insights into cTHY28’s function, a co-immunoprecipitation assay was developed to identify proteins that interact with cTHY28. Co-immunoprecipitated material from DT-40 bursal lymphocytes was analyzed using Western Immunoblot and SDS-Polyacrylamide Gel Electrophoresis methodology. Immunoprecipitated proteins isolated from polyacrylamide gels were subjected to mass spectrometric analysis. These results indicated that 3 putative proteins appear to have a direct protein-protein interaction with cTHY28: nucleolin, DNA topoisomerase I, and elongation factor-2. From a functional perspective, nucleolin is associated with pre-rRNA processing; DNA topoisomerase I relaxes supercoiled DNA during transcription; and elongation factor-2 is involved with protein translation at the ribosomal level. Interestingly, both DNA topoisomerase I and nucleolin co-localize with cTHY28 to the nucleolus, the site of RNA transcription and processing. Based on the functions of these interacting proteins, cTHY28 may play a role in rRNA processing. Future work will be focused on designing functional assays to analyze the putative role of cTHY28 in rRNA processing.

**Key Words:** cTHY28, nucleolin, DNA topoisomerase I, co-immunoprecipitation

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**185 Cost effectiveness of maintaining research chicken populations in situ or with cryopreserved semen or ovaries.** F. G. Silversides*, P. H. Purdy1, and H. D. Blackburn2, 1Agriculture and Agri-Food Canada, Agassiz, British Columbia, Canada, 2USDA-ARS National Animal Germplasm Program, Fort Collins, CO.

The cost of maintaining poultry populations has resulted in substantial losses of lines kept for research, and scientists’ calls for action have gone unheeded. To date the costs of alternatives to keeping live populations (LP) have not been considered. The costs of programs using LP, semen cryopreservation and reconstitution (SC), and ovary and semen cryopreservation and reconstitution (OSC) were evaluated over 20 yr using biological parameters of cryopreservation and population reconstitution that were derived from the literature. Costs for LP, SC, and OSC were evaluated by summing the compounded cost of preservation \[P(1+i)^n\], the sum of the compounded yearly costs of storage \[S(1+i)^n\] and the sum of the compounded yearly cost of recovery \[\Sigma R(1+i)^n\] where n = years of storage and i = compounding rate. Over 20 yr, costs for SC and OSC were from 3 to 20% of those associated with LP depending on the number of populations recovered, and the ability to rapidly reconstitute
populations using OSC made it the least expensive option. Keeping LP was most cost effective for periods of up to 3 yr. However, with longer periods, LP becomes increasingly difficult to justify and any research population that will not be used within 5 yr should be cryopreserved and in situ maintenance discontinued. The rapid reconstitution possible with OSC and SC (for single gene mutations) suggest that cryopreserved material could be included in short-term research projects and recovery costs included in the budget. Using the methods evaluated would reduce research costs and allow institutions to focus resources on investigating lines currently kept and developing new lines.

**Key Words:** genetic conservation, cryoconservation, semen, ovary

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186 Genetic polymorphism among broiler breeders as revealed by random amplified polymorphic DNA analysis.  F. S. Nassar*1, R. E. A. Moghaieb2, A. M. Abdou1, and F. K. R. Stino1, 1Department of Animal Production, Faculty of Agriculture, Cairo University, Giza, Egypt, 2Veterinary College, Giza, Egypt.

To characterize, the local broiler breeder female line that has been selected for increasing 6 wk body weight (Cairo B-2 line) and the control line a RAPD-PCR analysis was performed. DNA sample, collected from individuals of both lines, were subjected to RAPD-PCR analysis using 16 random primers. All primers used in the present study resulted in the appearance of PCR products with a variable number of bands. The genetic similarities between the lines tested were calculated by band sharing. According to our data it is possible to distinguish between Cairo B-2 and the control lines. The data indicated that a total of 200 and 196 RAPD markers were detected for Cairo B-2 and the control lines respectively. The genetic polymorphism detected from this study was 79% and 88.7% for Cairo B-2 and the control lines respectively. The genotypic specific markers for males and females from both lines were determined. The data indicate that 3 markers were found to be male specific markers (N13–805, N13–366, P3–1077), and 5 markers were defined as female specific markers (A4–2741, A4–1755, A4–735, C8–321, G14–3648) for Cairo B-2 line. However, 2 markers were detected as male specific markers (B10–2305 and N13–1513), and 5 markers were detected as female specific markers (A1–2737, A2–1648, A1–401, F15–525, G14–1158) for the control line. This study concluded that, the homogeneity percentages between all birds in Cairo B-2 line (21%) are higher than control line (11%). Moreover, these RAPD markers can be considered as useful markers that can help in marker-assisted selection breeding program aiming to improve the productivity of Cairo B-2 line.

**Key Words:** broilers, breeders, RAPD-PCR, polymorphism, genetic markers

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187 Utilizing piggyBac in transgenic chick strategies.  B. J. Jordan*, 1 M. R. Stark2, and R. B. Beckstead1, 1The University of Georgia, Athens, 2Brigham Young University, Provo, UT.

The chicken is a well-established model system for studying vertebrate embryogenesis, but creating transgenics has proven difficult. Viral infections have been predominantly used to insert transgenes and have been moderately successful, however, the rate of germ line infection is low and the virus is not easily manipulated in the lab. To increase efficiency and ease of production we are using piggyBac, a transposable element (TE) system, to generate transgenic chicks. The TE system utilizes a transposase enzyme, which recognizes a specific DNA sequence called a transposon. The enzyme excises the transposon from its original location and inserts it into another genomic location. The transposon contains a constitutively expressed GFP gene for tracking of insertion by fluorescent microscopy. piggyBac is delivered to cells using JetPEI, an in vivo transfection reagent. Chicks hatched from Stage X injections of JetPEI/piggyBac solutions showed GFP expression in multiple tissue types from all 3 germ layers. 6/19 males expressed GFP in the testes, with some GFP positive cells also staining positive with germ cell antibodies. We were also able to detect the GFP gene by PCR analysis of genomic DNA from the sperm of a sexually mature rooster, although transmission rate could not be determined. An alternative strategy to early embryo injections is using the sperm itself as carriers of DNA to the single cell oocyte. Preliminary experiments show that chicken sperm will take up exogenous DNA and transmit the DNA to oocytes, as confirmed by PCR analysis. This method does not induce integration into the genome however. Utilization of piggyBac in concert with sperm mediated gene transfer could be the protocol needed for efficient chick transgenesis.

**Key Words:** transgenic, transfection reagent, piggyBac, sperm-mediated gene transfer, germ cells

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188 Polymorphism and sequence analysis of ghrelin gene and its relationship with body weight in meat type of chicken.  M. E. Sadegh*, C. S. Nagaraja1, M. R. Jayashankar1, and H. N. Murthy1, 1Veterinary College, Bangalore, Karnataka, India, 2Veterinary College, Bangalore, Karnataka, India, 3Veterinary College, Bangalore, Karnataka, India, 4Veterinary College, Bangalore, Karnataka, India.

An investigation was carried out to study nucleotide sequencing and DNA polymorphism by PCR-RFLP of ghrelin gene in 4 strains of chicken. Genomic DNA was isolated from a total of 200 birds belonging to 4 Indian strains of chicken namely new Genotype, Punjab Broiler, Indian Cornish and University Male Line. A fragment of ghrelin gene, comprising of a partial intron 3, complete exon 4 and partial intron 4 was amplified. The products from each variety were digested with Hinf I. The RFLP pattern revealed 3 genotypes (LL, VV and GG) and 3 different alleles (L, V and G). Correlation of cGHRL/Hinf I patterns with 6th week body weight indicated significant differences among 4 strains. Nucleotide sequencing of the amplified fragment of GH gene of 4 strains were submitted to the NCBI GenBank (accession nos JN578259 and JN578261). Totally, 13 nucleotide variations were observed in the different strains when compared with public databases. The nucleotide sequence analysis indicated that the percent similarity of GHRL gene fragment of 4 strains were more than 99%.

**Key Words:** ghrelin gene, polymorphism, Hinf I, sequencing, nucleotide variation

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189 Residual feed intake and gain a new feed efficiency parameter in the turkey (*Meleagris gallopavo*).  O. W. Willems*, S. P. Miller1, and B. J. Wood2, 1Centre for the Genetic Improvement of Livestock, University of Guelph, Guelph, ON, Canada, 2Hybrid Turkeys, Kitchener, ON, Canada.

The use of residual feed intake (RFI), representing the residuals from a model regressing feed intake (FI) on weight gain (WG) and body...
weight (BW), by poultry breeders has been limited. This may be due to the common definition of RFI being independent of WG. Residual body weight gain (RG), a feed efficiency trait composed of residuals from a model regressing WG on FI and BW has also been proposed. In this study, a new trait for turkeys, residual intake and gain (RIG), combines the beneficial characteristics of both RFI and RG. Animals with superior RIG have, on average, greater WG and reduced FI. To assess the use of RIG in poultry, pedigree data for 15,830 tom turkeys over a 10-year interval were evaluated. Birds were measured for FI and WG over a 4-week period, from 16 to 20 weeks of age, during which they had ad libitum access to feed. RIG was calculated as the sum of −1*RFI and RG, both standardized to a variance of one. Table 1 shows daily feed intake (DFI), WG and average daily gain (ADG) of the 1% (n = 158) of animals ranked on RFI, RG and RIG, alongside number of days to achieve 10 kg weight gain (based on ADG) and FI to achieve 10 kg WG ((days to achieve 10 kg WG)*DFI). The best RFI birds consumed the least amount of feed, the RG birds the most and the RIG birds were intermediate. Similarly, the best RFI birds had the lowest ADG, the RG birds the highest and again the RIG birds were intermediate. At the top 1% level, the RIG birds consumed 0.27 and 0.46 kg less to achieve 10 kg WG than the RG and RFI birds, respectively. This small difference at the individual level may lead to large savings in feed costs over time.

### Table 1. Top 1% of birds

<table>
<thead>
<tr>
<th>Trait</th>
<th>DFI (kg)</th>
<th>WG (kg)</th>
<th>ADG (kg)</th>
<th>Days to 10 kg</th>
<th>FI to 10 kg</th>
</tr>
</thead>
<tbody>
<tr>
<td>RFI (kg)</td>
<td>0.47</td>
<td>6.09</td>
<td>0.22</td>
<td>46</td>
<td>21.61</td>
</tr>
<tr>
<td>RG (kg)</td>
<td>0.65</td>
<td>8.48</td>
<td>0.30</td>
<td>33</td>
<td>21.42</td>
</tr>
<tr>
<td>RIG</td>
<td>0.55</td>
<td>7.34</td>
<td>0.26</td>
<td>38</td>
<td>21.15</td>
</tr>
</tbody>
</table>

**Key Words:** turkeys, feed efficiency, RFI

Residual feed intake (RFI) is modeled so that feed intake (FI) is regressed on both weight gain (WG) and body weight (BW) and this allows RFI to be phenotypically independent from both. Similarly, residual body weight gain (RG) represents the residuals from the regression of weight gain on both FI and BW. Residual intake and gain (RIG) combines the beneficial characteristics of both RFI and RG such that RIG is independent of BW, but when used for selection it can increase WG and reduce FI simultaneously. To assess the effectiveness of RIG in poultry, pedigree data for 15,830 tom turkeys over a 10-year interval were evaluated. Birds were measured for FI and WG over a 4-week period, from 16 to 20 weeks of age, during which they had ad libitum access to feed. RIG was calculated as the sum of −1*RFI and RG, both standardized to a variance of one. A bivariate analysis was performed, fitting an animal model with hatch as a fixed affect in ASReml. Means, standard deviations and heritabilities for each feed efficiency and constituted trait were assessed. Means (SD) for FI, WG, FCR, RFI, RG and RIG were 18.62 (3.27), 6.41 (1.52), 3.00 (0.894) and 0.00 (1.902). FI, WG, FCR, RFI, RG and RIG had heritabilities (se) of 0.21 (0.02), 0.15 (0.02), 0.24 (0.02), 0.22 (0.02), 0.19 (0.02) and 0.21 (0.02), respectively. The heritabilities of RFI, FCR, FI and WG were similar to estimates in broiler chickens. RG and RIG heritability estimates were similar to estimates in beef cattle. RIG is a newly assessed trait in poultry, its heritability and beneficial relationships with both WG and FI make it an ideal trait for use as a selection criterion for feed efficiency.

**Key Words:** microarray, Campylobacter jejuni, innate immune response, cecum, broiler

191 Transcriptional profiling of innate immune response in broiler ceca following campylobacter jejuni infection. A. Nazmi1,2, J. Zhang1, X. Li1, C. Swaggerty2, M. Kogut1, H. Chiang1, Y. Wang1, K. Genovese1, H. Hi1, V. Dirita2, I. Pevzner1, and H. Zhou1, 2Texas A&M University, College Station, 3United States Department of Agriculture, Agricultural Research Service, College Station, 4University of Michigan, Ann Arbor, 5Cobb-Vantress Inc., Siloam Springs, AR, 6University of California-Davis, Davis.

*Campylobacter jejuni* (C. jejuni) is one of the most frequent bacterial causes of human gastroenteritis in the industrialized countries. C. jejuni colonizes the gastrointestinal tract of chickens especially ceca as a commensal organism. Chickens are considered the principle vector for human Campylobacteriosis with the consumption of contaminated poultry products. Understanding the host innate immune response following C. jejuni infection using microarray technology could lead new avenue for the development of strategies in the controlling C. jejuni colonization in broiler and reduce carcass contamination. Two genetically distinct broiler lines, previously characterized as resistant or susceptible to C. jejuni infection were orally inoculated with either mutant (MT), wild-type (WT) C. jejuni or PBS at day one after hatch. Cecal tissues were removed at 1 and 4 h post-inoculation (PI) to isolate mRNA which then applied to a whole genome microarray for a pair comparison between inoculated and control group. The signal intensity for each gene was normalized and data reported on the log2 scale. A mixed model including line, treatment, time point, array, dye, and all 2-way interactions among them were used to identify differentially expressed genes (P < 0.01). For the resistant line, there were 53 and 24 immune-related genes differently expressed at 1 h PI, and 23 and 22 genes at 4 PI in the MT-infected and WT-infected, compared with non-infected birds, respectively. Within the susceptible line, there were 7 and 6 immune-related genes significantly expressed at 1 h PI, and 44 and 12 genes at 4 h PI, respectively, when compared with the uninoculated controls. The results suggest the resistant line initiates strong host immune response early, and MT strain elicited more host response than wild-type strain. Further signal pathway analysis to understand the mechanisms of this host-pathogen interaction is underway.

**Key Words:** microarray, Campylobacter jejuni, innate immune response, cecum, broiler