**T93   Phenotypic and genotypic aspects of *Staphylococcus aureus* isolated from chronic subclinical infections in dairy goats.**   P. Moroni[1], G. Pisoni[1], C. Vimercati[1], M. Antonini[2], B. Castiglioni[2], P. Cremonesi[2], and P. Boettcher*[2], [1]*University of Milan, Milan, Italy*, [2]*Institute of Agricultural Biology and Biotechnology, National Research Council, Milan, Italy*.

The objectives of this study were to identify goats with chronic infections by *Staphylococcus aureus* (SAUR), isolate bacteria from these animals, genotype the bacteria to identify different strains, and perform tests of antimicrobial sensitivity. A herd of 75 Alpine goats in Northern Italy was monitored for a complete production season. Bacterial cultures were taken from each udder half during eight monthly visits. Goats with at least 2 consecutive positive tests for SAUR (n = 28) in the same udder half were identified as chronically infected. Goats with no infections in either udder half during any visit were considered healthy (n = 26). The bacteria isolated from one sample from each infected goat were genotyped based on variable numbers of tandem repeats in 6 genomic regions. One sample from each animal was also subject to a test for beta-lactamase production and to Minimum Inhibitory Concentration tests for 11 antimicrobial agents: benzylpenicillin, ampicillin, amoxicillin, amoxicillin plus clavulanic acid, cloxacillin, cephalonium, cephoperazone, oxytetracycline, doxicycline, kanamycin, and lincomicin. A linear mixed model was used to examine the relationship between chronic infection by SAUR and somatic cell score. This analysis involved 841 records. Factors in the statistical model were sample day, parity, infection status, goat, and udder half nested within goat. No genetic variability was observed among the bacteria isolated, suggesting that all were from the same strain. All SAUR isolates were negative for the beta-lactamase production test and no isolate was resistant to any of the antimicrobial agents used. Penicillins were the most effective drugs tested, however. As expected, SCS was significantly higher in infected goats (least-square mean = 7.55) than in healthy goats (LSM = 5.50). With regard to specific udder halves, mean SCS from infected udder halves (LSM = 8.02) was greater than in uninfected udder halves from the same goats (LSM = 6.44). No differences were observed in milk yield or fat and protein percentages between infected and healthy goats.

**Key Words:** Goat, Staphylococcus Aureus, Subclinical Infection

# Graduate Student Competition—CSAS

**T94   Validation of a new equation predicting digestible energy of forage for sheep.**   M. Vachon*[1,2], J. F. Bernier[1], G. Allard[1], A. Brégard[1], and D. Pellerin[1], [1]*Université Laval, Québec, Québec, Canada*, [2]*Centre d'expertise en production ovine du Québec, La Pocatière, Québec, Canada*.

Single-component equations are actually used to evaluate DE of forages for sheep in Quebec. Previous study pointed out that multi-component empirical models generally improve slightly the precision of digestibility determination. The aim of this project was to compare the precision of a new multi-component empirical model (new) to predict DE of forages fed to sheep (DE Mcal kg$^{-1}$ =3.245+0.035xCP%-0.024xADF%-0.003LEGUME% (R2=0.52;n=202)) with the equation actually used in Quebec (old) for grasses (DE Mcal kg$^{-1}$ =4.681-0.0573xADF% (R2=0.68;n=69)). Comparisons were made in two separate trials with 48 lactating and 46 pregnant ewes in a 2 X 2 factorial arrangement. Factors were two equations used to predict DE of forage (old vs. new) and two grass hays harvested at different stage. ME requirements were calculated with the NRC model (1985) and with a factorial model based on the NRC (1985) and ARC (1980). Residual ME (intake - requirements) was used to evaluate precision of equations. The new equation predicted more DE in forages so less concentrates were needed to meet energy requirements of ewes. Feeding costs were thus lower when the new equation was used. Lactating ewes lost more weight (-0.25 vs. -0.19 kg d$^{-1}$ p=0,01) and more body condition score (-0.61 vs. -0.33 p=0.05) and their lambs gained less weight (0.52 vs. 0.57 kg d$^{-1}$ p=0.04) when the new equation was used. Residual ME was closer to 0 (lactation: old 0.36 vs. 2.18 Mcal d$^{-1}$, new 1.12 vs. 2.94 Mcal d$^{-1}$ p<0.01; pregnancy: old -0.64 vs. -0.95 Mcal d$^{-1}$, new -0.16 vs. -0.46 Mcal d$^{-1}$ p<0.01) when the NRC model (1985) was used to calculate ME requirements. For lactating ewes, residual ME was closer to 0 (0.36 vs. 1.12 Mcal d$^{-1}$ p<0.01) with the old equation. For pregnant ewes, residual ME was not different from 0 (Student t, p<0.05 ) with the new equation but was different from 0 (Student t, p<0.05) with the old one. These results do not allow to recommend the systematic use of the new empirical model to predict forage energy for sheep.

**Key Words:** Digestible energy, Forage, Sheep

**T95   Nutrient digestibility of diets containing graded levels of meat and bone meal for pigs and ducks.**   S. A. Adedokun* and O. Adeola, *Purdue University, West Lafayette*.

Apparent digestibility of calcium (Ca), phosphorus, (P) and nitrogen (N) of diets containing meat and bone meal (MBM) were determined using 288 barrows with an average weight of 35 kg. Apparent N utilization was also determined in 288 ducks with mean weight of 3.4 kg. For each of 12 MBM samples, diets were formulated by substituting 0, 5, or 10 % MBM in a basal 170 g CP kg-1 corn-soybean meal diet; corn and soybean meal were adjusted at the same ratio to account for the substitution. Each diet was fed to 8 barrows in individual metabolism crates in a digestibility assay that employed a 5-d acclimation followed by a 5-d period of total collection of feces. Each of the diets was also fed to 8 ducks in a metabolism assay that employed a 4-d acclimation and 3-d period of excreta collection. The gross energy (GE), CP, crude fat (CF), ash, Ca, and P contents of the MBM samples, on per kg dry matter basis, ranged from 3,493 to 4,732 kcal, 496.7 to 619.1 g, 91.1 to 151.2 g, 200.3 to 381.9 g, 54.3 to 145.8 g, 25.6 to 61.7 g, respectively.. In most of the diets, there were increases in dietary Ca, P and CP with increase in substitution levels of MBM from 0 to 10 %. Calcium digestibility in pigs increased linearly (P < 0.05) for diets containing MBM samples 3 and 8 and decreased linearly (P < 0.05) for diets containing MBM sample 1. Phosphorus digestibility in pigs increased linearly (P < 0.05) with MBM samples 3, 7 and 10 with an increase in MBM substitution. Nitrogen digestibility was either unaffected (MBM 3 or 9) or decreased (MBM samples 2, 4, 5, 11 or 12, P < 0.05) in the pigs and an increase in N utilization (MBM samples 3 and 9, P < 0.05) for ducks. This study shows that the digestibility of N, Ca and P in diets supplemented with MBM compares favorably with that of the diet supplemented from inorganic sources when MBM replaced up to 10 % corn and SBM in the basal diet.

**Key Words:** Duck, Pig, Meat and bone meal

**T96   Growth performance, carcass characteristics and fat quality of pigs fed Manitoba-grown corn cultivars.**   F. O. Opapeju*, C. M. Nyachoti, and J. D. House, *University of Manitoba, Winnipeg, MB, Canada*.

An experiment was conducted to determine growth performance, carcass characteristics and fat quality of growing-finishing pigs fed diets based on two widely grown corn cultivars in Manitoba. Twenty-four Cotswold growing pigs (~41 kg initial BW) individually housed in floor pens were blocked by BW and sex and randomly allotted from within block to one of three diets to give eight replicate pigs per diet. Experimental diets consisted of a control based on barley and two corn based diets containing corn cultivar 1 or corn cultivar 2 as the main energy source. A three-phase feeding program for 20-50 kg (phase 1), 50-80 kg (phase 2) and 80-110 kg (phase 3) BW range was used. Diets for each phase contained 3.5 Mcal/kg DE but total lysine was 0.95%, 0.75% and 0.64% in phase 1, 2 and 3 diets, respectively. Average daily gain (ADG), average daily feed intake (ADFI) and gain to feed ratio (G:F) were monitored weekly during each phase. Pigs were slaughtered after reaching a minimum BW of 100 kg. There were no ef-

fects ($P > 0.05$) of diet on ADG (mean ± SE) (0.87 ± 0.04, 0.85 ± 0.05 and 0.90 ± 0.05 kg for phase 1, 2 and 3, respectively), ADFI (mean ± SE) (1.96 ± 0.07, 2.46 ± 0.08 and 2.86 ± 0.09 kg for phase 1, 2 and 3, respectively) and G:F (mean ± SE) (0.45 ± 0.02, 0.34 ± 0.02 and 0.31 ± 0.02 for phase 1, 2 and 3, respectively) in all the three phases. Carcass length, dressing percentage, loin eye area, loin depth, backfat thickness, belly firmness and L*, b* and a* fat color were similar ($P > 0.05$) across dietary treatments. Pigs fed the diet based on corn cultivar 2 had a higher ($P < 0.05$) amount of polyunsaturated fatty acids in their backfat compared with those fed the barley-based diet but the amount of saturated, monounsaturated and total unsaturated fatty acids in the belly fat and backfat were similar ($P > 0.05$) across dietary treatments. The results suggest that growth performance, carcass characteristics and fat quality of pigs fed diets based on Manitoba-grown corn cultivars and those fed the barley-based diet were comparable.

**Key Words:** Corn, Performance, Pigs

**T97  Bioavailability of phosphorus in peas for growing pigs.** A. M. Hawkins*[1], C. M. Nyachoti[1], B. A. Slominski[1], and H. A. Weiler[2], [1]*Department of Animal Science, University of Manitoba, Winnipeg, MB, Canada*, [2]*Department of Human Nutritional Sciences, University of Manitoba, Winnipeg, MB, Canada*.

The nutritional evaluation of field peas for swine has primarily focused on its energy and protein value. However, the bioavailability of phosphorus (P) in peas for pigs has only been examined to a limited extent. Thus, an experiment was conducted to determine the bioavailability of P in peas fed to growing pigs and to investigate bone mineral density using dual-energy x-ray absorptiometry as an alternative indicator for determining P bioavailability. Thirty-five individually housed barrows with an initial BW of 6.85 ± 1.40 kg (mean ± SD) were blocked on the basis of BW and randomly assigned from within block to seven semi-purified experimental diets to give five pigs per treatment. The test diets consisted of a cornstarch-soybean meal basal diet (0.6% Ca, 0.25% P), and the basal diet supplemented with 0.05, 0.10. or 0.15% P from monosodium phosphate (MSP) or common yellow pea (PEA). Feed and water were provided for ad libitum intake throughout the 5-wk study period. ADFI, ADG, and FE were measured weekly. At the end of the study, pigs were euthanised for collection of the femurs for measurements of bone mineral density. ADG (0.276, 0.341, 0.344 and 0.247, 0.275, 0.280 kg/d from MSP and peas, respectively) was linearly ($P < 0.05$) increased with incremental P supplementation, while improvement in gain:feed (0.470, 0.614, 0.634 and 0.452, 0.438, 0.426 kg/d from MSP and peas, respectively) was only linear ($P < 0.05$) for MSP but not for pea supplementation. ADG and bone measurements were regressed on supplemental P intake, and P bioavailability from peas was determined by the slope ratio technique. Estimates for the bioavailability of P (relative to MSP) for peas from growth rate and bone mineral density data were 43.29% and 37.28%, respectively. The P bioavailability value determined with the bone mineral density data in the present study was comparable with values determined in previous research.

**Key Words:** Peas, Phosphorus bioavailability, Growing pigs

**T98  True phosphorus digestibility and the endogenous phosphorus losses associated with barley for pigs.** Y. Shen*, R. R. Hacker, and M. Z. Fan, *University of Guelph, Guelph, Ontario, Canada*.

True phosphorus (P) digestibility and the endogenous P outputs associated with barley for pigs were determined by using the regression analysis technique. Two groups of four pigs, representing weanling and growing pigs with an average initial BW of 7.5 and 25.0 kg, respectively, were fitted with a T-cannula at the distal ileum. These two groups of pigs were each fed four semi-purified diets according to a 4 x 4 Latin square design. The diets were cornstarch-based and contained four levels of P, with 0.9, 1.6, 2.3, and 2.9 g/kg DM for the weanling pigs and 0.9, 1.7, 2.3, and 3.1 g/kg DM for the growing pigs, respec-

tively. The linearity between digestible P input and dietary P intake at both the ileal and the fecal levels was present only with the growing pigs ($P < 0.05$) but not ($P > 0.05$) with the weanling pigs. High dietary inclusions of barley in some diets might have affected the normal digestion of the feed in the weanling pigs. Thus, true P digestibility and the endogenous P outputs associated with barley were estimated by linear regression analysis only for the growing pigs. The true P digestibility (57.2 ± 11.6 vs. 64.7 ± 7.3%) and the endogenous P outputs (0.463 ± 0.230 vs. 0.507 ± 0.156 g/kg DMI) associated with barley were not different ($P > 0.05$) between the ileal and the fecal levels. Fecal true P digestibility was not affected by the higher (P<0.05) phytate degradation rate (84.0%) at the fecal level than that (51.7%) at the ileal level in the growing pigs. About 65% of the total P in conventional barley is digested and absorbed in growing pigs.

**Key Words:** Barley, True phosphorus digestibility, Pigs

**T99  Estimation of true phosphorus digestibility and the endogenous phosphorus losses associated with wheat for pigs.** Y. Shen*, R. R. Hacker, and M. Z. Fan, *University of Guelph, Guelph, Ontario, Canada*.

True phosphorus (P) digestibility, phytate-P degradation rates and the endogenous P outputs associated with a conventional wheat sample were measured in pigs by the regression analysis. Four weanling and four growing pigs, with average initial body weight of 7.7 and 28.4 kg, respectively, were fitted with a T-cannula and fed four diets according to a 4 x 4 Latin square design. Four cornstarch-based semi-purified diets, containing four levels of P at 0.9, 1.6, 2.2 and 2.8 g/kg dry matter intake (DMI) for the weanling pigs and 0.9, 1.4, 2.3 and 3.1 g/kg DMI for the growing pigs, were formulated from the wheat. The apparent ileal and fecal P digestibility in wheat were linearly affected (P<0.05) by P contents in the diets in the growing pigs but not ($P > 0.05$) in the weanling pigs. The increase in dietary P content from 0.9 to 3.1 g/kg DMI lead to a linear increase (P<0.05) in apparent ileal and fecal P digestibility in the growing pigs from 5.2 to 25.8% and from 9.0 to 31.0%, respectively. Phytate P degradation was not affected (P>0.05) by the dietary P levels. True P digestibility and the endogenous P outputs associated with the wheat were determined to be 33.5 ± 6.8% at the ileal level and 41.2 ± 4.1% at the fecal level with the endogenous P outputs being 0.320 ± 0.143 at the ileal level and 0.341 ± 0.086 g/kg DMI at the fecal level, respectively, in the growing pigs. The higher phytate-P degradation rate at the fecal level (53.4%) than that (28.9%) at the ileal level contributed little to the true fecal P digestibility in the growing pigs. True fecal P digestibility measured in the selected conventional wheat sample for growing pigs is somewhat lower than expected. More experiments need to be conducted to measure true P digestibility in wheat samples for pigs.

**Key Words:** True phosphorus digestibility, Pigs, Wheat

**T100  Persistence of the *cp4 epsps* transgene in ruminal and duodenal fluids from sheep fed diets containing Roundup Ready® canola meal.** T. Alexander*[1,2], R. Sharma[1], W. Dixon[2], E. Okine[2], and T. McAllister[1], [1]*Agriculture and Agri-Food Canada Research Centre, Lethbridge, AB, Canada*, [2]*University of Alberta, Edmonton, AB, Canada*.

The increased use of genetically modified plants over the last nine years has created interest in the fate of transgenic plant DNA throughout animal digestive tracts. The present study examined the persistence of transgenic DNA encoding the synthetic CP4 EPSPS protein in ruminal fluid (RF) and duodenal fluid (DF) collected from sheep fed either a high fiber (HF, 15.22% DM; n = 3) or low fiber (LF, 7.37% DM; n = 3) diet containing 15% Roundup Ready® canola meal (DM basis). Wethers were restricted to 95% of *ad libitum* intake and fed once in the morning. Digesta samples were collected at 1, 4, 7, 10, 13, 17, 21, and 25 h after feeding. Immediately after collection, whole digesta samples were divided into two equal portions. One portion was frozen in liquid nitrogen and later freeze-dried. The second portion was centrifuged to obtain a supernatant free of plant cells. DNA was extracted from the freeze-dried material using a CTAB

method and from the supernatant using a Qiagen DNeasy Plant Mini Kit. A TaqMan® PCR assay was used to quantify the *cp4 epsps* transgene in 245 ng of extracted DNA from whole and supernatant samples of RF and DF. Fiber content did not affect the persistence of the *cp4 epsps* transgene in RF or DF (P > 0.05). In whole RF, the *cp4 epsps* copy number was greatest for the HF and LF diets (2635 and 2432 copies, respectively) 1 h after being fed and eventually decreased to below the limit of quantification (less than 20 copies) by 21 h after feeding. In contrast, the *cp4 epsps* copy number in whole DF peaked at 7 h after feeding for both HF and LF treatments (245 and 278 copies, respectively) and decreased to below the limit of quantification by 21 h. The transgene was not detected in any of the supernatant samples devoid of plant cells. This study suggests that the transgenic DNA detected in RF and DF was mainly associated with solid undigested plant material.

**Key Words:** Genetically modified, Transgene, Real-time PCR

# Meat Science and Muscle Biology: Meat Quality Prediction and Enhancement

**T101   Prediction of monounsaturated fatty acid in the rib eye marbling of Japanese Black by image analysis using high resolution digital image.** K. Kuchida*[1], Y. Hirayama[1], A. Oka[2], E. Iwamoto[2], and M. Fukushima[3], [1]*Obihiro University of Agriculture and Veterinary Medicine, Obihiro-shi, Hokkaido, Japan*, [2]*Hyogo Prefectural Agricultural Institute, Kasai-shi, Hyogo, Japan*, [3]*Hyogo Prefectural Hokubu Agricultural Institute, Wadayama-cho, Hyogo, Japan*.

Evaluation of beef meat quality based on objective metrology and eating quality will be needed in the future, although the evaluation now depends more on the judgment by the naked eye. The purpose of this research was to predict the ratio of monounsaturated fatty acid (MUFA) of marbling fat in the rib eye muscle by detailed image analysis using high resolution carcass images. Japanese Black (29 steers and 17 females) cattle, which were slaughtered at 24-30 months (average: 27.7 months), were used in this study. The ratio of marbling area to rib eye area (FATPER), overall coarseness of marbling (O_COARSE), coarseness of the largest marbling particle in rib eye (M_COARSE), coarseness of single marbling particle (S_COARSE), ratio of minor and major axis of rib eye (MM_RATIO), and complexity of rib eye shape (COMP) were calculated by image analysis. The original images of rib eye were converted into binary images, which were then thinned by 5 and 10 rounds while maintaining the connection of pixels. The hairline (width of line being 1 pixel) of the thinned image was retained (hairline image). The pixels of each hairline, second moment, maximum length, pattern width, pattern direction, equivalent circular diameter, degree of circularity, ruggedness degree, circumference length, number of hairlines and total area were calculated for the hairline image by image analysis. MUFA was obtained by an official method. The range of MUFA was 51.0-62.5% (average: 56.7%), and the correlation coefficient of MUFA with marbling score and the O_COARSE were 0.15 (NS) and 0.47 (p<0.01), respectively. As the result of stepwise regression analysis, the M_COARSE, average of circumference length of hairline image, green color component of marbling, MM_RATIO and COMP were selected for the multiple regression equation for the prediction of MUFA ($R^2$=0.82). For the confirmation of the equation, an additional 10 steers were analyzed. The MUFA could be predicted using different data set ($R^2$=0.73).

**Key Words:** Image Analyisis, Monounsaturated Fatty Acid, Japanese Black

**T102   Development of photography equipment for the cross section of beef and its use in the evaluation of beef marbling and color of rib eye.** K. Takahashi*[1], K. Kuchida[1], T. Hori[2], M. Nami[2], T. Honma[2], H. Kotaka[3], and H. Tsukuda[4], [1]*Obihiro University of Agriculture and Veterinary Medicine, Obihiro, Hokkaido, Japan*, [2]*Hokkaido Industrial Research Institute, Sapporo, Hokkaido, Japan*, [3]*Hayasaka Science and Engneering Corporation, Sapporo, Hokkaido, Japan*, [4]*Livestock Improvement Association of Japan, Makubetsu, Hokkaido, Japan*.

In Japan, the area, marbling and color of rib eye of Wagyu are economically important traits at the purchasing by buyer. Although marbling and meat color are subjectively evaluated currently, an objective method is more desirable from the viewpoint of equitable evaluation. The aim of this study was to develop a photography equipment (to) that could obtain clear images of beef carcass cross-section and to evaluate marbling and meat color using the equipment. The view angle of the equipment was 384mm×318mm and the resolution of the digital camera (Kodak DCS Pro 14n) combined with the equipment was 13.5 million pixels. A super wide lens (Nikkor Ai AF ED 14mm F2.8D) was attached to this digital camera. Two line lightings of white LED (CCS Co. Ltd. LND-300H - SW-DF) were used. The rib eye images of the cross-section between the 6th and 7th ribs of 240 Japanese Black steers were analyzed by computer image technique. Nine variables (marbling percentage, marbling coarseness, etc.) were calculated for the estimation of the Beef Marbling Standard (BMS) number, and 108 variables (R, G and B components of color of marbling or lean, etc) calculated for the estimation of Beef Color Standard (BCS) number were computed as image analysis traits from these images. The BMS and BCS numbers assigned by the grader were predicted using these image analysis traits by multiple linear regression analysis. Four variables were selected in the multiple regression equation of the BMS number ($R^2$ = 0.84). Percentages of 71.7% and 96.7% for the differences between the BMS numbers predicted by image analysis and assigned by the grader were within ±0 and within ±1, respectively. The multiple regression equation of the BCS number was composed of 5 image analysis traits ($R^2$=0.74). Ratios of the difference between BCS number predicted by image analysis and BCS number assigned by grader being ±0 and within ±1 were 81.6% and 100%.

**Key Words:** Beef Carcass, Marbling, Meat Color

**T103   Prediction of BMS number by image analysis and comparison of estimated BMS numbers in different cross sections of Holstein steers.** Y. Hamasaki*, K. Kuchida, S. Hidaka, K. Shimada, and M. Sekikawa, *Obihiro University of Agriculture & Veterinary Medicine, Obihiro-shi, Hokkaido, Japan*.

In Japan, the 6-7th rib of carcass cross section has been used in meat quality evaluation of beef. Marbling scores in *M. longissimus thoracis* are classified into 12 levels and have a large economic impact. Marbling scores evaluated by different graders have some discrepancy in the same carcass and even in the same muscle when the section is different. The aims of this study were to develop a prediction method of the BMS (Beef Marbling Standard) number by image analysis and to investigate the difference between BMS numbers in the 6-7th ribs and those in other areas. Digital images of the 6-7th cross section from 61 Holstein steers were used to predict BMS number with a multiple regression equation. The ratio of marbling to rib eye area (FATPER), the coarseness of marbling and the shape of rib eye were considered as independent variables, and the BMS number evaluated by a grader was a dependent variable for the multiple regression analysis. The multiple regression equation was applied to 4 cross sections, which were cut in 2.5 cm intervals from the 6-7th cross section toward the direction of the lumbar of 18 other Holstein steers. Selected variables of the multiple regression equation for estimating the BMS number were FATPER, the area of the largest marbling particle, coarseness of a single marbling particle and rib eye area ($R^2$ = 0.71). The differences of the image analyzed BMS numbers between the 6-7th cross section and the other 3 cross sections were not large, ranging from -0.99 to 0.72. Samples with large differences of the BMS numbers among the cross sections contained a huge marbling particle in the rib eye. After removing the huge marbling particle by image processing, the BMS number was predicted again using the multiple regression equation, and the differences of the BMS numbers between the 6-7th cross

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