

(2.64 LU/ha and 500 kg concentrate/cow) and a high output per hectare (HC) pasture system (2.85 LU/ha and 1,200 kg concentrate/cow). A total of 126, 128 and 140 animals were used during the years 2006, 2007 and 2008, respectively. HighNA had the greatest milk and solids corrected milk (SCM) yields, HighNZ had the lowest milk yield but similar SCM yield to LowNA group. Increased stocking rates combined with concentrate supplementation increased milk production per cow and overall farm output. HighNA and HighNZ genotypes had greater odds of being served within the first 24 days of the breeding season, becoming pregnant to first service and being pregnant after 42 days of the breeding season compared to the LowNA group. Both HighNA and HighNZ animals also had a lower hazard of being culled compared to the LowNA animals. Concentrate supplementation at pasture had no effect on fertility performance. There was no genotype by FS interaction for any measures recorded. These results demonstrate the EBI as a total merit index to improve reproductive capacity while maintaining milk production performance.

Key Words: genotype, feed system, fertility performance

409 Consequence on reproduction of two feeding levels with opposite effects on milk yield and body condition loss in Holstein and Normande cows. E. Cutullic^{*1}, L. Delaby¹, G. Michel², and C. Disenhaus¹, ¹INRA UMR1080 Dairy Production, Rennes, France, ²INRA UE326 Le Pin-au-Haras, Exmes, France.

The objective of this study was to evaluate the respective effects of milk yield and body condition (BC) loss on cows' postpartum repro-

ductive status taking breed differences into account. 105 Normande (dual-purpose) and 98 Holstein cows were assigned to a low or high feeding level (L-group: 50% grass silage and 50% haylage in winter, no concentrate at grazing; H-group: 55% maize silage, 15% alfalfa hay and 30% concentrate, 4kg concentrate at grazing). Milk progesterone assays led to determine commencement of luteal activity (CLA), postpartum ovarian activity profile, ovulation detection rate and late embryo mortality. Data were analysed by variance-covariance and logistic regression models. In both breeds, L-group cows had a lower 100-day average daily milk yield (MY) than the H-group cows but lost more BC (0-5 scale) (21.5 vs. 30.9 kg/day, -1.38 vs. -0.94 unit, N=102 and 101; P<0.001). Feeding level effect on MY was greater for Holstein than for Normande cows (+10.9 vs. +8.0 kg/day; P<0.05). As expected, Normande cows had shorter CLA, less prolonged luteal phase cycles and higher calving rate than Holstein cows (P<0.01). Feeding level had little effect on CLA and ovarian activity profile. In both breeds, ovulation detection rate was higher in the L-group (77% vs. 60%, N= 254 and 282; P<0.001). At 1st and 2nd inseminations, conception rate was improved in the H-group (74% vs. 57%, N=125 and 138; P<0.01), especially for Holstein cows (73% vs. 48%; P<0.01). As late embryo mortality frequency was very high in the H-Group Holstein cows (30% vs. 9%, N= 64 and 64; P<0.01), difference in calving rate was not significant between feeding groups (P>0.25). Owing to feeding level effects, MY and BC loss could affect reproduction at different stages. Consistent with the literature, a greater BC loss coincides with reduced conception rate. High milk yield coincides with depressed ovulation detection and embryo survival.

Key Words: reproduction, milk yield, body condition loss

Breeding and Genetics: Swine Breeding

410 Performance and carcass composition of pigs selected for residual feed intake on restricted and ad libitum diets. N. Boddicker*, D. Nettleton, N. Gabler, M. Spurlock, and J. C. M. Dekkers, Iowa State University, Ames.

Understanding the biology behind genetic differences in feed efficiency is important to develop selection strategies to improve efficiency. To this end, a line of Yorkshire pigs selected for lower residual feed intake (LRFI) was developed. The objective of this study was to evaluate the 5th generation of the LRFI line against a random control line (CTRL) for performance, carcass and chemical composition, and overall efficiency. Forty barrows from each line were paired by age (~132 d) and weight (74.8±9.9 kg), and randomly assigned to 1 of 4 feeding levels in individual pens in 10 replicates: 1) ad libitum (adlib), 2) 75% of adlib (A75%), 3) 55% of adlib (A55%) and 4) weight stasis (WS). Pigs were on test for 6 weeks with feed intake adjusted once or twice per week for each pig. Although initial BW did not differ between lines (p=0.49), all results were adjusted for initial BW. The adlib LRFI consumed 8% less feed (p=0.15) with no difference in growth rate versus the CTRL. However, the A55% LRFI gained 10% more (p<0.01) than the CTRL on the same amount of feed. Despite attempts to hold the WS pigs at constant BW for six weeks, the LRFI gained BW while consuming 11% less feed than the CTRL (p=0.05). The LRFI line also had a higher dressing percentage (p<0.03) and lower visceral weights than the CTRL, but this was significant only for the A75% level (p<0.02). Based on chemical analysis of the empty carcass, the LRFI line had lower fat% and greater water% than the CTRL, but this was significant only for the adlib level (p=0.08). There were no line differences in protein% and ash%. In conclusion, pigs selected for LRFI consumed less feed for the same rate of gain but differed in carcass composition, indicat-

ing differences in the partitioning of energy. LRFI pigs also had lower viscera weights and required less energy to maintain BW, indicating possible differences in maintenance requirements. Further analysis will focus on differences between retained and consumed energy. *This research was funded by grants from the National Pork Board and the Iowa Pork Producers Association.*

Key Words: residual feed intake, performance, carcass composition

411 Effect of selection for residual feed intake on feeding behavior and daily feeding patterns in pigs. J. M. Young*, W. Cai, and J. C. M. Dekkers, Iowa State University, Ames.

Residual feed intake (RFI) is a measure of feed efficiency defined as the difference between observed and predicted feed intake based on average requirements for growth and maintenance. The objective of this study was to evaluate the effect of selection for lower RFI on feeding behavior traits (FBT) and to estimate the relationship between FBT and RFI. Data were from 3 parities from the 4th and 5th generations of a selection experiment for lower RFI (LRFI) and a random control line (CTRL) were analyzed by parity. Lines were mixed in pens of 16 and evaluated for FBT obtained from a single-space electronic feeder (FIRE©) over a growing period of ~3 months prior to ~115 kg. The following FBT were evaluated as averages over the entire test period (TP) and over the first (TP1) and second half (TP2) of the test period: number of visits per day (NVD) and per hour (NVH), occupation time per day (OTD), per visit (OTV) and per hour (OTH), feed intake per day (DFI), per visit (FIV) and per hour (FIH), and feeding rate per visit

(FRV). Models used included fixed effects of line and feeder, covariates of onage and DFI, and random effects of pen, on-test group, sire, and litter. Repeated measures models were used to analyze feeding patterns during the day. LRFI pigs had a significantly lower DFI than CTRL pigs for all 3 data sets. With adjustment for DFI, line differences in FBT were in the same direction for all 3 data sets but differed in significance and size. FIV, FIH, NVD, and NVH did not differ between lines but the trend was for LRFI pigs to have fewer visits, in particular during peak eating times. LRFI pigs had a higher FRV and lower OTD, OTV, and OTH than CTRL pigs but this was not significant for all datasets. Residuals correlations of RFI were positive with DFI and NVD, although its strength differed between datasets. In conclusion, feed efficiency may be affected by feed intake behavior because selection for RFI has resulted in pigs which spend less time eating and eat faster. *Funding provided by the National Pork Board, the Iowa Pork Producers Association, and National Needs Fellowship grant no. 2007-38420-17767.*

Key Words: swine, feeding behavior, residual feed intake

412 Longitudinal random regression analysis of growth and feed intake in selection lines for residual feed intake in Yorkshire swine. W. Cai*, H. Wu, and J. C. M. Dekkers, *Iowa State University, Ames.*

A 5-generation selection experiment in Yorkshire pigs for feed efficiency consists of a line selected for lower residual feed intake (LRFI) and a random control line (CTRL). The objectives of this study were to use random regression models to evaluate the effect of LRFI selection on daily feed intake (DFI), body weight (BW), backfat (BF) and loin muscle area (LMA) along the growth trajectory and to estimate genetic parameters. Data from ~3 to ~8 months of age on 586 boars and 495 gilts were used, along with data on generations -1 and 0, with data on the LRFI line from all generations and on the CTRL line from generation 5. The average number of measurements for DFI, WT, BF, and LMA was 85, 14, 5, and 5. Random regression models were fitted with pen by on-test group as fixed effect and second-order Legendre polynomials of age as fixed curves for each generation by line and also as random curves for additive genetic and permanent environment effects. Different residual variances were used for the first and second half of the test period. 3-trait analyses for DFI, WT, and BF and single-trait analyses for LMA were run by sex. For boars from 90 to 210 d of age, estimated heritability of DFI and WT had S-shaped increasing trends, but for BF and LMA, estimates initially increased until 200 d and then decreased. For gilts, estimated heritability of WT was constant across age but initially increased and then remained constant for DFI, BF, and LMA. In generation 5, compared with CTRL boars, LRFI boars had lower average genetic curves for DFI and WT, especially towards the end of the test period; estimated line differences (CTRL-LRFI) for DFI and WT were -31 g/d and -7 g at 90 d and 209 g/d and 4384 g at 210 d. LRFI boars also tend to have lower BF and LMA at the end of the test period. In conclusion, LRFI selection has resulted in a lower feed intake curve toward maturity and a slightly lower body weight curve.

Key Words: longitudinal analysis, pigs, residual feed intake

413 Impact of genetic social interactions on relationships between average daily gain and feeding pattern in pigs. C. Y. Chen*¹, I. Misztal¹, S. Tsuruta¹, W. O. Herring², J. Holl², and M. Culbertson², ¹*University of Georgia, Athens,* ²*Smithfield Premium Genetics Group, Rose Hill, NC.*

The objective was to examine social genetic effects on correlations between average daily gain (ADG, g), daily feed intake (DFI, g), daily feeder occupation time (DOT, min), and daily feeding rate (DFR, g/min). A total of 547 Duroc boars were housed in 41 pens (size=12 to 15 pigs, area=14.3 m²), each equipped with one FIRE feeder and allowed *ad libitum* feeding. Traits were averaged over the entire test period from about 103 to 158 d of age and weight from 41 to 92 kg. Social genetic effects (including, excluding), pen (random, fixed) and linear covariates (pen sizes and initial age or weight) were fitted differently in single trait animal models for ADG and feeding pattern traits. Fixed effect of year and random effect of litter were also in the model. Variance components were estimated by REML. Initial results for ADG indicated confounding of social genetic effects and other effects (e.g. litter and pen). Therefore, six sets of parameters for ADG (heritability about 0.19) were evaluated based on estimates in literature with variance components scaled appropriately. Positive and negative signs of direct-social genetic covariances were interpreted as heritable cooperation and competition. Egoistic and altruistic pigs were classified as pigs with higher direct and social genetic values, respectively. Estimates of heritability were 0.18, 0.38, and 0.42 for DFI, DOT, and DFR. Correlations of estimated breeding values between ADG and DFI, DOT, and DFR were 0.46, 0.04, and 0.29 for egoistic pigs. With cooperation for altruistic pigs, those correlations were 0.36, 0.02, and 0.25. With competition for altruistic pigs, the slow eating rate ($r = -0.31$) was considered as a consequence of eating during less busy hour of feeding. The decreased feed intake ($r = -0.53$) indicated that altruistic pigs fail to compensate for the competition.

Key Words: feeding behavior, genetic correlation, social interactions

414 Genetic relationships of individual pig birth weight with weaning weight, off-test weight, feed intake, backfat and loin depth. J. S. Fix*¹, J. W. Holl², W. O. Herring², J. P. Cassady¹, C. Maltecca¹, and M. T. See¹, ¹*North Carolina State University, Raleigh,* ²*Smithfield Premium Genetics Group, Rose Hill, NC.*

Studies have shown low birth weight pigs are poorer performing and less likely to survive to harvest. The objective was to examine the potential for selection of individual pig birth weight and its genetic relationships with performance traits. Variance components were estimated using Large White (LW) and Landrace (LR) for birth weight (BWT) (127,188; 93,273), weaning weight (WW) (105,760; 78,131), off-test BW (OTW) (45,278; 42,407), ADFI (2,959; 1,914) backfat depth (BF) (26,842; 25,858) and loin depth (LD) (26,789; 25,840) from data provided by Smithfield Premium Genetics. Cross fostering (12.6%) was completed within 24 h of birth. Pigs were weaned at 21.7±0.01 d and removed from test at 171±0.02 d of age. Pigs with ADFI data were fed using FIRE® feeders during the last portion of test period. Breed specific 6 trait models were used for analyses. Models included fixed effects of sex, farm, parity (birth and nurse sow), cross foster status, and contemporary group (BWT and WW: farrowing group (yr-mo); OTW, LD and BF: off-test group (yr-wk); ADFI: contemporary group (sex-yr-wk)); covariates of number of fully formed pigs (linear and quadratic), wean age (linear and quadratic), off-test age, OTW, ADFI; random effects of animal, maternal (birth dam), litter (birth or nurse). Analyses were conducted using GIBBS2F90 and POSTGIBBSF90 with 100,000 cycles, burn-in period of 20,000 and every 20th sample stored thereafter. Direct heritability estimates (LW, LR): BWT (0.06, 0.06), WW (0.11, 0.08), OTW (0.25, 0.29), BF (0.52, 0.45), LD (0.33, 0.25), ADFI (0.30, 0.31). Maternal heritability estimates (LW, LR): BWT (0.12, 0.11), WW (0.10, 0.08), OTW (0.09, 0.09), BF (0.08, 0.08), LD (0.07, 0.07), ADFI (0.17, 0.16). Direct genetic correlations (LW, LR) between BWT and WW,

OTW, BF, LD, ADFI: (0.54, 0.54), (0.48, 0.55), (-0.23, -0.16), (-0.19, -0.01) and (0.11, 0.24), respectively. Estimated direct heritability for BWT was low. Low direct heritability estimates for BWT combined with high favorable genetic correlations with OTW suggest birth weight could be increased through selection for OTW.

Key Words: genetic parameters, birth weight, performance traits

415 Breed differences in swine temperament and its phenotypic relationship with performance. C. L. Yoder*¹, C. Maltecca¹, J. P. Cassady¹, S. Price², and M. T. See¹, ¹North Carolina State University, Raleigh, ²Ivey Spring Creek Farms, Goldsboro, NC.

Nucleus populations of Chester White (CW), Duroc (D), Landrace (L), and Yorkshire (Y) boars and gilts (n=2466) were used to estimate breed differences for temperament and its relationship with performance. Backfat (BF), loin depth (LD), off-test weight, estimated percent lean (LEAN), and three temperament scores: loading score (LS), scale score (SS), and vocal score (VS) were recorded. All scores ranged from 1 (calm) to 5 (highly excited). While loading into the scale LS was recorded, SS and VS were recorded while in the scale. Temperament scores were evaluated as categorical traits with a statistical model including fixed effects of breed, sex, farm, date of scoring, and off-test weight as a covariate. Statistical models for BF, LD, off-test weight, and LEAN included fixed effects of breed, sex, farm, LS, SS, VS, and appropriate interactions. Traits BF, LD, and LEAN were adjusted to the mean off-test weight (116.6 ± 0.54 kg). Breed differences for LS, SS, and VS were estimated as odds ratios. The odds of a higher LS were greater (1.33; P < 0.05) for L vs. D. CW were more likely (P < 0.01) to have higher SS than D (2.18) and Y (1.85), respectively. Landrace had a greater (P < 0.01) probability of a higher SS and VS compared to CW (1.52, 1.95), D (3.31, 4.99) and Y (2.80, 2.15). For VS, CW were 2.56 (P < 0.01) times more likely to be higher than D. Pearson's Correlations (P < 0.01) for SS with VS, BF, LD, off-test weight and LEAN were 0.29, -0.18, -0.10, -0.15 and 0.09, respectively. Pearson's Correlations for VS with off-test weight and BF were -0.07 and -0.11, respectively. An increase of one SS resulted in 0.87 ± 0.09 mm less BF (P < 0.01), 0.71 ± 0.13 mm less LD (P < 0.01), and 1.57 ± 0.21 kg less off-test weight (P < 0.01). Landrace were more excited and vocal in the scale than Chester White, Duroc and Yorkshire. Landrace were more difficult to load than Duroc. Chester White were more excited in the scale than Duroc and Yorkshire, and more vocal than Duroc. Pigs with lower SS were heavier, fatter, and had greater loin depth.

Key Words: pigs, breed, temperament

416 Genetic parameters for litter traits and piglet survival in Norsvin Landrace. B. Zumbach*¹, P. Madsen², and B. Holm³, ¹Norsvin, Hamar, Norway, ²Aarhus University, Tjele, Denmark, ³Norsvin USA, Rochester, MN.

The study examined the genetic background of piglet mortality both as a litter trait and as a trait of the individual piglet in the Norsvin Landrace. Data included 20,531 and 7,332 1st and 2nd parity litters, respectively, and 229,651 piglets from 17,822 1st parity sows collected from 2001 to 2008. Litter traits analyzed were # piglets born alive (LB), # stillborn piglets (SB), # piglets dying during the suckling period (DS), total # piglets dying until weaning (TD), # weaned (W), within litter SD at 3 wk (SD_LW3), and litter weight at 3 wk corrected by # piglets weighed at 3 wk (LW3). Individual survival was measured at birth, after birth

until the age of 3wk, and at 3 wk. Heritability (h²) estimates for litter traits in 1st and 2nd parities were 0.11±0.01 and 0.10±0.02 for LB, 0.08±0.01 and 0.09±0.02 for SB, 0.07±0.01 and 0.05±0.01 for DS, 0.11±0.01 and 0.11±0.01 for TD. Based on h² estimates, TD is as well apt as a selection trait as LB. Genetic correlations (rg) between LB and SB in 1st and 2nd parity were -0.04±0.10 and 0.29±0.17, between LB and DS 0.66 ±0.06 and 0.47±0.12; rg between TD and SB in 1st and 2nd parity were 0.75±0.05 and 0.79±0.08, between TD and DS 0.90±0.02 and 0.92±0.03. While selection for LB increases DS, selection for low TD should reduce both, SB and DS. In 1st and 2nd parity rg between LB and W were 0.79±0.04 and 0.80±0.06; rg among TD, W and LW3 were not significantly different from 0 in both parities; rg between SD_LW3 and LW3 were 0.54±0.07 and 0.43±0.12 in 1st and 2nd parity; rg between SD_LW3 and TD was slightly positive. Selection for LB increases efficiently W at the cost of TD. LW3 as a mother ability does not counteract this relationship. Direct h² for individual piglet survival was about 2% from birth to 3 wk. Maternal h² decreased from birth (2.1%) to 3 wk (1.4%). Total h² was about 3% from birth to 3 wk. The rg between direct and maternal genetic effects were not significantly different from 0. Sow and piglet genotype contribute to piglet survival.

Key Words: piglet survival, genetic parameters, sow productivity

417 Marker assisted selection using simulated IGF2 gene in Canadian Landrace. M. Jafarikia*, B. Sullivan, and L. Maignel, Canadian Centre for Swine Improvement, Ottawa, ON, Canada.

Marker Assisted Selection (MAS) can increase the accuracy of selection in comparison to accuracy from conventional Best Linear Unbiased Prediction (BLUP). One of the major genes in the pig is Insulin-like growth factor 2 (IGF2) which has a large effect on muscle mass. The objective of this study was to investigate the advantage of using IGF2 paternal alleles on the accuracy of selection in MAS using simulated data. A population with almost one million pigs was simulated using the QMSim package (Schenkel and Sargolzaei, 2008). This simulated population was based on the Canadian Landrace population which existed in the national database managed by the Canadian Centre for Swine Improvement (CCSI). Data was simulated using heritability of 25% and with 15% of the phenotypic variance under the effect of the simulated IGF2 gene. Selection was at random because when simulation was performed with a major gene such as IGF2 and selection was by using BLUP, the major gene became fixed after a few generations. The proportion of genotyped animals was approximately 0.05% of the population and mostly chosen from recent generations. A software program was developed for estimation of genotype probabilities of the entire pedigree using the genotype information of relatively few genotyped animals. Estimated paternal allele probabilities of the simulated IGF2 gene were used as a covariate in the model. The observed accuracy of Estimated Breeding Value (EBV) for BLUP and MAS for genotyped animals were 71% and 80%, respectively.

Key Words: IGF2, marker assisted selection, BLUP

418 A DNA based test for evaluating and improving pork colour in Canadian pigs. B. Uttaro*¹, M. Jafarikia², W. Van Berkel³, S. Wyss², B. Sullivan², and S. Chen⁴, ¹Agriculture and Agri-Food Canada, Lacombe Research Centre, Lacombe, Alberta, Canada, ²Canadian Centre for Swine Improvement, Ottawa, Ontario, Canada, ³Western Swine Testing Association, Lacombe, Alberta, Canada, ⁴University of Guelph, Labora-

atory Services Division, Guelph, Ontario, Canada.

Meat colour is an important characteristic of pork quality but quantitative selection requires sacrifice of animals. Meat colour and single nucleotide polymorphisms (SNPs) of exon 14 and partial codon sequences of SLC44A3 gene of 500 pigs were used to examine the association of this gene with meat colour and change of colour during storage. Significant differences ($p \leq 0.01$) were found among breeds for subjective colour (NPPC; Scale 1-6). Duroc (4.45 ± 0.07) and Lacombe (4.49 ± 0.09) had significantly darker loins than other breeds: Yorkshire (4.16 ± 0.07), Landrace (3.94 ± 0.08) and crossbreds (3.98 ± 0.06). Females (4.25 ± 0.05) were darker on average than castrates (4.16 ± 0.06). Thirteen SNPs were found in the SLC44A3 gene. Four of the 13 SNPs were in the coding region but only one resulted in an amino acid change. Three SNPs at base pair (bp) positions of 234, 381 and 386 were selected for analysis based on the following criteria: minor allele frequency above (5%) and no confounding with other SNPs. Defining the haplotypes of the three SNPs revealed four different haplotype alleles in the sampled pigs. SNP at bp 386 showed significant association with NPPC colour ($p \leq 0.05$), and a significant effect of haplotypes was also found within breeds ($p \leq 0.05$). Loin colour (Minolta CIE L*, a*, b*) was recorded on days one, four and seven post-mortem, and colour differences calculated. The greatest change in L* was observed during dark storage (days 1 to 4) with little change during storage in light (days 4 to 7). A significant difference between L* values as well as change in L* was observed among breeds ($p \leq 0.05$) and gilts tended to remain darker than castrates.

Key Words: meat colour, SLC44A3 gene, pork

419 Estimation of the IGF2 effect on backfat and lean muscle depth in Canadian Landrace. M. Jafarikia*, B. Sullivan, L. Maignel, and S. Wyss, *Canadian Centre for Swine Improvement, Ottawa, ON, Canada.*

IGF2 is a paternally expressed gene located at the distal tip of porcine chromosome 2. Allelic variation of this gene is associated with 15-30% of the phenotypic variation in muscle mass and 10-20% of the phenotypic variation in backfat thickness. Canadian Landrace with approximately one million records was used to investigate the proportion of the phenotypic variance in backfat thickness and muscle mass explained by IGF2. The genetic variance was estimated as $\sigma_{IGF2}^2 = 2pq\alpha^2$ where σ_{IGF2}^2 , p, q and α represent IGF2 variance, frequency of paternal A, frequency of paternal G and allele substitution effect respectively. The traits under study included backfat and lean muscle depth adjusted to 100 kg live weight. The statistical models included the probability of inheriting the IGF2 allele from sire as a covariate along with contemporary group and sex as fixed effects. The GLM procedure of SAS was used for the analysis. In order to determine the paternal allele origin, a genotyping probability software was developed to estimate the paternal allele probabilities of all the animals in the pedigree using information from

a limited number of genotyped animals from recent generations. The numbers of AA, AG and GG genotypes were 456, 304, 38, respectively. Using the homozygote genotypes (AA, GG), the total number of known paternal alleles was 494. The number of animals with known paternal alleles increased to 36,371 after using the genotyping probability estimation software. The estimated paternal A over G allele substitution effects were -1.28 mm and +2.05 mm and the estimated variances were 0.61 mm² and 1.55 mm² for backfat and lean muscle depth, respectively. The estimated variances were 14% and 11% of the observed phenotypic variance of backfat and lean muscle depth, respectively. The observed variance for backfat corroborated the range reported in previous studies but for lean muscle depth, a lower variance was found than the range reported in previous studies on other swine populations.

Key Words: IGF2, variance, backfat and lean muscle depth

420 Proximal promoter of the pig HMGCR gene: Structural and functional study. A. Cánovas*¹, R. Quintanilla¹, J. M. Reecy², M. Marqués³, and R. N. Pena¹, ¹IRTA. *Genética i Millora Animal., Lleida, Spain*, ²Iowa State University, Ames, ³INDEGA. *Universidad de León, León, Spain.*

HMGCR is the rate-limiting enzyme in the biosynthesis of cholesterol. We have studied the role of the HMGCR gene in pig lipid metabolism by means of expression and structural analysis. Animals came from a high intramuscular fat commercial Duroc line used in the production of fine quality cured ham. The experiment was based on a half-sib design, generated by mating five parental boars with 385 females and using only one male offspring per litter. We characterized the mRNA expression profile of the porcine HMGCR in six tissues involved in lipid metabolism. HMGCR is expressed at high levels in the duodenum and back fat. In contrast, heart and liver had lower HMGCR mRNA expression levels. In addition, we amplified the proximal promoter (600 bp) of this gene and identified two SNP at positions -239 and -16 bp. In silico analysis of the distal and proximal promoter SNPs revealed that they may potentially affect the binding of myogenic bHLH family members (e.g. myoD, myogenin, myf5 and myf6), and Ets-2 family members, respectively. The pig HMGCR promoter region exhibited a high level of conservation (72 to 86% sequence identity across species) with conserved motifs for several transcription factors. Furthermore, we evaluated the interaction between HMGCR:c.-239G>T promoter SNP and promoter activators and inhibitors in hepatic (HepG2) and muscle (C2C12) cell lines. In C2C12 and HepG2 transfected cells, we observed that insulin (1 μ M), increased the transcriptional activity of the HMGCR G allele promoter, whereas 25-hydroxycholesterol (12.5 μ M) also inhibited the transcriptional activity of the G allele promoter. Our findings indicate that HMGCR may play an interesting role in the genetic variability of lipid and cholesterol metabolism in pigs.

Key Words: pig, meat quality, lipid metabolism

Dairy Foods: Dairy Foods 1

421 Value-added components derived from whey. W. Modler*, *Agriculture Canada (formerly, Centre for Food & Animal Research, Ottawa, Ontario, Canada), Kemptville, Ontario, Canada.*

Initially, whey products, such as roller dried whey powder, had poor functionality and limited food product application. Technological advances in evaporation and spray drying, along with the development of demineral-

ization and electro dialysis technology, led to further improvements in functionality in whey-based powders. The next generation of products consisted primarily of WPC and WPI prepared primarily through the development of membrane technology, particularly microfiltration. More recently, improvements have provided cleaner separations, improved membrane performance and durability. In addition, nanofiltration and microfiltration have provided additional tools for whey processors for