190 Effect of feeding reduced crude protein and phosphorus diets on pig compartmental and whole body mineral masses and accretion rates.

R. Hinson*[1], B. Hill[1], M. Walsh[1], D. Sholly[1], S. Trapp[1], J. Radcliffe[1], A. Sutton[1], A. Schinckel[1], B. Richert[1], G. Hill[2], and J. Link[2], [1]*Purdue University*, *West Lafayette, IN*, [2]*Michigan State University*, *East Lansing*.

Pigs (Exp. 1 = 98 and Exp. 2 = 148) were allotted by sex and BW to determine the effects of feeding a control (CTRL), corn-SBM based diet or a low nutrient excretion (LNE) diet, with reduced CP + synthetic amino acids, low phytic acid corn, and phytase, on carcass, visceral, and blood mineral contents and masses. Pigs were split-sex phase fed, three nursery diets for a 5-wk nursery period (Exp. 2) and two grower and two finisher diets for a 16-wk grow-finish (G-F) period (Exp. 1 and 2). Pigs were housed two-five pigs/pen and five pens/sex/treatment (trt) in G-F. Individual pig weights and pen feed consumption were recorded bi-weekly. Five or six pigs/sex were harvested at the start of each experiment to determine initial composition and six pigs/sex/trt were harvested at the end of the nursery period (Exp. 2) and 10 pigs/sex/trt were harvested at wk 8 and 16 of the G-F period (Exp. 1 and 2) for determination of tissue pool compositions. Tissues were assayed for: DM, Ash, N, P, Ca, Zn, Fe, Cu, Mg, and Mn. There were no differences in nursery, grower, or finisher whole body tissue mass between treatments. However, total mass and accretion rates of P, Ca, and Mg decreased and Zn and Mn increased when LNE diets were fed during the nursery period (Exp. 2 only; $P < 0.05$). Grower period ash, P, Ca, Mg, and N (Exp. 2) masses and accretion rates of ash, P, Ca, Mg, Fe (Exp. 1), Zn (Exp. 2), Cu (Exp. 2) decreased when pigs were fed LNE diets ($P < 0.05$). During the finisher period, whole body ash (Exp. 2), P, Ca, Mg, N (Exp. 2) decreased and accretion rate of Zn (Exp. 2) increased ($P < 0.05$) when pigs were fed LNE diets. Overall, total tissue accretion rate was not different between treatments, however whole body accretion rates of ash (Exp. 2), P, Ca, Mg, and N (Exp. 2) were decreased when pigs were fed LNE diets from weaning to market. There were differences in individual mineral accretion rates by the different tissue pools at different phases of the pigs growth cycle, however, the carcass is the largest pool and has the greatest influence on the whole body mineral accretion rates.

Key Words: Pigs, Phosphorus, Whole Body Mineral Accretion

191 Pigs housed under deep litter and conventional housing systems have different growth paths to a similar carcass composition.

D. Suster[1], D. J. Henman[2], D. J. Cadogan[3], and F. R. Dunshea*[1,4], [1]*Primary Industries Research Victoria*, *Werribee, Victoria, Australia*, [2]*QAF Meat Industries*, *Corowa, NSW, Australia*, [3]*Feedworks*, *Hamilton, Qld, Australia*, [4]*University of Melbourne*, *Parkville, Victoria, Australia.*

Three replicates of 120 boars and gilts were weaned into deep litter (rice hulls and straw) pens with an additional 60 pigs of each sex weaned into groups of 20 housed under conventional systems (raised weaner cots and then concrete flooring). All pigs were located in the same airspace with a stocking density of 0.65 pigs/m^2. Randomly allocated focus pigs were used for dual energy X-ray absorptiometry analyses at various time points to determine body composition. In the immediate post weaning period, conventionally housed pigs ate more (199 vs. 170 g/d, $P < 0.01$) and grew faster than deep litter pigs (189 vs. 154 g/d, $P < 0.05$). However, feed intake was higher ($P < 0.05$) in pigs housed in the deep litter system between 8 and 85 days of age. Over the final growth phase from 114 until 149 days of age, feed intake (2,726 vs. 2,551 g/d, $P < 0.05$) and daily gain (897 vs. 808 g/d, $P < 0.05$) were higher in conventionally-housed pigs. Over the finisher phase, gilts consumed more feed (2,379 vs. 2,289 g/d, $P < 0.05$) than boars probably because of social interactions between boars housed in groups. Pigs raised in deep litter systems deposited more ($P < 0.05$) lean and fat tissue than conventionally housed pigs up until about 60 and 80 days of age, respectively after which time the conventionally housed pigs deposited more of each tissue. The rate of lean tissue gain decreased in gilts but remained elevated in boars over the latter stages of the study. Hot carcass weight and backfat were not affected by either housing system. These data suggest that under the same relatively high stocking density there is little difference in the final carcass composition and overall growth performance of pigs housed under either conventional conditions or in deep litter. However, there were quite clear differences in the pattern of growth and tissue deposition with the deep litter pigs initially eating more and growing faster before slowing down.

Acknowledgements: Supported in part by Australian Pork Limited

Key Words: Deep Litter, Pig, Body Composition

Physiology and Endocrinology II

192 Differential expression of superoxide dismutases (SODs) in bovine corpus luteum during estrous cycle and pregnancy.

R. K. Putluru*, C. N . Lee, and Y. S. Kim, *University of Hawaii at Manoa*, *Honolulu.*

In the tropics, lower conception rates are common in dairy cattle. While many factors contribute to a successful pregnancy, an important ingredient is a healthy functional corpus luteum (CL) for the maintenance of pregnancy. Previous studies in rabbits have shown that the generation of reactive oxygen species (ROS) including superoxides may play a role in the regression of CL and subsequent luteolysis. Studies in pregnant rats also showed that the up-regulation of superoxide dismutase (SOD), a ROS scavenging enzyme, is involved in the rescue of the CL from luteolysis. The objective of this study was to investigate the presence and expression of different types of SODs in the bovine CLs at different stages of the estrus cycle (1st, 2nd, 3rd and 4th) and pregnancy. CL samples (n=155) were collected from a local slaughter house and classified into different stages based on morphological classification. CL samples (0.25 gms) were homogenized in 20 ml of PBS buffer. Protein concentration of each CL was measured by Lowry method, and equal amount of protein from each sample was subjected to SDS-PAGE. The fractionated proteins were transferred onto a nitrocellulose membrane and immunoblotted against commercially available anti-MnSOD and anti-Cu/ZnSOD antibodies. The Mn-SOD and Cu/Zn-SOD were quantified using densitometry analysis. Mn-SOD was highly expressed in the pregnant CLs and 3rd and 4th stage CLs of the estrus cycle. In contrast, Cu/Zn SOD was equally expressed throughout the estrus cycle and pregnancy. Present results suggest that the Mn-SOD is probably involved in the maintenance of bovine pregnant corpus luteum.

Acknowledgements: We would like to thank local slaughter house staff and the local Dairy industry for their support.

Key Words: Superoxide Dismutase, Bovine Corpus Luteum, Estrus Cycle

193 Effects of changes in systemic progesterone in the first few days after ovulation on uterine retinol binding protein and folate binding protein gene expression in cattle.

R. McNeill[1,2], R. Fitzpatrick[1], J. Sreenan[1], and D. Morris*[1], [1]*Teagasc, Research Centre*, *Athenry, Co. Galway, Ireland*, [2]*National Diagnostics Centre, National University of Ireland Galway*, *Galway, Ireland.*

Low systemic progesterone in the first week after AI is associated with a low probability of embryo survival in dairy cows. Progesterone may affect embryo survival by altering uterine gene expression and ultimately uterine function. The objective of this study was to establish the relationship between systemic progesterone during the first week after AI and bovine uterine gene expression. Heifers (n=24) were blood sampled twice daily from the day of ovulation (day 0) and on the basis of their systemic progesterone concentrations were divided into high or low groups on day four. Half of each group was, in turn, supplemented with exogenous progesterone (CIDR) from day 4 to day 8, resulting in a total of four groups, low control (LC), high control (HC), low supplemented (LS) and high supplemented (HS). Uterine endometrial tissue was harvested post mortem on day 6 or day 8 and snap frozen in liquid nitrogen. The effects of changes in systemic progesterone on uterine gene expression was measured using candidate and global gene approaches. Data were analyzed as a 2 x 2 factorial using analysis of variance. High systemic progesterone concentration up to day 4 was associated with increased ($P<0.01$) uterine retinol binding protein (RBP) mRNA expression on day 6 but not on day 8. In contrast supplementation with exogenous progesterone between days 4 and 6 or days 4 and 8 did not alter RBP mRNA expression ($P>0.05$). There was a positive ($P<0.05$) linear relationship between progesterone and folate binding protein (FBP) mRNA expression on day 6 after ovulation but not on day 8. These results indicate that uterine gene expression is very sensitive to small changes in systemic progest-

erone in the first few days after AI. Suboptimal progesterone during the first few days after AI may therefore result in altered uterine gene and protein expression and increased embryo loss.

Key Words: Cattle, Uterus, Gene Expression

194 Withdrawn.

195 Hepatic gene expression profiling in cows with early postpartum ketosis using a bovine 13,000 oligonucleotide microarray.

J. J. Loor*, R. E. Everts, H. M. Dann, D. E. Morin, S. L. Rodriguez-Zas, H. A. Lewin, and J. K. Drackley, *University of Illinois*, *Urbana*.

We used a simple model for induction of ketosis (K) in early postpartum Holstein cows to examine liver gene expression profiles using microarray technology. Cows had ad libitum (142% of NRC requirements) or restricted (85% of requirements) DMI during the dry period. All cows were fed a common lactation diet after parturition. At 4 DIM, 7 cows classified as healthy after a physical examination were fed at 50% of DMI at d 4 from d 5 to signs of K or until 14 DIM. Another group of 7 healthy cows served as controls (H). Liver was biopsied at 10-14 (K) or 14 DIM (H). A microarray consisting of 13,257 unique oligonucleotides (70-mers) was used for transcript profiling. Annotation was based on similarity searches using BLASTN and TBLASTX against human, mouse, and bovine UniGene databases, the human genome, and the cattle TIGR database. Cy3- and Cy5-labelled cDNA from liver and a reference standard were used for hybridizations (28 microarrays). Loess-normalized log-transformed ratios were used to detect differential expression. ANOVA using a False Discovery Rate of $P = 0.20$ identified 3,513 differentially expressed genes. Hierarchical clustering of those genes showed that relative expression between K and H differed by 37%. Ketosis resulted in 76 downregulated genes with expression levels 2-fold or higher. There were 37 upregulated genes with K showing expression levels 2-fold or higher. Genes with key functions in stress, inflammation, and signal transduction had <2-fold expression in cows with K. Ketosis resulted in >2-fold decrease in expression for 2 genes involved in fatty acid desaturation, 2 in acetyl-CoA metabolism, and 1 in intracellular triglyceride transport. Other downregulated genes (>1.5-fold) in K were associated with regulation of transcription, insulin signaling, cytokine-mediated signaling, urea cycle/metabolism, and gluconeogenesis. Our data show that altered hepatic function due to ketosis early postpartum is associated with complex changes in transcript expression patterns.

Key Words: Microarray, Dairy Cows, Ketosis

196 Mammary gene expression profiling in cows fed a milk fat-depressing diet using a bovine 13,000 oligonucleotide microarray.

J. J. Loor*[1], L. Piperova[2], R. E. Everts[1], S. L. Rodriguez-Zas[1], J. K. Drackley[1], R. A. Erdman[2], and H. A. Lewin[1], [1]*University of Illinois*, *Urbana*, [2]*University of Maryland*, *College Park*.

We studied the effects of a milk fat-depressing diet (MFD) on mammary gene expression patterns using microarray technology. Six lactating Holstein cows were randomly assigned to control (CON) or MFD (HCO; 25% forage, 70% concentrate, 5% soybean oil) in a single reversal design for 3-wk periods. Mammary tissue was biopsied in wk 3 of each period. A microarray consisting of 13,257 unique oligonucleotides (70-mers) was used for transcript profiling. Annotation was based on similarity searches using BLASTN and TBLASTX against human, mouse, and bovine UniGene databases, the human genome, and the cattle TIGR database. Cy3- and Cy5-labelled cDNA from mammary and a reference standard were used for hybridizations (24 microarrays). Loess-normalized log-transformed ratios were used to detect differential expression. ANOVA using a False Discovery Rate of $P = 0.20$ identified 2,175 differentially expressed genes. Hierarchical clustering of those genes showed that relative expression between CON and HCO differed by 60%. A total of 241 genes were downregulated ≥2-fold and 150 were upregulated ≥2-fold with HCO. Among genes associated with fatty acid metabolism 18 were downregulated and 5 were upregulated ≥1.5-fold with HCO. Twenty-six transcription factors were differentially expressed with 8 being downregulated and 3 upregulated ≥1.5-fold with HCO. Expression for *SREBF1* did not differ. Results confirmed HCO downregulated (≥1.5-fold) *FASN* and *ACACA* but also *SCD*, *LPL*, *FABP3*, *ACAS2*, *SLC27AC*, and *ACSL1* among other lipogenic genes. Differentially expressed genes with HCO included 21 associated with insulin action, 24 with glucose metabolism, and 27 with cytokine action. Mammary from HCO had >3-fold downregulation for a gene encoding a novel nuclear protein responsible for normal triglyceride synthesis and induction of key lipogenic genes (e.g. *PPARs*, *CEBPs*) in mice. Our data show that milk fat depression is associated with complex changes in mammary transcript expression patterns.

Key Words: Microarray, Dairy Cow, Milk Fat Depression

197 Transcriptional regulation of mammary gland sensitivity to thyroid hormones during the transition from pregnancy to lactation.

A. V. Capuco*, E. E. Connor, and D. L. Wood, *USDA-ARS, BARC, Bovine Functional Genomics Laboratory*, *Beltsville, MD*.

Thyroid hormones are galactopoietic and appear to assist in establishing the mammary gland's metabolic priority during lactation. Expression patterns for genes that can alter tissue sensitivity to thyroid hormones and thyroid hormone activity were evaluated in the mammary gland and liver of Holstein cows at dry-off, 7, 25, 40 and 53 days into the dry period, and 14 and 90 days into lactation. Transcripts for the three isoforms of iodothyronine deiodinase, type I (*DIO1*), type II (*DIO2*) and type III (*DIO3*) and transcripts for the thyroid hormone receptors alpha1 (THRa1), alpha2 (THRa2) and beta1 (THRb1) were evaluated. Tissues for this purpose were obtained at slaughter from 3 to 6 cows per physiological state. The *DIO3* is a 5-deiodinase that produces inactive iodothyronine metabolites, whereas *DIO1* and *DIO2* form the active thyroid hormone, triiodthyronine, from the relatively inactive precursor, thyroxine. Low copy numbers of *DIO3* transcripts were present in mammary gland and liver during all physiological conditions. *DIO2* was the predominant isoform expressed in mammary gland and *DIO1*, the predominant isoform expressed in liver. Quantity of *DIO1* mRNA in liver tissues did not differ ($P>0.05$) with physiological state, but tended to be lowest during lactation. Quantity of *DIO2* mRNA in mammary gland increased during lactation ($P<0.05$), with copy numbers at 90 d of lactation 6-fold greater than at days 25 and 40 of the dry period. When the ratios of *DIO2/DIO3* were evaluated, the increase was even more pronounced (>100-fold). Quantity of THRb1 mRNA increased during lactation, whereas THRa1 and THRa2 did not vary with physiological state ($P>0.05$). Data support a role for increased expression of mammary THRb1 and *DIO2* as means to increase thyroid hormone activity in the mammary gland during lactation.

Key Words: Mammary Gland, Iodothyronine Deiodinase, Thyroid Hormone Receptor

198 Influence of parity, seasonal acclimatization, and recombinant bovine somatotropin (rbST), on diurnal patterns of physiological responses to thermal stress in cattle.

B. C. Pollard*, M. D. Estheimer, M. E. Dwyer, P. C. Gentry, E. L. Annen, D. A. Henderson, C. M. Stiening, and R. J. Collier, *University of Arizona*, *Tucson*.

Twelve mid-lactation, multiparous (M) Holstein cows and twelve late-gestation, nulliparous (N) Holstein heifers were assigned to one of two studies in January (W) or June (S) of 2004. Animals were balanced for parity and rbST treatment then were randomly assigned to one of two environmental rooms and were exposed to thermoneutral (TN) or two heat stressing environments (heat stress [HS]; heat stress plus solar [HSS]) in three, fourteen day periods arranged in an incomplete crossover design. Physiological data (sweating rate [SR], respiration rate [RR], rectal temperature [RT] and surface temperature [ST]) were

collected on d 6 of each period at bihourly intervals for analysis over a 24 h day. Data was analyzed using a repeated measures mixed model that included main effects, time fitted as a heterogenous first order variance-covariance structure, and appropriate two-way and time interactions. Overall, rbST increased SR (P=0.09), but had no effect on ST (P=0.64), RT (P=0.31), or RR (P=0.95). There was an effect of rbST within season, as rbST produced greater RR in W than in the S (P<0.10). For seasonal comparisons, SR did not differ between S and W (P=0.94), but RT (P=0.07), ST (P<0.001) and RR (P<0.01) were higher in S than W. Also, ST, RT, and RR were increased in M compared to N (P<0.001) although M and N displayed no differences in SR (P=0.35). Highest SR and RR were measured in cows exposed to HSS. Environment by period interactions indicate that previous heat exposure within the trial diminishes the response to heat stress in later periods implicating acclimation to heat during the course of the study. Results indicate that sweating rate in cattle is influenced by rbST. These data indicate that rbST does not increase stress load in dairy cattle, and commercial use of rbST during period of heat stress is possible in well-managed herds.

Key Words: Bovine Somatotropin, Heat Stress, Dairy Cattle

199 The influence of parity, acclimatization to season, and recombinant bovine somatotropin (rbST) on diurnal patterns of prolactin and growth hormone in Holsteins exposed to heat stress. B. C. Pollard*[1], M. D. Estheimer[1], M. E. Dwyer[1], P. C. Gentry[1], W. J. Weber[2], E. Lemke[2], L. H. Baumgard[1], D. A. Henderson[1], B. A. Crooker[2], and R. J. Collier[1], [1]*University of Arizona*, *Tucson*, [2]*University of Minnesota*, *Saint Paul*.

Twelve mid-lactation, multiparous (M) cows and twelve late-gestation, nulliparous (N) heifers were assigned to one of two studies in January (W, 6M and 6N) or June (S, 6M and 6N) of 2004. Animals were balanced for parity and rbST treatment, randomly assigned to one of two environmental rooms and exposed to thermoneutral (TN) or two heat stressing environments (heat stress [HS]; heat stress plus solar [HSS]) in three, 14 day periods in an incomplete crossover design. Sweating rate, (SR), respiration rate (RR), rectal temperature (RT) and surface temperature (ST) were measured and blood samples were collected on d 6 of each period at either hourly or bihourly intervals for 24 h. Data was analyzed using a repeated measures mixed model which included main effects, time fitted as a heterogenous first order variance-covariance structure, and appropriate two-way and time interactions. Means were declared different when P<0.05. Serum growth hormone (GH) was elevated by rbST, and was greater in W and M than in S and N. Serum GH was less in HS and HSS than TN. There were no interactions of GH and time and no observed diurnal change in GH. Parity had no effect on serum prolactin (PRL), but PRL was increased in HS and HSS compared to TN and the rise in PRL was greater in W than S. Spearman rank correlations indicated positive relationships between PRL and several variables (SR; r=0.42; RT, r=0.307; RR r=0.480, and ST, r=0.476) but GH was only correlated with RT (r=0.117). Results suggest GH and PRL have important roles in the regulation of physiological parameters related to heat stress.

Key Words: Prolactin, Growth Hormone, Heat Stress

200 Leaking cows: Physiological and anatomical reasons. M. Rovai*, M. Kollmann, and R. M. Bruckmaier, *Techn. Univ. Munich*, *Germany*.

Milk leakage (*I. lactis*) is considered as an important factor of infection risk. The aim of this study was to identify the main possible causes of leaking in two dairy farms differing in breed but with similar production level: Herd A: Red Holstein cows (n=30); 28kg/d and Herd B: BraunviehxBrown Swiss cows (n=15); 26kg/d. Herd A was classified into *I. lactis* and Control group, whereas Herd B was only a Control group. For statistical analysis, the Proc Mixed procedure of SAS was used. Effects of parity number, degree of udder filling and udder diseases were also analyzed. Milk samples (foremilk and main milk fraction) were collected twice, as well as the milk leakage (*I. lactis* group) at different intervals from 0-5 h prior to milking. Teat traits (external and internal), milk flow, milk fractions, intramammary pressure (IMP), and oxytocin (OT) blood pattern were also obtained. Fat content did not present differences between milk leakage and foremilk. However, fat increased (P<0.001) during milking in response to milk ejection (+2.64% for main milk samples). *I. lactis* cows had about 9% shorter sphincters than Control groups while all other teat traits did not present any differences. Milk flow curves showed higher (P<0.001) milk yield, peak and average flow rate for *I. lactis* contrasting with both Control groups. Quarter cisternal yield of *I. lactis* tended to be superior (P=0.064; 0.49 vs. 0.30 and 0.22kg for *I. lactis* and Control group from Herd A and Herd B, respectively), while percentage of cisternal and alveolar milk was similar between groups. The higher IMP (P<0.001) for *I. lactis* group both before and after udder preparation (*I. lactis*: 4.0 and 6.4kPa, Control: 2.0 and 5.0kPa; respectively) could explain this phenomenon. The OT blood concentration was low until the start of udder preparation, and increased in response to the milking stimulus reaffirming the hypothesis of absence of milk ejection in leaking cows. Overall, leaking causes were not related to milk production, incidence of mastitis, age or stage of lactation. Milk losses are likely due to the large amount of cisternal milk, which creates pressure and leaking, and consequently does not represent milk ejection.

Key Words: Leaking Cows, Dairy Cows, Milk Losses

201 Effect of extended lactation on fertility of divergent Holstein-Friesian genotypes within a seasonal pasture-based dairy system. C. Burke*, J. Roche, and E. Kolver, *Dexcel Limited*, *Hamilton, New Zealand*.

Holstein-Friesian dairy cows with a predominance of North American (NA) ancestry exhibit excessive depletion of body condition score (BCS) and reduced pregnancy rates when constrained by managerial decision rules within a seasonal pasture-based system. However, the NA genotype does have potential for superior lactation persistency as compared with New Zealand bred (NZ) Holstein-Friesians. Reproductive characteristics are reported from a study that aimed to exploit this feature by relaxing the constraints of season and diet. The design was a 2 x 3 factorial with main effects of genotype (NA or NZ) and grain supplement (0, 3 or 6 kg DM/cow/d grain). Cows (n = 56) calved on 28 July 2003 (±3.5 d SEM) and were mated in October-November (Year 1). Pregnancy diagnosis was performed and pregnancies terminated in December 2003 with the intention of extending lactations to 670 d. All cows were mated again in October-November 2004 (Year 2). Cows were managed as a single group fed generously on pasture with high-energy grain supplements offered daily on an individual basis during each of the twice-daily milkings. Cows calved in similar BCS (5.8±0.2; 1 to 10 scale) but NA had a lower (P<0.05) BCS than NZ cows at PSM in Year 1 (4.0±0.3 vs. 4.5±0.2) and Year 2 (6.9±0.3 vs. 5.1±0.3). The net energy (NE_L) of milk production (MJ/d) per 100 kgBW was similar (P>0.1) among strains at PSM in Year 1 (16.9±0.4 MJd), but greater (P<0.01) in NA (11.1±0.7 MJ/d) as compared with NZ cows (7.8±0.7 MJ/d) at PSM in Year 2. Pregnancy rate by 42 d mating (PR42) in Year 1 was greater (P<0.01) in NZ (62%) as compared with NA cows (26%). Ultrasound examinations of the reproductive tracts 2 to 4 wks before PSM in Year 2 found mostly normal ovaries and uteri, consistent with cycling cows. The PR42 at Year 2 improved (P<0.05) for NA (52%) as compared with earlier in lactation but remained less (P<0.05) than NZ cows (76%). The NA-type cow was better suited to an extnded lactation system, but the reduced fertility of NA cows was only partially mitigated by removing the constraint of having to re-establish pregancy at 12 wks in lactation.

Key Words: Fertility, Genotype, Lactation

202 Localization of Interleukin-18 and its receptor in somatotrophs of bovine anterior pituitary gland. Y. Nagai*, T. Nochi, K. Watanabe, K. Watanabe, and T. Yamaguchi, *Tohoku University*, *Sendai, Japan*.

A pro-inflammatory cytokine, interleukin 18 (IL-18), induces intracellular expression of IL-1 and release of IL-6. IL-1 and IL-6 have been detected in anterior pituitary cells, suggesting that IL-18 is produced in anterior pituitary cells and serve as a mediator of immuno-endocrine regulation in anterior pituitary gland. In the present study, we addressed this hypothesis by investigating intracellular localization of IL-18 and its receptor in the bovine anterior pituitary gland. Twelve cattle of Japanese Black and Holstein were used. The anterior pituitary gland were freshly removed and subjected to RT-PCR, western bloltting, in situ hybridization and immunohistochemical analysis. Immuno-laser microdissection was performed to confirm mRNA expression in IL-18-immunnoreactive cells. IL-18 mRNA and protein was detected in the anterior pituitary tissue by RT-PCR and Western blotting. In situ hybridization showed that IL-18 mRNA were constantly localized in the anterior pituitary cells. Immunohistochemistry of IL-18 and specific hormones revealed the presence of IL-18 in bovine somatotrophs. Furthermore, the expression of GH mRNA in IL-18 immunoreactive cells was confirmed by immuno-laser microdissection. These results first demonstrated that somatotrophs produced IL-18. Subsequently, the distribution of IL-18 receptor alpha (IL-18R α) was investigated in the anterior pituitary gland to understand IL-18 signal among anterior pituitary cells. Bovine IL-18R α cDNA was partially sequenced and detected in the anterior pituitary gland by RT-PCR. Immunohistochemistry of IL-18R α, IL-18 and GH showed that IL-18R α was expressed in IL-18 immunoreactive cells and somatotrophs. In conclusion, we found that IL-18 and IL-18R colocalized in somatotrophs of bovine anterior pituitary gland. Our results suggest that IL-18 acts on somatotrophs as an immuno-endocrine mediator through autocrine pathway.

Acknowledgements: Grant-in-Aid for Scientific Research (B) (No.13460122) from the Ministry of Education, Science and Culture of Japan.

Key Words: IL-18, Somatotroph, Immuno-Endocrine

Production, Management and the Environment: Impact of Culling Rate on Dairy Profitability

203 Historical examination of culling of dairy cows from herds in the United States.

H. D. Norman* and E. Hare, *Animal Improvement Programs Laboratory, Agricultural Research Service, USDA*, *Beltsville, MD*.

Dairy producers need cows that reproduce, stay alive, and produce well, but information on culling rate and herd life has not always been readily available so that producers can minimize cow losses. A recent examination of cow survival in Dairy Herd Improvement herds provided information on culling rate since 1980. Cows were excluded if the herd discontinued testing during their productive period or they were sold for dairy purposes. Survival rates for individual parities were the fraction of cows with an opportunity to calve that did calve. Number of parities by breed and year of first calving was determined to provide an indicator of herd life before culling. Survival rates for second through eighth parities were 73, 50, 32, 19, 10, 5, and 2%, respectively, for Holsteins. Survival to second parity was 72% for Ayrshires, 69% for Brown Swiss, 66% for Guernseys, and 75% for Jerseys; corresponding survival to fifth parity was 22, 23, 15, and 26%. Although survival to second parity declined only slightly after 1980, survival to later parities dropped substantially. Survival rates for Holsteins were 77, 57, 39, 24, 14, 8, and 4% in 1980 for second to eighth parities but declined to 74, 49, 28, 16, 8, 4, and 1% in recent years. Mean number of parities declined from 3.2 for Ayrshires, 3.2 for Brown Swiss, 2.8 for Guernseys, 3.2 for Holsteins, and 3.4 for Jerseys that first calved in 1980 to 2.9, 2.9, 2.4, 2.8, and 3.2 for cows that first calved in 1992. Across calving years, about 36, 26, and 17% of Holsteins were first-, second-, and third-parity cows, respectively. Mean calving age ranged from 44 mo for Guernseys to 49 mo for Brown Swiss, a decline from earlier estimates, and recent years show a continuing decline. The increase in culling rate and subsequent reduction in mean calving age must be driven by dairy management choices rather than a decline in genetic merit of the population as genetic estimates indicate that substantial genetic improvement is being made in productive life.

Key Words: Culling, Herd Life, Survival

204 The impact of timing of the culling event on profitability in dairy herds.

R. Cady*, *Monsanto*, *St. Louis, MO*.

Every cow is eventually culled. Thus, it is not a question of if a cow will be culled, but rather when she will be culled. Culling is primarily an economic risk management practice, influenced by existing economic conditions, risk tolerance of the dairy management team, and dairy cattle management skills. The only exceptions to this would be loss due to death, theft, or cows that are simply too difficult to manage (eg. kickers).

Knowledge of three factors is necessary to successfully manage culling: 1) how often does the event occur (turnover), 2) when does the event occur (timing), and 3) why the event occurred at that time (reason). The cow's life is a continuum from birth to death, divided into a growth and maturation process followed by a series of parturition/lactation events. Thus, the risk of cull is more than a simple function of increasing risk with increasing time because the initiation of each new lactation increases the risk of cull every time it occurs. Subsequent pregnancy reduces the likelihood of being culled.

Internal and external, controllable and uncontrollable factors influence culling. An example of an uncontrollable risk is increased culling associated with age. An external uncontrollable factor is beef price. Many factors however are within management purview, such as mitigating disease incidence, changing risk tolerance, production level, reproductive performance, transition cow care, and herd long-term growth goals.

Culling management is more complex than simply reducing herd turnover rate. There is an optimum time to cull a cow based on her productive, reproductive and health status and probability for future economic success. Culling too early limits profitability through the loss of the ability to recover costs of investment. Culling too late limits profitability because of lost opportunity to gain higher profits with a more profitable cow. Opportunity exists to better manage the timing of cull events.

Acknowledgements: Dr. Sandra Godden, University of Minnesota, Dr. Steve Stewart, University of Minnesota

Key Words: Culling, Risk Managment, Profitability

205 Culling: nomenclature, definitions and some observations.

J. Fetrow*[1], K. Nordlund[2], and D. Norman[3], [1]*Univeristy of Minnesota*, *St. Paul*, [2]*University of Wisconsin*, *Madison*, [3]*USDA AIPL*, *Beltsville, MD*.

In advance of the Discover Conference on Culling in Dairy Herds in October, 2004, a subcommittee was formed for the purpose of laying out a proposed set of definitions of terms relating to culling on dairy farms. This paper is the product of that effort. In addition to the specific charge, the committee has chosen to make some observations on the general topic of culling in dairy cattle and on appropriate ways to examine the underlying factors surrounding the exit of cows from a dairy.

Key Words: Dairy, Culling

206 The effect of animal removal on herd internal growth rate.

A. Skidmore*, *Blue Seal Feeds, Inc.*, *Londonderry, NH*.

The decision making process and reasons for removing an animal from a herd has been extensively studied. This study was designed to evaluate the effect of animal removal on herd size and herd internal growth rate. An inventory control model was adapted to develop a simple model for evaluation. Herd size is very dynamic and dependent on many factors. The factors that influence the dynam-