cristaline microcelulose pellet with 15 mg of naloxone. And, group 3 was injected with saline solution at the same intervals as group 1. Testosterone in plasma samples was determined by RIA at the beginning of the experiment and at 7, 15 and 21 days during treatment. During the non-breeding season testosterone levels in naloxone treated bucks was significantly increased from a control concentration of 0.5 ng/ml to a plasmatic concentration of 1.7 ng/ml, and 1.6 ng/ml of naloxone as compared with 0.5 ng/ml in the control group ($p<.01$). When bucks were treated during the breeding season (autumn) the administration of naloxone did not affect the concentration of plasma testosterone. It was concluded that naloxone antagonism was more effective when administered to bucks in the non-breeding season.

Key Words: Bucks, Testosterone, Naloxone

Animal Behavior & Well Being: Housing environments

620 Behavioral and physical variation among cloned litters of pigs. G. S. Archer*[1], T. H. Friend[1], J. Piedrahita[2], C. H. Nevill[1], and S. Walker[2], [1]*Department of Animal Science, Texas A&M University, College Station,* [2]*College of Veterinary Medicine, Texas A&M University, College Station.*

A series of tests were used to quantify the variation in food preference, temperament, and time budgets of two genetically identical cloned Duroc litters (n = 5,4) and their matched naturally bred controls (n = 4,4). Food preference was determined for all pigs using apples, bananas, crackers, and carrots. Each food type was offered ten times per trial for two trials. To assess variation in temperament a Towel Test, Back Test and Pick-up Test were used. The Towel Test consisted of recording the average time for each pig to remove a towel from its head ten times in each of three trials. The Back and Pick-up Tests were conducted only on the second set of matched litters at 7 weeks of age. They consisted of counting the number of vocalizations and escape attempts each pig made during one-minute of restraint when held on its back and picked up by a person. Time budgets of the pigs were determined for three consecutive 24 h periods at three different ages using time-lapse video. Time spent lying in bedding, lying on concrete, standing, feeding, and play/fighting was quantified. An F-test was used to determine if any differences in variation between litters existed. The cloned litters were found to be similar or more variable ($P < 0.05$) than the naturally bred controls: in their preference for the foods in thirteen of the sixteen comparisons; in five of the eight comparisons during the Towel Test; in all four comparisons in the Back and Pick-up Tests; and in all ten of the comparisons in the time budget analysis. Physical variation among the clones was also observed: one clone had curly hair while the rest had straight hair, one clone developed hyperkeratosis while the others did not, and one clone had 13 teats and the rest had 14. These results indicate that environmental and epigenetic phenomena have major effects on the behavior and physical development of cloned pigs and question the feasibility of using cloning by nuclear transfer to replicate animals with specific behavioral or physical characteristics.

Key Words: Clone pig, Variation, Behavior

621 Effect of stressors on serum concentration of acute phase proteins and performance in pigs. C. Pineiro*[1], E. Lorenzo[1], J. Morales[1], E. Gomez[2], and G. G. Mateos[3], [1]*PigCHAMP Pro Europa S.A., Spain,* [2]*CPP Hontalbilla, JCyL, Spain,* [3]*UPM, Spain.*

Two trials were conducted to assess the effect of stressors on serum concentration of acute phase proteins (APP), pig-MAP (MAP) and haptoglobin (HPT), and performance of pigs. In trial 1 we studied the effect of room temperature in young piglets. A total of 208 piglets were allotted at weaning (21 d) into two identical rooms with eight pens of 13 piglets each. Room temperatures were reduced from 32 C at 28 d to 28 C at 40 d in the control group (CON) and from 26 C at 28 d to 24 at 40 d in the cold room (COOL). From 40 to 60 d room temperature was identical for both groups. From 21 to 28 d of age COOL piglets grew less (73 vs 119 g/d; $P = 0.0003$) and had worse feed conversion (1.17 vs 2.05 g/g; $P = 0.0003$), than CON piglets, but the differences disappeared thereafter. From 21 to 28 d of age APP concentrations increased (0.74 vs 1.2 mg/ml for MAP and 0.22 vs 0.37 mg/ml for HPT at 21 and 28 d, respectively; $P < 0.05$). At 40 d of age APP concentrations decreased in CON group but not in COOL group (1.02 vs 0.75 mg/ml for MAP; $P = 0.12$ and 0.43 vs 0.10 mg/ml for HPT; $P = 0.006$ for COOL and CON groups respectively). In trial 2 we studied in growing pigs (74 to 116 d of life) the effects of feeding frequency on the same parameters. A total of 240 pigs were randomly distributed in 24 pens. The experimental treatments consisted of pigs fed ad libitum (AL) or disorderly (DIS). Total feed intake was kept constant in both groups. From 74 to 102 d of age, AL pigs grew more than DIS pigs (542 vs 482 g/d; $P < 0.05$) but no differences were observed at the end of the trial. Serum APP were higher for the DIS group than for the AL group ($P = 0.004$ for MAP and $P = 0.001$ for HPT). We conclude that stressors impair pig performance and that the impairment can be detected through measuring the variation in serum concentration of Pig-MAP and HPT. When the stressors disappears pigs compensate for the losses in performance and serum levels of APP return to basal levels.

Key Words: Stressors, Acute phase proteins, Pig performance

622 Effects of pre-natal stress on immunological response and weight gain during the grower finisher period. M. J. Toscano*[1], K. A. Scott[1], H. K. Smith[1], J. E. Cunnick[2], M. J. Daniels[3], and D. C. Lay, Jr.[1], [1]*USDA-ARS-MWA-LBRU,* [2]*Iowa State University,* [3]*University of Florida.*

Pre-natal stress, stress applied to the pregnant dam which potentially affects development of subsequent young, works through unclear mechanisms. In the current study, sows received one of two treatments once a week during d 42 to d 77 of gestation: injections of ACTH (i.v., 1 IU/kg BW) (ACTH, n=19), or forcefully moved up and down an alley and received 3 shocks from a standard electric prod over a 10-min-period (ROU, n=15). A third group served as a control and received no treatment (CONT, n=18). Subsequent progeny were separated into groups of 6 (2 pigs/trt/grp) upon weaning. To assess the affect of the treatments on immunological function, at 106 ± 0.51 d of age, a single pig from each litter received a 6-mm punch biopsy to assess healing and then regrouped with other test pigs maintaining groups of six. A base blood sample was taken before the procedure (d 0) and then d 2, 4, 7, 9, 11, 14, 21, 28, 35, 42. To provide a record of punch biopsy healing, digital pictures were taken of the wound at each sampling time until d 21. Collected blood provided an immunological cell profile and each wound picture was scored for severity by 3 observers blind to treatments. Average daily gain from farrowing to d 146 ± 1.0 of age was calculated. Granulocytes as a percentage of white blood cells was least in the ACTH group followed by CONT and ROU, respectively (51.5 ± .82 vs. 53.4 ± .94 vs. 56.08 ± .84 %; $p<.05$). Eosinophils tended to be least ($p>.08$) in the CONT, followed by ROU and ACTH, respectively (1.9 ± .13 vs. 2.01 ± .14 vs. 2.14 ± .34 5^{10} cells/L). A score given to biopsy healing progress was most improved in ROU, followed by CONT and ACTH, respectively (2.12 ± .06, 2.26 ± .06 , 2.34 ± .06; $p > .04$). Average daily gain was not affected by treatment (.65 ± .01 kg/d, $p>.45$). Our results suggest pre-natal stress is a factor in granulocyte production and the body/s ability to heal a small biopsy. Continued research is needed to develop a complete understanding of pre-natal stress/s effects.

Key Words: Pre-natal stress, Swine , Immune

623 Evaluation of drop versus trickle feeding for crated and penned pregnant gilts: productivity measures. J. McGlone*[1], J. Morrow[2], and J. Smith[1], [1]*Texas Tech University,* [2]*USDA-ARS.*

Eighty three Camborough-22 (PIC USA) gilts with known estrus dates were used to determine the effects of two penning systems (crates vs. pens of 5) and feeding system (drop fed vs. trickle fed) on reproductive performance. The four treatments were arranged in a 2 X 2 factorial. Drop-fed gilts (DROP) received their entire 2.7 kg daily meal in a single drop. Trickle-fed (TRICK) gilts were fed 2.7 kg over a 30 min period. Gilts with a known estrus date and a predicted next estrus date were randomly selected and moved from their acclimation group pen to their assigned treatment. Estrus detection, maintenance of pregnancy and litter performance measures were collected. Measures of behavior and physiology will be reported elsewhere. Overall farrowing rate was not different among treatments. However, more gilts were not bred (not detected in estrus) among penned (4.9%) than crated gilts (0.0%). Fewer gilts recycled after mating when in TRICK-Pen (15%) than in TRICK-Crate (25%), DROP-Pen (29.2%), or DROP-Crate (24.2%) treatments.

Other measures (mean SEM) not significantly influenced by treatments included: gilt body weights at breeding (135.6 ± 2.7 kg), farrowing (205.0 ± 2.02 kg) or weaning (189.4 ± 2.82), backfat thickness (11.05 ± 0.57), and per litter measures of pigs born alive (10.9 ± 0.61), pigs born dead (1.13 ± 0.28), piglet birth weights (1.7 ± 0.04 kg), number weaned (8.8 ± 0.57), preweaning survival (87.0 ± 3.9%), piglet weaning weight (6.21 ± 0.14 kg) and shoulder lesions (scored 0-3 with 0 = no lesion; 0.53 ± 0.13). Overall reproductive rates and sow and litter productivity were similar for gilts in the four treatments. Differences in estrus detection and recycle rates after mating were probably due to ease of animal observation in the different systems. In conclusion, productivity of breeding and gestating gilts was similar in the four systems evaluated.

Key Words: Pig, Welfare, Housing

624 The effects of dietary sodium bicarbonate on abnormal behavior and heart rate in sows. J. N. Marchant-Forde*[1] and E. A. Pajor[2], [1]*USDA-ARS,* [2]*Purdue University*.

Many oro-nasal behaviors are considered to be stereotypic and abnormal and have been implicated as an indicator of poor welfare in swine. There is some evidence in other monogastric species to suggest that oral stereotypies serve a pH buffering function and reduce ulceration of the stomach resulting from restricted feeding practices. Stomach ulceration is prevalent in swine and a weak link between stereotypies and ulceration has been established. The objective of this study was to determine whether the incidence or types of oro-nasal behaviors were affected by dietary sodium bicarbonate. Sixteen sows housed in gestation crates were subjected to change in diet for 2 wk of a 6-wk experimental period, with each animal therefore acting as its own control. During wks 1 & 2 and wks 5 & 6, all sows were fed standard commercial ration. During wks 3 & 4, all sows were fed a diet containing 2% sodium bicarbonate but identical to normal diet in other ingredients and total energy content. Behavior and heart rate were recorded on the middle day of each week from 0.5h before feeding to 2h after feeding and analysed to determine incidence and durations of oro-nasal behaviors and heart rate responses to feeding. Sows spent 46.2% of the pre-feeding observation period engaged in oro-nasal behaviors, increasing to 55.23% of the post-feeding period (P<0.05). The main pre-feeding behaviors were nosing the crate (NC = 11.7%) and bar biting (BB = 11.6%). The main post-feeding behaviors were nosing the floor (NF = 22.3%) and sham chewing (SC = 10.2%). The post-feeding durations of BB and NF were both lower after the diet contained bicarbonate (BB wks 1&2 = 330s, wks 3&4 = 166s wks 5&6 = 175s, P<0.01, NF wks 1&2 = 2010s, wks 3&4 = 1412s, wks 5&6 = 1140s, P<0.05), but the post-feeding incidence of nosing the trough (NF) increased (wks 1&2 = 192s, wks 3&4 = 514s, wks 5&6 = 559s, P<0.001). The heart rate response to feeding was higher (p<0.01) in wk 4 (163bpm) than any of the other wks (151 bpm). The results suggest that the addition of dietary bicarbonate may affect both the performance of feeding-related stereotypic behaviors and the cardiac response to feeding. Further investigation is required to elucidate the mechanisms by which bicarbonate may be acting.

Key Words: Swine, Stereotypies, Well-being

625 Effect of housing systems on implantation in sows. L. Anil*, S. Baidoo, R. Walker, J. Deen, R. Morrison, and S. Anil, *University of Minnesota, Saint Paul, Minnesota*.

A study was conducted to evaluate the effect of housing systems during breeding and gestation in sows on subsequent reproductive performance in terms of piglets born alive, mummies and stillborn piglets. The 3 housing systems were; 1.Sows bred and reared for their entire gestation in stalls (TS, n = 87), 2. Sows bred and reared for their entire gestation in pens with electronic sow feeder (TP, n = 49) and 3. Sows bred and maintained in stalls for 28 days and then transferred to pens with electronic sow feeder for the rest of gestation (PS, n = 43). Analysis of variance was performed to compare the housing systems. The mean born alive varied significantly among the housing systems (TS 11.71 ± 0.27; TP 10.27 ± 0.41; PS 10.42 ± 0.39; $P< 0.01$). The difference between PS and TP housing systems was not significant. However, significant differences ($P< 0.01$) were found between the TS and TP and between TS and PS. Litter weight (kg) showed the same trend as that of born alive (18.33 ± 0.35, 16.77 ± 0.59 and 16.74 ± 0.58 for TS, TP and PS respectively with $P< 0.05$). There was no difference among the groups in terms of farrowing rate, mummies and stillborn. Sows housed in stalls and pens during gestation are equally susceptible to factors causing stillborn and mummies and therefore, there was no difference among sows with respect to mummies and stillborn. There was no difference in farrowing rate among sows, as farrowing success is independent of litter size. The higher live born numbers in stall-housed sows indicates the beneficial effect of stall housing in reducing stress during the implantation period.

Key Words: Gestation, Implantation, Housing

626 Swine Welfare Assurance Program. A. K. Johnson*, E. A. Lautner, and P. L. Sundberg, *National Pork Board*.

Recently in the US there has been intense marketing interest in animal welfare and on-farm production guidelines. Multiple communications with the marketing sector indicate that animal welfare assurances may be transferred back to the producer. The National Pork Board's (NPB) Animal Welfare Committee (AWC) has worked with an international panel of experts to develop a program by which pork producers can objectively assess pig welfare on the farm. The Gestating Sow Welfare Index was the first phase of this collaboration and concentrated on gestating sow welfare. The index was tested in early 2002 by animal and veterinary experts. Results were presented to the AWC who expanded the program to include the farrowing sow and the neonatal piglet, nursery and finisher pigs. It has been renamed the Swine Welfare Assurance Program (SWAP). Three sections of SWAP will assess swine welfare. The first is an evaluation of records, which assesses herd health and nutrition and caretaker training. The second is animal observations, which assesses regularity of animal observation, body condition score, euthanasia, and handling and movement. Third is an assessment of the facilities, which evaluates facility conditions emergency support and continuing assessment and education. SWAP was tested on farm in late 2002 and modifications and refinements to the program have been completed. SWAP Instructor Teams (SIT) will train Certified SWAP Educators (CSE) who will educate producers and provide assessments. SWAP will benefit producers by providing them with a voluntary, uniform, producer-developed tool to help maintain market availability or open up new marketing avenues if selling to a market that asks for information about animal welfare. SWAP can also help producers evaluate and track animal performance and welfare over time and identify weaknesses in management, nutrition or health programs before they become welfare and production problems. SWAP will also demonstrate the US pork producers' commitment to the welfare of their animals.

Key Words: Assessment, Swine, Welfare

627 Factors affecting cow preference for stalls with different freestall bases in pens with different stocking rates. W. K. Fulwider* and R. W. Palmer, *University of Wisconsin-Madison*.

Stall use was monitored using a closed circuit television system in a 4-row, 104-stall freestall barn. Stall status was recorded four times each day, 1400, 2000, 0400, and 0900h, for a 6-month period, 6/19/02 to 12/17/02. Two measures of cow preference, stall with cow lying or stall occupied (cow lying or standing in stall) were recorded. The objective was to compare percentages of cow preference measures for each factor affecting use of stalls with different freestall bases. Six factors were analyzed: freestall base, distance to closest water, stall location within a stall type section (End vs. NotEND), row of stalls (INTERIOR vs. EXTERIOR (wall side)), inside barn temperature (TEMP), and length of time animals exposed to freestall bases (XPOSR). One pen had a low stocking rate (LowSR, 65%), six different freestall bases, [cork-based mattresses-CMATR; foam-based mattresses, FMATR3, FMATR4; rubber-based mattresses RMATR2, waterbeds (WATR), and rubber mat (RMAT4)], and cows were milked with a robotic milker. The other pen had a 100% stocking rate (100%SR), seven different freestall bases [foam-based mattresses-FMATR1, FMATR2; rubber-based mattresses RMATR1, RMATR2; and rubber mats, RMAT1, RMAT2, and RMAT3], and cows were milked twice daily in a herringbone parlor. Each pen was analyzed separately because of different stocking rates. Freestall bases were grouped with 3 to 8 stalls/section and randomly placed in each row. Results show significant differences (P< .05) between a number of freestall bases for lying and occupied. Stall usage for the 100%SR side for lying was FMATR1 (62%), RMATR1 (59%), RMATR2 (57%), FMATR2 (52%), RMAT1 (51%), RMAT2 (43%), RMAT3 (42%), whereas, occupied was FMATR1 (91%), RMATR2 (85%), RMATR1 (84%), FMATR2 (81%), RMAT1 (73%), RMAT3 (65%), and RMAT2 (64%). Stall usage for the LowSR side for lying was FMATR3 (49%), FMATR4 (35%), RMATR2

(35%), WATR (32%), CMATR (18%), and RMAT4 (16%), whereas, occupied was FMATR3 (62%), FMATR4 (50%), RMATR2 (46%), WATR (40%), CMATR (25%), and RMAT4 (23%). Results show foam- and rubber-based mattresses to be superior to rubber mats.

Key Words: Freestall base, Cow preference, Stocking rate

Breeding & Genetics: Molecular genetics and analyses of microarray data

628 Analysis of gene expression patterns in the cattle digestive system. S. L. Rodriguez-Zas*[1], M. R. Band[2], R. E. Everts[1], B. R. Southey[1], Z. L. Liu[1], and H. A. Lewin[1,2], [1]*University of Illinois at Urbana-Champaign, Urbana, IL,* [2] *W. M. Keck Center for Comparative and Functional Genomics, University of Illinois, Urbana, IL.*

Scant information is available on the levels of gene expression in the digestive system of cattle. A study was conducted to characterize transcript profiles in rumen, large intestine, small intestine and reference samples. The absolute intensities obtained from cDNA microarrays that included 7653 cattle and control sequences were used as indicators of the transcript levels. The experimental design included dye-swaps totaling six arrays and sequences were duplicated within array. Data normalization included a LOWESS fit to remove dependencies between tissue effect and average expression level. The remaining variation was analyzed using a linear mixed effects model including the effects of array, dye, gene, and gene by tissue. A total of 218 sequences were significant at P< 10 to the -6 power, of which 28 were significant at P< 10 to the -9 power. The 99.9% bootstrap confidence interval limits of tissue contrasts indicated that 625 genes were expressed at different levels between large and small intestines, 448 were different between the large intestine and rumen, and 401 were different between the small intestine and rumen. Multiple sequences associated with fatty acid metabolism were over expressed in the rumen with respect to the small and large intestines. This result is consistent with the high fatty acid absorbance that occurs in the wall of the rumen. In agreement with the high cell turnover rate of the intestinal epithelium, some Caspase genes were significantly under-expressed in the rumen, when compared to small and large intestines. These results augment the understanding of the gastrointestinal tract development, differentiation, and function and can be used in nutritional programs to optimize feed efficiency and metabolism.

Key Words: Cattle, Digestive system, Microarray

629 Analysis of microarray data: are you better off by replicating genes or arrays? R. Rekaya*, *The University of Georgia.*

Maximizing information content of gene expression experiments is essential for successful application of the technology. The way data is collected (design) and analyzed determines the information content of a study and the power of detection of true changes. Gene expression technology is still very expensive especially for animal agriculture applications. As a result, most expression experiments have less than a dozen chips. Given the noisy data we are dealing with, such small number of arrays will have little power for detecting genuine changes. One way of increasing power is to increase the number of arrays. However, this option is not the most cost effective way. An alternative approach is to replicate genes within array without increasing the number of arrays. This approach allows the control of within-chip variation. To demonstrate the importance and benefits of modeling on-chip variation and compared with the simple approach of increasing the number of arrays, a simulation study was carried out. A mixed linear model including the fixed effect of treatment, a random affect for on-array variation at each gene with variance ${\sigma^2}_g$ and the residual term (between arrays variation) with variance ${\sigma^2}_e$ was fit to the normalized expression level. Three cases of within array replication where each gene was replicated 2, 4 and 8 times were considered. Also, we varied the ratio of variances $R={\sigma^2}_g/{\sigma^2}_e$ from 0.01 to 1. For each combination of number of on-chip replication and variance ratio, 50 datasets with 10 arrays and 200 genes were simulated. For small variance ratio (0.2), the power of the design with on-chip replication was 2.5, 3.6 and 3.9 fold greater than the design without gene replication. The difference in power decreases with the increase of the ratio of variances. However, it remains significantly greater for the design with on-chip replication. In fact, at a ratio of 1, the within chip replicate design remains twice more powerful. Similar power was obtained using 4 arrays with 4 on-chip replication and 10 arrays without gene replication. Results indicate that on-chip replication is a cost effective way to increase power.

Key Words: Microarray, Power, Replicate

630 Normalization, replication, and significance tests in cDNA microarray experiments. G. J. M. Rosa*, R. J. Tempelman, S. Suchyta, S. A. Madsen, J. L. Burton, and P. M. Coussens, *Michigan State University, East Lansing, MI.*

Spotted cDNA microarray experiments are being increasingly used in animal science to compare gene expression of tissues under different biological states, such as different environmental stress conditions or a time course. These experiments generate large, complex, and noisy data sets, which must be appropriately analyzed for satisfactory mining of important biological information. Several procedures have been proposed for normalizing the data regarding different kinds of biases and sources of systematic variation, e.g. intensity- or spatially-dependent dye biases. Also, a variety of statistical approaches have been suggested for the determination of significant differences between mean expression signals. We apply and contrast some of these methodologies, using robust local regression technique, ANOVA models and mixed model approaches. Four microarray experiments are used to illustrate these methods and to discuss their advantages and drawbacks. The experiments were conducted at the Center for Animal Functional Genomics at Michigan State University, using a bovine-specific cDNA microarray system containing 3,888 total spots representing 709 bovine EST clone inserts, 345 amplicons of known genes derived from bovine sequence, and numerous blank and control gene spots. The first dataset derives from a self-self hybridization trial where the same tissue sample was arrayed with two fluorescent dyes, in a reverse labeling experiment. A second loop design experiment was used to monitor gene expression profile changes in blood neutrophils collected from cows multiple times as they proceeded through parturition. The other two experiments compare gene expression profiles of peripheral blood cells from control and Johne's disease positive cows. Special attention in the statistical analyses is given to spatial variability, the use of control genes for data normalization, biological replication, multiple testing and the false positive rate. Some suggestions for further research on the statistical treatment of microarray data are outlined, including the use of mixtures and thick-tailed processes, and different alternatives for modeling heterogeneity of variances across genes and slides.

Key Words: Microarray, Normalization, Significance test

631 Accounting for genotyping errors in QTL analyses. G. J. M. Rosa*, *Michigan State University, East Lansing, MI.*

Construction of genetic maps and the identification of QTL should involve genetic data of high fidelity. However, the rate of mistyping is considerable in most genotypic data, substantially reducing statistical power on detection of linkage between loci and associations between markers and phenotypic traits. Checks for genotyping errors are then crucially important prior to gene mapping analysis based on traditional statistical methods. Common strategies include comparison of duplicate samples, independent calling of alleles, and Mendelian-inheritance error checking. These strategies, however, are not able to detect all errors. A statistical approach that simultaneously infers upon genotyping error rates and allows for the possibility of miscoded genotypes in QTL analyses is presented. The methodology treats observed marker genotypes as phenotypes with a penetrance function that links these variables (which include errors) to the actual (unknown) genotypes. The model includes an additional parameter, which describes the probability of genotype miscoding. A Bayesian approach based on Markov chain Monte Carlo methods is adopted. Backcross data sets with 150 or 300 individuals, genotyped for 5 loci (including some missing data), and with recombination rates between adjacent loci ranging from 0.01 to 0.15 were simulated. Miscoding probabilities were 0, 1, 3 and 5%. Analyses were conducted ignoring or contemplating miscoding in the model.