heterozygous (Nn), 1.06 vs. 1.01 Kg, respectively. However, there were not statistical differences between groups on days to 100 Kg, back fat and loin area. Nevertheless, contrary to the current literature, a tendency of best performance for homozygous (NN) pigs was observed in our experimental conditions. There was no genotype X sex interaction, both sexes having similar performance.

Key Words: Test performance, Halothane gene, Pig

769 Performance Levels, Genetic Parameters and Genotype-Health Interactions for Production Traits in Pigs. R. Bergsma*[1], E.F. Knol[1], J.W.M. Merks[1], and G.J. Van Groenland[2], [1]*IPG, Institute for Pig Genetics, Beuningen,* [2]*TOPIGS, Vught, The Netherlands*.

Replacement boars and gilts are potential carriers of infectious agents for pig production farms. Demand for healthy breeding stock is increasing. Consequently, production facilities of these animals should be of high health. However, from a genetic point of view questions should be raised whether 1) genetic trend realized under high health conditions (SPF) will be expressed in the same magnitude under conventional conditions, and 2) selection under SPF will, in the long term, decrease genetic disease resistance. SPF in the current analysis was defined as controlled free of Pseudorabies, PRRS, TGE, *Mycoplasma hyopneumoniae, Actinobacillus pleuropneumoniae, Brachispira hyodysenteriae, Pasteurella multocida* (DNT), *Streptococcus suis* (Type II), endoparasites and ectoparasites. On the conventional farms used, some, but not all, of the pathogens were present. Data analysis of a genetically linked structure of 2 SPF farms and 3 conventional farms for fertility traits, and 3 SPF- and 2 conventional farms for finishing traits yielded different performance levels under SPF for: Total Number Born (TNB, +0.7), Gestation Length (GL, -0.5 d), Nurse sow PreWeaning Mortality (PWM, -1.4 %), Test Growth (25-80 kg; TG, +143 g/d), and Ultrasonic Backfat (USB, +0.58 mm). Heritability tended to be higher only for TNB (0.13 vs. 0.10) under SPF. Genetic correlations between traits measured under SPF and under conventional conditions were positive and high (r_g >0.8) for Stillborn, TNB, and TG and moderate (0.5< r_g <0.8) for GL, PWM, and USB. It is concluded that selection under the defined SPF conditions will not markedly reduce genetic trend on farms with a conventional health status. A genetic decrease in resistance is difficult to detect. Using health and performance data of SPF sired offspring in a conventional environment will help to control this potential risk.

Key Words: Pigs, Genotype Health Interaction, SPF

770 Sustainable Outdoor Pork Production. W. P. Tynan*, J. G. Gentry, A. K. Johnson, H. A. Rachuonyo, J. F. Smith, and J. J. McGlone, *Texas Tech University, Lubbock, Texas/USA*.

A Sustainable Pork (SP) Research and Demonstration Farm was developed based on past research and the following conditions. The objectives of the SP Farm were to develop a precisely defined production technology. Acceptable criteria include that the farm does not use waste lagoons; uses no more land than a conventional indoor production system and should have no negative impact on the land. The farm may use no more labor than a conventional system and must be economically competitive. Neither may the farm have an offensive odor. It must be viewed as a positive member of the rural community. Plants used as groundcover must uptake the nutrients the animals add to the soil and recycle them by retaining carbon, nitrogen and other nutrients in a solid form. Finally, the farm should contribute healthy meat to the segment of consumers who wish to protect the environment, the animals and the workers. This niche market may be available in the United States now. Started "from scratch" on grassland that was in the Conservation Reserve Program for ten years, the farm shows the feasibility of successfully operating a 300-sow farrow-to-finish pig production outdoor sustainable farm. The farm has completed two years of operation. Production of piglets began in January 1999 and approximately 15,000 piglets have been weaned and finished outdoors. There were no health problems in the herd of 300 sows that received no sub-therapeutic antibiotics. Meat is sold to the public under the trademarked Sustainable Pork® label at the Texas Tech University Meats Laboratory. Visitors to the farm are impressed by the absence of odor due to the maintenance of ground cover and the manner in which the sows and piglets live a healthy, active life style. Consumers may consider their meat to be of better quality and taste panel results confirm the consumer perception of better taste in some trials. Soil analyses indicate that the farm's program of maintaining groundcover, which is being fertilized by the animals, has prevented a buildup of some nutrients in the soil. This production system works well in a dry, warm climate.

Key Words: Outdoors, Pigs, Environment

771 Evaluation of three genetic populations of pigs for response to four levels of ractopamine. A. P. Schinckel*[1], C. T. Herr[1], B. T. Richert[1], and M. E. Einstein[1], *Purdue University*.

Gilts (n = 300; BW = 83.5 kg) were allotted to pens (n = 60) by weight in a 3 × 4 factorial arrangement of treatments in a randomized complete block (n = 5) with three genotypes (G) and four ractopamine levels (RL): 1) control, 0 ppm; 2) 5 ppm; 3) 10 ppm; and 4) 20 ppm RAC to evaluate the effects of ractopamine (RAC) on growth performance in a four week trial. All pigs were fed an 18.6% CP, 1.1% lysine diet. The weekly pen data were fitted to numerous linear, nonlinear and biphasic equations of ractopamine level (RL), and either duration of time (DRAC, midweek days on RAC), or weight gain (WTGRAC, kg) on RAC. The values of DRAC and WTGRAC were set to zero for the control treatment. The RAC response was also divided into two phases: (1) RL1, 0 for control and 5 for all other RAC treatments, and (2) RL2, (RL-RL1) for RAC treatments 2, 3, and 4. For ADG (kg/d), the equations included the fixed effects of block, G and week on test ($p < .01$) and either a biphasic [0.0186 RL1 + .0272 $(RL2)^{.007}$] or nonlinear function {.113 [1 - exp (-.713 RL)]} of RL level. For gain:feed (G:F), the models included the fixed effects of week ($p < .01$) and either a biphasic linear (.0084 RL1 + .0013 RL2) or nonlinear function {.0513 [1 - exp (-.717 RL)]}. The partial sums of squares accounted for by the biphasic functions were 4.4 and 8.9% greater than the nonlinear functions for ADG and G:F, respectively. For daily feed intake (ADFI, kg/d), the equation with the lowest RSD included the fixed effects of block, G, week, and -.0068 RL2 ($p < .01$). The change in the RAC response with WTGRAC were not significant ($p > .50$) for any variable. The predicted linear change in RAC response to DRAC were small for ADG (-.0035, p = .19), G:F (-.0008, p = .49), and ADFI (-.0026, p = .31). The regression analyses indicated that the three variables respond differently to increasing RL. The biphasic and nonlinear functions of RL resulted in different predicted RAC responses. The RAC response did not significantly change over the duration of the 28-day feeding trial.

Key Words: Ractopamine, Genetic, Finishing

ASAS/ADSA Animal Health: Dairy, Beef Cattle, and Other Species

772 Parenteral vitamin E for prevention of retained placenta in dairy cows. S. LeBlanc, K. Leslie*, T. Duffield, K. Bateman, J. Ten Hag, and J. Wallace, *University of Guelph, Guelph, Ontario, Canada* .

Immune function is suppressed, and the risk of infectious and metabolic disease is increased in periparturient dairy cows. Several studies have shown improved immune function and decreased risk of RP or mastitis in transition cows supplemented with vitamin E in feed and/or parenterally. However, these benefits are not universally reproducible and may depend on baseline vitamin E and selenium status of animals, and other factors. Additionally, a fraction of animals will demonstrate hypersensitive reactions to parenterally administered vitamin E. The objective of this study was to investigate the effect of vitamin E administered subcutaneously to prepartum cows on the incidence of periparturient health problems. A total of 1184 cows in 20 herds were randomly allocated to receive either a single SC injection of 3000 IU vitamin E (d-α-tocopherol) or placebo approximately one week prior to expected calving date. Incidence of peripartum disease (retained placenta, milk fever, metritis, ketosis, displaced abomasum, clinical mastitis, and lameness) was recorded. Data were analyzed in SAS using the GENMOD procedure including herd as a random effect. The risk factors for RP and the effect of vitamin E on RP were different between primiparous and multiparous cows. Therefore, these parity groups were modeled separately. Occurrence of dystocia was offered to the models but was not a signifi-

cant effect. There were no hypersensitive reactions following treatment. Overall, there was no association between vitamin E injection and any disease except RP. Among primiparous animals, treatment reduced the probability of RP by 40% (P = .06), with no interactions with season or time of administration relative to calving. Among multiparous cows, occurrence of milk fever or twins were significantly associated with increased risk of RP. Even excluding affected cows, there was no significant effect of vitamin E on the risk of RP in parity 2 or greater. Analysis of the pharmacokinetics of vitamin E in 18 animals suggests that after a single SC injection of 3000 IU, peak circulating vitamin E level is reached in 1 week, and returns to baseline level after 2 weeks.

Key Words: Retained Placenta, Vitamin E, Transition Cow

773 The incidence and impact of clinical endometritis in dairy cows. S. LeBlanc[1], K. Leslie*[1], T. Duffield[1], K. Bateman[1], and G. Keefe[2], [1]*University of Guelph, Ontario Veterinary College,* [2]*University of Prince Edward Island, Atlantic Veterinary College.*

Endometritis is a localized inflammation and/or infection of the uterus characterized by delayed involution of the uterus, and associated with chronic bacterial uterine infection and purulent uterine discharge. Diagnosis and treatment of endometritis are a source of controversy among veterinarians, fuelled by a lack of large-scale clinical trials with an objective case definition and economically meaningful outcomes. The objectives of this study were to assess diagnostic criteria for endometritis, and to quantify the impact of endometritis on reproductive performance. A total of 1910 cows on 26 farms were studied. The occurrence of dystocia, twins, retained placenta and metritis were recorded. Every cow was examined once between 20-33 DIM, with an external inspection and vaginoscopic examination, followed by rectal palpation of the genital tract for collection of objective data (cervical diameter, location, size, texture and symmetry of the uterus, and ovarian structures). The character of the discharge was scored. Subsequent reproductive performance and culling were monitored for all cows. Multivariate survival analysis was used to identify the factors that predicted longer time to pregnancy (days open), accounting for cows that failed to become pregnant. Adjustment was made for clustering of cows within herds. There were 606 animals (32%) that had visible purulent discharge, but only cows with muco-purulent or worse discharge, or cervical diameter > 7.5 cm after 26 DIM, had significantly reduced pregnancy rate. Using this case definition, the prevalence of endometritis was 21%, and affected cows had an increase of 17 median days open compared to normal cows (140 vs. 123 median days open, respectively). Among cows with endometritis, 69% were diagnosed by vaginoscopy. Given vaginoscopy, only cervical diameter was associated with reduced pregnancy rate; all uterine palpation findings had no predictive value for time to pregnancy. Herd level prevalence of endometritis ranged from 7% to 31%. Endometritis significantly impairs reproductive performance, but identification of affected individuals depends on objective assessment and consideration of the interval from calving to diagnosis.

Key Words: Endometritis, Reproduction, Vaginoscopy

774 The influence of negative energy balance on udder health. K. Leslie, T. Duffield, S. LeBlanc, and J. Ten Hag, *University of Guelph, Ontario Veterinary College.*

There is growing evidence that the mechanisms of udder defence are impaired in periods of negative energy balance and hyperketonemia. Two recent experiments, involving approximately 1000 periparturient dairy cows in Ontario, were utilized to investigate the association between subclinical ketosis and subsequent mastitis. In the first study, 951 cows were blood sampled at 1, 2, 3, 6, and 9 weeks after calving. Overall, 15.1% of cows (39 of 258) with subclinical ketosis had clinical mastitis, as compared to 10.1% (70 of 693) non-ketotic cows ($p< 0.05$). In cows with ketosis during the first week postpartum, 18.1% had clinical mastitis. In multi-variable regression analysis, it was found that parity, calving in summer and fall seasons, and being ketonemic at a threshold of greater than or equal to 1400mol/L BHB were all significantly associated with an increased risk of clinical mastitis. The associations between subclinical ketosis and elevated SCC were also studied. Of cows with ketonemia for two or more weeks in the postpartum period, 21.6% had an elevated SCC, as compared to 13.6% of cows without chronic ketonemia. In the second study, 1142 cows in 20 herds had blood samples collected during the week before calving and in the first week postpartum. Mastitis was monitored as a producer diagnosis of clinical signs in the first 30 days in milk. Using this definition, there was 9.7% lactational incidence rate of clinical mastitis (111 cases). Of cows with serum BHB greater than or equal to 1400 mol/L in the week before calving, 28.6% subsequently had clinical mastitis, as compared with 8.7% of cows that were non-ketonemic prepartum. The results of these two studies add to the growing evidence that negative energy balance and subclinical ketosis is associated with increased rates of mastitis.

Key Words: Negative Energy Balance, Subclinical Ketosis, Mastitis

775 The effects of metaphylactic treatment with tilmicosin on the incidence of bovine respiratory disease in growing dairy replacement heifers. D.G. Schmidt*[1], J.E. Shirley[1], E.C. Titgemeyer[1], M.V. Scheffel[1], and D.G. McClary[2], [1]*Kansas State University, Manhattan,,* [2]*Elanco Animal Health, Greenfield, IN.*

One hundred forty four Holstein heifers were used to evaluate the efficacy of a metaphylactic tilmicosin treatment on the incidence of bovine respiratory disease (BRD). Heifers were moved from individual calf facilities at 56 d of age to an off-site (5 h transport) facility, weighed on arrival, ranked by weight, and alternately assigned to pens (6 heifers/pen). Pens with similar weight heifers were paired and randomly assigned to control or tilmicosin treatment. Pens (12/treatment) served as the experimental unit in a randomized block design. Tilmicosin (10 mg/kg of body weight) was administered immediately after pen assignments were completed (day of arrival) to calves in the treatment group. Individuals unaware of treatments conducted health observations twice daily. Incidence of clinical BRD was observed in 2.8 and 4.2 percent of control and tilmicosin treated heifers, respectively. One relapse (clinical signs of BRD within 21 d after treatment) occurred in a tilmicosin treated heifer, and one new episode (clinical signs of BRD after 21 d from first treatment) was observed in a control heifer. Heifers treated with tilmicosin gained more weight ($P<0.05$), consumed more feed ($P<0.05$), and were more efficient ($P<0.05$) during the first 28 d after treatment. Improved performance during the first 28 d in the tilmicosin treated group is presumed to be due to a reduced incidence of sub-clinical BRD.

Key Words: Dairy heifer, Tilmicosin, Bovine respiratory disease

776 On-farm batch pasteurization destroys Mycobacterium paratuberculosis in waste milk. J. Stabel*[1], *USDA-ARS, National Animal Disease Center, Ames, IA.*

A recent dairy survey conducted in 1996 by the National Animal Health Monitoring System suggests between 20 to 40% of dairy herds in the United States have some level of Johne's disease in the herd. This figure will continue to increase unless producers implement management regimes that will help control the spread of this disease within their herd. The neonatal calf is the target for infection with Mycobacterium paratuberculosis, the causative agent of Johne's disease. Calves become infected via exposure to the bacterium through contaminated feces, bedding, colostrum, and milk. Shedding of viable M. paratuberculosis has been documented in the colostrum and milk of infected dams. This study evaluated the efficacy of on-farm pasteurization to destroy M. paratuberculosis in waste milk fed to calves in order to circumvent this mode of transmission. In three replicate experiments, waste milk was experimentally inoculated with M. paratuberculosis and heated at 150degF for 30 minutes. No viable bacteria were recovered after 28 weeks of incubation. These results suggest that batch pasteurization of waste milk contaminated with M. paratuberculosis was effective at generating a clean product to feed to young calves.

Key Words: Mycobacterium paratuberculosis, Johne's disease, Pasteurization

777 Effect of environmental stressors on ADG, serum retinol and α-tocopherol concentrations, and incidence of bovine respiratory disease of feeder steers. N. K. Chirase*[1,3], L. W. Greene[1,3], C. W. Purdy[2], R. W. Loan[3], R. E. Briggs[4], and L. R. McDowell[5], [1]*Texas Agricultural Experiment Station, Amarillo and West Texas A&M University, Canyon,* [2]*USDA/ARS, Bushland, TX,* [3]*Texas A&M University, College Station,* [4]*USDA/ARS, Ames, IA,* [5]*University of Florida, Gainesville.*

Environmental stressors are frequently encountered in confined animal feeding operations. An experiment was conducted to determine the effect of Micotil® and feedyard dust exposure on ADG, serum vitamins A (Vit A) and E (Vit E) concentrations, and incidence of bovine respiratory disease (BRD) of feeder steers. One hundred and twenty crossbred feeder steers (average BW 185 kg) were purchased in Morristown, TN and transported to Bushland, TX. One half of the steers received Micotil (1 ml/30 kg BW s.c.) in TN. Simulated dust storm was produced by having steers in an enclosed canvas tent. Calves were allotted randomly into 3 dust exposure groups: 1) Control (not exposed to tent or dust, 2) Tent (enclosed in tent without dust) and 3) Dust (exposed to dust suspension inside tent), and nested within Micotil® treatments. There were four dust application events each lasting 4 h. Calves were weighed and blood samples taken in Morristown (d -3), arrival (d 0) and every 7 d for 28 d. The data were subjected to the analysis of variance using the General Linear Models procedure of SAS. Transportation stress reduced (P<0.001) serum Vit E concentrations from 7.10 to 1.95 ug/ml. There was no interaction (P>0.05) between the antibiotic and dust treatments. On d-28, the mean ADG of tent and dust groups was lower (P<0.02) than the controls (0.77 vs 1.26 kg/d). Similarly, the mean serum Vit E concentration of these steers was also lower (P<0.05) than the controls (1.88 vs 2.11 ug/ml). Micotil® treatment sustained (P<0.001) serum Vit A and E concentrations of steers. As incidence of BRD increased (0 to 6), serum Vit A and E concentrations decreased (P<0.001) as well as ADG. These results suggest that environmental stressors decrease serum antioxidants corresponding with decreases in ADG.

Key Words: Steers, Simulated dust, Serum antioxidants

778 Influence of dietary antioxidant vitamins on performance of feeder steers exposed to simulated feedyard dust. N. K. Chirase*[1,3], L. W. Greene[1,3], C. W. Purdy[2], R. W. Loan[3], D. R. George[1], and J. Avampato[1], [1]*Texas Agricultural Experiment Station, Amarillo and West Texas A&M University, Canyon,* [2]*USDA/ARS Bushland, TX,* [3]*Texas A&M University, College Station.*

Feeder cattle often encounter many environmental stressors such as dust. An experiment was conducted to determine the effects of short term (28 d) feeding of vitamins A (Vit A) and E (Vit E) on the performance of beef steers exposed to feedyard dust. Thirty six (36) crossbred feeder steers (average BW 260 kg) were allowed 28 d to recovered from transit stress and sickness and assigned randomly into four groups of 9 steers. Steers were housed in pens equipped with calan gate feeders for individual feed intake measurement. The diets consisted of 1) Control (Vit A = 20,240 IU/kg DM; Vit E = 300 IU/kg DM) and 2) Antioxidants (Vit A = 60,700 IU/kg DM; Vit E = 760 IU/kg DM). The diets and dust treatments were arranged in a 2 X 2 factorial design. Steers were trained to feed from calan gates, adapted to diets for 14 d and assigned the following dust treatments: 1) Control (not exposed to tent or dust and 2) Dust (exposed to dust suspension inside tent). Simulated dust storm was produced in an enclosed canvas tent. There were six consecutive daily dust events each lasting 4 h. Steers were weighed every 8 d. The data were subjected to the analysis of variance using the General Linear Models procedure of SAS. An interaction occurred between the dust and antioxidants for feed intake and ADG on d 8 and 17. Steers fed the control diet and not exposed to dust consumed less (P < 0.08) feed and gained less (P < 0.05) weight than all other groups. Although not significant (P> 0.05), the feed to gain ratio for steers not exposed to dust was 36% greater than those exposed to dust (8.0 vs 5.9). The feed to gain ratios of steers fed the control and antioxidant diets were not different (P>0.05). These results suggest that short term feeding of dietary antioxidants during the receiving period to reduce oxidative stress requires additional investigation.

Key Words: Steer performance, Simulated dust, Antioxidant vitamins

779 Relative contribution of nitric oxide (NO)- synthase (NOS) isoforms to hepatic NO production following low-level in vivo endotoxin (LPS)-challenge in cattle. T. Elsasser*, S. Kahl, E. E. Connor, and D. Carbaugh, *USDA, Agricultural Research Service, Beltsville, MD* .

Nitric oxide, synthesized from arginine by different isoforms of NOS, mediates many aspects of inflammatory response to bacterial toxins. Type-II NOS, induced primarily in macrophages 4 to 6 h after LPS, has been identified in other cell types as well; Type-III NOS, constitutively present in several cell types, is modulated by cofactor availability. The present research evaluated the temporal relationship between increases in plasma nitrate (NOx, the stable breakdown product of NO) after LPS and relative activity of Type-II and Type-III NOS in liver. Calves were challenged with either 0 (saline, n = 6, CON) or 3 μg/kg LPS (E. coli 055:B5, iv, jugular, n = 6, L) with serial blood samples obtained for plasma analysis. Plasma NOx increased after 3h (P < 0.02) and peaked at 6 to 8 h after a secondary rise initiating at 4 h post LPS. In a subset of calves (n = 4) liver biopsy samples were obtained 8 h after LPS for characterization of NOS isoforms by immunohistochemistry (IHC) and enzyme assay. Localized by IHC, both isoforms were present in CON; less than 5% of cells were positive for Type-II NOS while 36% of cells (P < 0.002 vs Type-II) immunostained for Type-III NOS . After LPS, Type-II positive cells increased to 18% in L (hepatocytes, Kupffer cells, and infiltrating monocytes). With the use of selective NOS-type inhibitors both isoforms were identified in CON (2.9% of total NOS activity - Type-II). Type-II activity (pmol citrulline/min/mg protein) averaged 0.052 and 0.445 (SEM = 0.12, P < 0.002) in CON and L, respectively. Type-III activity averaged 1.68 and 1.97 (SEM = 0.15, NS) in CON and L, respectively. While the activity of Type-II NOS increased 9-fold with LPS (P < 0.01), the relative contribution of Type-II to total NOS activity after this dose of LPS was 18.4%. The data suggest that early increases in plasma nitrate after LPS arise predominantly from Type-III NOS with secondary increases contributed from lower levels of Type-II NOS.

Key Words: Endotoxin, Cattle, Inflammation

780 Influence of estrus on somatic cell count in dairy goats. S McDougall* and M Voermans, *Animal Health Centre, Morinsville, New Zealand.*

The effect of estrus on the somatic cell count (SCC) in goats' milk was examined by inducing estrus in half of a group of 48 seasonally anoestrus dairy goats. Goats were blocked by infection status and ranked by SCC from the three preceding herd tests and then randomly allocated to three treatment groups: (a) an intravaginal progesterone releasing insert for 12 days and with equine chorionic gonadotropin (eCG) and dinoprost tromethamine 2 days before insert removal (Short; n = 12), (b) a intravaginal progesterone releasing insert for 17 days and with 500 i.u. of eCG on the day of insert removal (Long; n = 12), or (c) left as untreated controls (Control; n = 24). The bacteriological status of each gland of each enrolled goat was determined before and after synchronization (d -23 and d 13) and SCC and milk yield were determined on days -2, 0, 1, 2, 3, 4, 14, 25 where day 0 was the day of intravaginal insert removal. A general linear model was used to test the effect of treatment group on Log 10 SCC and milk yield on each day. The value on day -2 was used as covariate in all models. There was no difference in age, SCC or prevalence of intramammary infection preceding synchronisation among treatment groups (P > 0.1). The Short group were in estrus before the Long group who were in turn in estrus before the control group (1 (1-1) vs. 2 (2-2) vs. 11 (9-13) days, median days to estrus (upper and lower 95% confidence intervals) for Short, Long and Control groups, respectively; P < 0.05). The log 10 SCC was higher in the Short than Control group on days 1 to 4 (3.28 +/- 0.10 vs. 2.57 +/- 0.08; 3.17 +/- 0.11 vs. 2.71 +/- 0.08; 2.93 +/- 0.11 vs. 2.63 +/- 0.08; 2.95 +/- 0.12 vs. 2.55 +/- 0.09, mean and sem for Short vs. Control on days 1 to 4, respectively, all P < 0.05). Log 10 SCC of the Long group were higher than the Control group on days 2 and 4 (3.01 +/- 0.10 vs. 2.71 +/- 0.08; 2.84 +/- 0.11 vs. 2.55 +/- 0.09, mean and sem for Long vs. Control on days 2 and 4, respectively, both P < 0.05). There was no difference in milk yield on any day (P > 0.1) or in prevalence of intramammary infection between groups. This data indicates that estrus was associated with an increase in SCC and that the increase in SCC was independent of any change in milk yield.

Key Words: Goat, Somatic Cell Count, Estrus

781 Associations between porcine leptin and leptin-receptor marker genotypes and immune parameters. M.F.W. te Pas*[1], A.H. Visscher[1], E.J. van Steenbergen[2], E.F. Knol[2], K.H. de Greef[1], T.A. Niewold[1], and L.L.G. Janss[1], [1]*ID-Lelystad,* [2]*Institute for Pig Genetics*.

Leptin is an adipocyte-secreted hormone that affects diverse traits like food intake, body fatness, reproduction, and immune response. Leptin acts through activation of the leptin-receptor on target cells. Leptin deficiency is associated with excessive fatness, suppressed reproductive function, and reduced immune function. Reduced leptin-receptor function is also associated with excessive fatness. Both leptin expression levels and leptin marker genotype has been associated with back fat thickness in certain, but not all, pig breeds. The relationship between leptin and leptin-receptor genotypes and immune parameters is still unknown. The purpose of this study was to evaluate the association between leptin and leptin-receptor genotypes and immune parameters. Ninety immune parameters were measured in 202 AI boars from 4 different lines from 2 pig breeding organizations. Immune parameters were grouped in 1) lymphocyte stimulation tests, 2) lymphocyte cell numbers, and 3) lymphocyte cell membrane markers CD4 and CD8. Pigs were genotyped for 1) a leptin marker as described by Stratil et al. (Anim. Genet. 28: 371-372), and 2) two leptin-receptor intronic PCR-RFLP#s. Associations were evaluated with several statistical models including models that evaluated the association of each individual marker genotype and the immune parameters separately, and models that included the genotypes and interactions of both genes. The results indicate that leptin marker genotypes show good association with the lymphocyte stimulation tests and the cell membrane markers. Leptin-receptor genotypes associated to lymphocyte stimulation tests, lymphocyte cell numbers, and cell membrane markers, but associations were less significant than for the leptin gene. Interactions between the leptin and leptin-receptor genotypes were shown for the cell membrane markers. The relation between pig health and leptin and leptin-receptor genotypes remains to be established.

Key Words: Pig, Leptin Genotype, Immune Capacity

782 Profiling intestinal microbial populations with the *cpn60* molecular diagnostic. J.E. Hill[1], A.G. Van Kessel*[2], R.P. Seipp[1], L. Hawkins[1], M. Betts[1], J. Marshall[2], and S.M. Hemmingsen[1], [1]*National Research Council Plant Biotechnolgy Institute, Saskatoon, SK,* [2]*University of Saskatchewan, Saskatoon, SK*.

Conventional methods for identifying and quantifying microorganisms in complex communities such as those found in the intestine are costly, labour intensive, offer limited species differentiating capacity and fail to identify unculturable organisms. We designed a single set of degenerate PCR primers which can be used to amplify a target gene, *cpn60*, present, usually in single copy, in the genomes of all eukaryotes and eubacteria. We used these "universal" primers to characterize the microflora in pig intestine. Total genomic DNA was isolated from pig faeces by two different extraction methods and subjected to universal *cpn60* primer PCR at two different annealing temperatures. The resulting PCR amplicons were cloned, resulting in 4 libraries of partial *cpn60* sequences. To date, 266 randomly selected clones have been sequenced. Analysis showed the presence of 77 distinct sequences appearing in frequencies ranging from 1 to 50 out of 266. The majority of pairwise DNA sequence identities for the sampled sequences were between 50 and 70%, indicating that the sequences likely represent many different genera. A comparison of cloned sequences to a database of *cpn60* sequence data permitted the classification of library sequences into taxonomic subclasses, in some cases to the genus level, consistent with those identified in the intestine by classical methods. Preliminary data suggest that template extraction method and PCR parameters affect the composition and diversity of the resulting library. We are currently collecting sequencing data from 1800 additional library clones and are developing hybridization and realtime PCR approaches to quantitatively profile intestinal bacterial colonization. Profiling technology based on *cpn60* has significant potential to improve understanding of the interrelationships among intestinal colonization, age, nutrition, health status and animal performance.

Key Words: Intestinal Microbiology, *cpn60*, Molecular Diagnostic

783 Evidence for Transfer of Tylosin and Tylosin-Resistant Bacteria in Air from Swine Production Facilities using Sub-Therapeutic Concentrations of Tylan in Feed. J. A. Zahn*, J. Anhalt, and E. Boyd, *National Swine Research and Information Center, USDA-ARS, Ames, IA*.

Macrolides are an important class of antibiotics used in human and veterinary medicine for therapy and prevention of diseases caused by Gram-positive bacteria, and as animal growth promotants. Tylosin belongs to the class of 16-membered macrolide antibiotics, and has been used exclusively in veterinary medicine for treatment of animal diseases or for enhancing animal growth rate. Antibiotic resistance studies have recently focused on tylosin residues and tylosin-resistant bacteria (TRB) in animal products or in effluent streams from animal production facilities as potential routes for transfer of antibiotic resistance to humans. However, these studies have not considered aerial transfer from point sources as a significant route in human exposure. This study quantified the concentration of tylosin and TRB in air from three mechanically ventilated swine (finisher stage) confinements using tylosin at sub-therapeutic concentrations (20 $g*ton^{-1}$) in feed. Tylosin residues and culturable bacteria in air at exhaust fans were trapped on absorbent resins or impinger samplers, respectively. Tylosin concentration was determined by high-performance liquid chromatography-electrospray tandem (MS-MS) mass spectrometry following solvent desorption of absorbent resins. The number of culturable bacteria and culturable, TRB were determined by plating on standard plate count agar containing no tylosin or 50 $\mu g*mL^{-1}$ tylosin, respectively. The mean concentration of TRB (49,400 16,700 $CFU*m^{-3}$) accounted for approximately 80% of the total culturable bacteria (62,100 18,300 $CFU*m^{-3}$) present in air streams from confinements, with Corynebacterium the predominant genus of TRB. The mean concentration of tylosin in the air from the three confinements was shown to be 8.1 5.3 $ng*L^{-1}$ of exhaust air. Feeder operation, ventilation rate, and animal activity were shown to be the most significant variables influencing emission rate of tylosin and culturable TRB from the swine confinements. The results indicate that aerial transfer of antibiotics and antibiotic-resistant bacteria from swine confinements may represent an important, and previously overlooked mechanism for transfer of antibiotic resistance to humans and to the environment.

Key Words: Antibiotic Resistance, Tylosin, Swine Production

784 Evaluation of Mannan Oligosaccharide on the microflora and immunoglobulin status of sows and piglet performance. K. E. Newman*[1] and M. C. Newman[2], [1]*Venture Laboratories, Inc., Lexington, KY,* [2]*University of Kentucky, Lexington, KY*.

A number of studies have demonstrated improvements in production parameters and mortality with the inclusion of Mannan oligosaccharide (MOS) to the diet. Documented effects include increased macrophage activity and serum immunoglobulins. In addition, alterations in fecal bacterial populations have also been noted with MOS inclusion in the diet. Twenty- four sows were divided into two treatment groups by parity to evaluate the effect of MOS on fecal bacterial populations, sow colostrum immmunoglobulin levels and piglet performance to weaning. All sows received a fortified corn-soy diet. Treated sows received 5-g MOS per day from approximately 14 days pre-farrowing throughout the lactation. Control sows received no supplementation (C). MOS treated sows had higher levels of IgM than untreated sows (440 vs. 316 mg/dl; P=0.0366). Colostrum IgG levels were also numerically increased in sows receiving MOS (4215 vs. 3565 mg/dl; P=0.1615). Colostrum immmunoglobulin levels were also numerically greater 24-h post-farrowing in sows receiving MOS than unsupplemented sows (IgG 1572 vs. 1130 mg/dl; IgM 227 vs. 184 mg/dl). No effect of MOS supplementation was noticed on colostrum IgA concentrations. Piglet mortality was unaffected by treatment. Piglet weights were determined at 7, 14 and 21 days and greater when sows were supplemented with MOS than unsupplemented sows (Day 7: C - 3.14kg, MOS - 3.61kg; Day 14 C - 4.92kg, MOS - 5.62kg; Day 21 C - 6.57kg, MOS - 7.61kg $P<0.05$). Sow fecal bacterial concentrations were unaffected by treatment. The exact mechanism of the improved performance seen in the piglets from sows receiving MOS is not fully understood, but improved immune status of the piglets may provide an aid in performance by controlling sub-clinical problems. Further investigations on the nutrient profiles of colostrum may be warranted to better explain improved piglet performance.

Key Words: mannan oligosaccharide, immunoglobulin, sow

785 Biosecurity measures of spray-dried plasma protein in weanling pigs. J.M. Campbell*[1], B.S. Borg[1], L.E. Russell[1], J. Polo[1], and J. Pujols[2], [1]*APC, Inc., Ames, IA,* [2]*CRESA, Barcelona, Spain.*

The experimental objective was to evaluate safety of spray-dried plasma protein after oral administration in weanling pigs by monitoring clinical, serological, and performance results. Thirty-six pigs (13.6 kg body weight) were randomly assigned to dietary treatments consisting of control (soybean meal) or 8% plasma. Diets were formulated to contain 1.20% lysine due to continuous administration for 2 months after weaning. Individual body weights and feed intake were determined on d 0, 21, 42, and 63 post-weaning. Clinical observations were monitored daily. Blood samples were obtained on d -14, 0, 21, 42, and 63 post-weaning for serological testing. Average daily gain was improved ($P < 0.10$) from d 22-42 and 0-42 due to plasma consumption compared to control pigs. Average daily feed intake and feed efficiency tended towards ($P > 0.10$) improvement. During the experiment, no clinical signs were associated with oral plasma consumption; however, control pigs had mild clinical symptoms and one death. Serological results of all blood samples from control and plasma treated pigs were negative for antibody presence against the following viruses: porcine parvovirus (PPV), Aujeszky's disease virus (PRV), porcine respiratory and reproductive syndrome virus (PRRS), and bovine viral diarrhea virus (BVD). The plasma used in the study was devoid of titers for PRV, PRRS, and BVD, but positive for PPV. In summary, results indicate that oral administration of plasma had no adverse effects on clinical or performance parameters. Serological results indicate no transmission of disease from plasma for the period from a 14 to 63 kg pig.

Key Words: pigs, spray-dried plasma protein

ASAS/ADSA Breeding and Genetics: QTL Detection and Mapping

786 Fine scale mapping of QTL using of linkage and linkage disequilibrium. T.H.E. Meuwissen*[1] and M.E. Goddard[2,3], [1]*Institute fo Animal Science & Health, Lelystad, The Netherlands,* [2]*University of Melbourne, Melbourne, Australia,* [3]*Victoria Institute of Animal Science, Melbourne, Australia.*

Genome wide scans for QTL in livestock populations have revealed many QTL carrying chromosomal regions. However, the size of these regions is rather large: > 30cM. Linkage disequilibrium has proven useful for the fine mapping of mono-factorial diseases in humans. A Quantitative Trait Loci (QTL) mapping method is presented that combines the information from linkage analysis and linkage disequilibrium mapping. The method is based on predicting an Identity By Descent (IBD) probability matrix between all haplotypes of the animals at the putative QTL position. By using this IBD-matrix as a correlation matrix between haplotypes, the variance associated with the putative QTL and the likelihood of the data can be estimated using REML variance component estimation. This likelihood can be maximised over all putative QTL positions in order to find the maximum likelihood position of the QTL. The matrix of IBD probabilities is predicted using 1) the identities of marker alleles in the region surrounding the QTL (linkage disequilibrium information); 2) recombinations within the marker haplotypes that occurred in the genotyped and pedigreed animals (linkage analysis information). The information on the IBD probabilities comes from two parts of the pedigree: 1) say 100 early generations where no pedigree and no genotyping information is available (but effective population size was assumed known); 2) say 2-5 generations where pedigree and genotypes are available. Background genes are accounted for by including a polygenic term in the REML variance component estimation.

Key Words: fine scale mapping, linkage analysis, linkage disequilibrium

787 Evaluation of statistical models and permutation tests for detecting gametic imprinting in QTL scans. H. K. Lee[1], J. C. M. Dekkers*[2], R. L. Fernando[2], and M. F. Rothschild[2], [1]*National Livestock Research Institute, Korea,* [2]*Iowa State University, Ames, IA.*

Recently, De Koning et al. (PNAS, 2000) detected imprinted QTL in an F2 swine breed cross based on significance of paternal and maternal imprinting effects against a no-QTL model. They did, however, not test for deviations from Mendelian inheritance. Our objective was to develop and evaluate such tests. Breed cross regression interval mapping was implemented using the following QTL models: Mendelian (additive and dominance effects), full imprinting (separate maternal and paternal allele effects plus dominance), paternal imprinting (only paternal expression), and maternal imprinting. Tests of each model against the no-QTL model and tests of full imprinting against the Mendelian (Full/Mend), paternal and maternal imprinting models were used in a decision tree to determine presence and mode of inheritance of QTL. Chromosome-wise significance levels were derived by permutation (20,000 replicates). For the Full/Mend test, data were permutated by shuffling paternal against maternal coefficients within individual. Permutation test thresholds were compared to true values obtained from replicate (10,000) simulation of data under the null hypotheses (512 progeny from 8 F1 sires and 32 dams). The QTL was either fixed in alternate breeds or segregating at different frequencies (.7 and .3). The Full/Mend test had higher F-value significance thresholds than tests against the no-QTL model. For fixed QTL, thresholds for Full/Mend derived by permutation underestimated simulated 10, 5, and 1% chromosome-wise type I error rates, but by less than 1.5, 0.6, and 0.3%. Simulation thresholds were slightly more stringent for segregating QTL. As a result, the permutation test underestimated simulated type I error rates slightly more (<1%). Similar work is ongoing to validate tests of full against paternal or maternal imprinting. In conclusion, statistical models and permutation tests can be used to determine presence and mode of inheritance of QTL, although true type I error rates may deviate slightly from desired rates. Supported by USDA CSREES # 00-52100-9610.

Key Words: QTL detection, Imprinting, Permutation test

788 A Bayesian approach for constructing genetic maps when genotypes are miscoded. G. J. M. Rosa*[1,2], B. S. Yandell[2], and D. Gianola[2], [1]*UNESP - Botucatu, SP/Brazil,* [2]*UW - Madison, WI.*

The increased availability of information on genetic markers has created opportunities for understanding quantitative inheritance and for developing novel strategies for genetic improvement in agriculture, such as exploitation of quantitative trait loci (QTL). A QTL analysis relies on having accurate genetic marker maps. At present, however, statistical methods for map construction ignore the possibility that molecular data are read with error. Often, there is ambiguity about at least some genotypes, and ignoring this phenomenon can affect inferences adversely. Here, a Markov chain Monte Carlo Bayesian approach is presented for constructing genetic maps (gene ordering and genetic distances) when there is some random miscoding of genotypes. A probability of miscoding is incorporated in the calculation of recombination events, assuming Haldane's mapping function. Samples from the joint (conditional) posterior distributions of recombination rates and gene order are obtained with the Metropolis-Hastings algorithm. Missing marker genotypes are imputed from Bernoulli distributions. Backcross data sets were simulated, with 100 or 300 individuals, genotyped for 5 loci (including some missing data), and with recombination rates between adjacent loci ranging from .02 to .18. Miscoding probabilities were 0, 2, 4 and 5%. Analyses were conducted ignoring or contemplating miscoding in the model. Results indicate that unless there is certainty that genotypes are coded correctly, it may be safer to use our alternative, robust, procedure, as it provides more reliable inferences about genetic maps. An analysis of *Brassica napus* is presented to illustrate how the procedure works in practice.

Key Words: Genetic map, Miscoding genotype, Bayesian inference

789 The extention of mixed model equations to finite normal mixture models for marker assisted analysis of quantitative traits. Yuefu Liu*, *University of Guelph, Guelph, Canada.*

The marker-based analysis of quantitative traits, such as marker assisted genetic evaluation, is characterized by the mixture model since the QTL genotypes are not observable. It is, therefore, important to develop a general statistical procedure for mixture model analysis. In this study, a set of mixture model equations was derived based on the normal