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POSTER PRESENTATIONS
Animal Health: Immunology

W1 Absorption of total immunoglobulin G in dairy calves fed a colostrum replacement. J. A. Elizondo-Salazar*[1], R. F. Leuer[1], J. M. Campbell[2], and A. J. Heinrichs[1], [1]*The Pennsylvania State University*, *University Park*, [2]*APC, Inc.*, *Ankeny, IA*.

Proper colostrum management is an important step in preventing disease in neonatal calves, but failure of passive transfer of immunity is still a problem in the US dairy industry. It is generally considered that transfer of passive immunity is adequate if serum IgG concentration is > 10 g/L in colostrum-fed calves. Colostrum replacers providing ≤ 125 g of globulin protein have increased in popularity and are designed to be an alternative to colostrum. However, it is important to make sure these products are effective and are capable of providing adequate serum Ig concentrations. The objective of this study was to evaluate the effect of a commercially available serum-based colostrum replacement product on serum total IgG concentration. The study included 28 Holstein calves (14 males and 14 females) from a single dairy. Calves were bottle fed a single package of colostrum replacer (125 g IgG; Acquire, APC, Inc.) mixed in 2 L of warm water. After colostrum replacer feeding, calves were fed whole milk for the second and third feeding at 10% of birth weight daily in 2 feedings. Blood samples from all calves were collected at 24 h after birth and analyzed for total IgG concentration using single radial immunodiffusion. Overall, plasma IgG levels were 10.8 ± 2.4 g/L and indicated successful passive transfer of immunity. There were no significant differences in serum IgG levels attributable to gender (females: 10.3 ± 2.1 g/L; males: 11.1 ± 2.6 g/L), birth weight (> 41.5 kg: 11.1 ± 2.5 g/L; < 41.5 kg: 10.1 ± 2.4 g/L), age at first feeding (> 60 min: 11.4 ± 3.0 g/L; < 60 min: 10.3 ± 2.0 g/L), or time of d at first feeding (a.m.: 11.3 ± 2.7 g/L; p.m.: 10.0 ± 1.9 g/L). Results indicate that the colostrum replacer evaluated in this study provided adequate IgG concentrations for newborn calves when fed according to label directions and thus can be considered an effective alternative to colostrum in dairy calves.

Key Words: Colostrum Replacer, Dairy Calf, Immunoglobulin G

W2 Feeding heat-treated colostrum does not affect growth parameters in pre-weaned heifer calves. J. A. Elizondo-Salazar*, R. F. Leuer, and A. J. Heinrichs, *The Pennsylvania State University*, *University Park*.

Colostrum not only provides nutrients and passive immunity for the newborn calf, but it can also have profound effects on their development. Heat-treatment of colostrum reduces IgG concentrations yet increases IgG absorption, but effects on short- and long-term calf performance are unknown. For this reason, a study was conducted to evaluate effects of feeding heat-treated colostrum on calf growth. First milking colostrum with > 50 g IgG/L (measured by colostrometer) was collected from Holstein cows and frozen at -20°C until a total of 106 L were accumulated. Once collected, colostrum was thawed at 4°C and pooled in a commercial batch pasteurizer to create a uniform batch. Colostrum was mixed at 4°C for about 20 min. 53 L of colostrum were transferred to 1.89 L containers and frozen at -20°C until feeding. The remaining 53 L were heated at 60°C for 30 min, transferred to 1.89 L containers, and then frozen at -20°C until feeding. A total of 28 calves weighing ≥ 35 kg at birth were systematically enrolled into 1 of the 2 treatment groups. Calves were separated from their dams at birth before suckling occurred. For the first feeding, 3.8 L of colostrum were bottle fed by 1 to 2 h of age. To ensure that all calves received an equal amount of colostrum, an esophageal feeder was used in calves with reduced appetite. For the second and third feeding, pasteurized whole milk was fed at 5% of birth BW. Subsequently, calves were fed milk replacer (20% CP, 20% fat) at 10% of birth BW in 2 daily feedings until week 5. Growth measures including heart girth, hip height, BW, and withers height were taken at birth and weekly 4 h post a.m. feeding. Total serum protein at 24 h of age was 5.6 and 5.5 g/L for the heated and unheated colostrum, respectively. No differences were detected between treatment groups for any of the variables. Weight at 2, 4 and 6 wks of age was 191.0, 235.6, and 288.2 kg for calves receiving heat-treated colostrum and 196.7, 242.9, and 297.8 kg for calves receiving untreated colostrum. The results of this study indicate that feeding heat-treated colostrum did not negatively impact growth in pre-weaned heifer calves.

Key Words: Colostrum, Growth, Heifer Calves

W3 The use of a mini-batch pasteurizer is a suitable system for small farms. J. A. Elizondo-Salazar*, R. F. Leuer, B. M. Jayarao, and A. J. Heinrichs, *The Pennsylvania State University*, *University Park*.

The adoption of commercial on-farm pasteurization systems for the purpose of pasteurizing non-saleable milk and colostrum has resulted

in significant health and economic benefits for calves and producers, respectively. However, these systems are expensive and not suitable for small farms. With this in mind, a Mini-Batch Colostrum/Milk pasteurizer is available in the market and we wanted to determine its performance on different liquid calf feeds. A 3 × 2 factorial design with 3 replicates was used. Three different liquid feeds (first milking colostrum, transition milk, and waste milk) at 2 different volume levels (full capacity = 12 L and half capacity = 6 L) were pasteurized at 63°C for 30 min. 10 mL samples were taken before and after pasteurization and frozen to -20°C. All samples were thawed at 4°C and evaluated for standard plate count (SPC), coagulase-negative staphylococci (CNS) count, environmental streptococci (ES) count, coliform (CC) count, gram-negative noncoliform (NC) count, *Streptococcus agalactiae* (SAG) count, and *Staphylococcus aureus* (SA) count. Total IgG levels were determined in all colostrum samples using radial immunodiffusion. Viscosity was also measured using a digital viscometer. The mini-batch pasteurizer effectively reduced SPC, CC, NC, ES, CNS, and SA ($P < 0.01$). However, pasteurization denatured IgG ($P < 0.01$) and increased the viscosity in colostrum samples. The effects were greater when small batches were used. The findings of the study suggest that a mini-batch pasteurizer can be used as an on-farm pasteurization system to effectively pasteurize transition milk and waste milk. However, for colostrum only full batches should be used and a lower temperature could help reduce the denaturing of immunoglobulins.

Table 1.

Liquid feed	Period	SPC (CFU/mL)	CC (CFU/mL)	Viscosity (Pa•s)	Total IgG (g/L)
Colostrun Full	Pre	215,444[a]	200,000[a]	0.464[a]	123.1[a]
Colostrum Full	Post	115[b]	0[b]	4.642[b]	96.3[b]
Colostrum Half	Pre	200,000[a]	175,000[a]	0.215[a]	119.2[a]
Colostrum Half	Post	54[b]	10[b]	100.000[b]	45.2[b]
Transition Full	Pre	1,841[a]	120[a]	0.022	—
Transition Full	Post	4[b]	0[b]	0.022	—
Transition Half	Pre	53,133[a]	62,145[a]	0.046	—
Transition Half	Post	9[b]	0[b]	0.046	—
Waste Full	Pre	45,788[a]	642[a]	0.022	—
Waste Full	Post	3[b]	0[b]	0.022	—
Waste Half	Pre	6,240[a]	71[a]	0.010	—
Waste Half	Post	3[b]	0[b]	0.010	—

$P < 0.01$

Key Words: Pasteurization, Immunoglobulin, Liquid Calf Feeds

W4 Animal performance and blood gas variables of steers pulled and/or treated for Bovine Respiratory Disease. K. M. Bischoff*, L. Carlos-Valdez, B. P. Holland, L. O. Burciaga-Robles, D. L. Step, and C. R. Krehbiel, *Oklahoma State University*, *Stillwater*.

Bovine Respiratory Disease (BRD) is the most economically important disease in cattle. The objective was to characterize performance, blood gases and metabolites of high-risk steers diagnosed with BRD. Steers were evaluated daily for clinical signs associated with BRD (depression, appetite, respiratory stress, and temperature). Steers identified as morbid were assigned a depression score (1=mild to 4=moribund) and pulled to a processing facility where rectal temperature and BW were recorded. Two blood samples were collected; one for blood gas and the second for serum haptoglobin analysis. If a steer had a rectal temperature greater than 40°C, an antimicrobial was administered. If a steer did not meet the rectal temperature criteria, no antimicrobial was administered unless the animal had a depression score of 3 or 4. During the first 21 d, a total of 89 out of 240 steers were enrolled in the study. For data analysis, steers were grouped based on whether they were pulled but not administered an antimicrobial (PULL), or had received one (TX1), two (TX2), or three (TX3) antimicrobial treatments. From the 89 animals enrolled, there were 19 PULL, 23 TX1, 29 TX2, and 17 TX3. Depression scores were lower ($P<0.001$) for PULL compared with TX1, TX2 and TX3. Arrival BW was greatest ($P=0.005$) for PULL and TX1, intermediate for TX3, and lowest for TX2. Average daily gain tended ($P=0.09$) to be greatest for PULL steers. Rectal temperature was lowest ($P<0.001$) for PULL as fever (>40°C) was prerequisite for the remaining groups. Haptoglobin concentration at arrival was not different ($P=0.57$) among treatments. Blood variables including pH, pO2, glucose, lactate, hematocrit, sodium, and SO2 were not affected ($P>0.10$) due to number of antimicrobials administered. Calcium concentrations were lowest ($P=0.02$) for PULL, intermediate for TX1 and TX2, and greatest for TX3. In addition, K was greater ($P<0.001$) for TX1 vs. PULL; TX2 and TX3 were intermediate. Bicarbonate and pCO2 were lower ($P<0.03$) in TX1 and TX2 steers. Our results suggest that some blood gases and metabolites are altered by BRD, and may be useful indicators of disease.

Key Words: Blood Gas, Bovine Respiratory Disease, Cattle

W5 Relationship between total microbial colostrum contamination and IgG absorption in newborn dairy calves. M. Terre*[1] and A. Bach[1,2], [1]*IRTA-Unitat de Remugants*, *Barcelona, Spain*, [2]*ICREA*, *Barcelona, Spain*.

Fifteen newborn Holstein calves (41.2 ± 6.15 kg BW) from 5 different farms were used to study the relationship between colostrum microbial contamination and IgG absorption 6 h after colostrum consumption. Furthermore, colostrum bacteria contamination from the udder to different colostrum containers was also studied. Within 5 h after each calf birth, an initial blood sample was obtained before colostrum was fed, and calves were weighed to estimate plasma volume concentration (assuming plasma represented 8% BW). After that, a first-milking colostrum sample was collected directly from the udder. Then, a second colostrum sample was obtained from the milking bucket, and a third sample was taken from the bucket or teat-feeder where calves were fed to perform total bacterial counts in Nutrient Agar plates and total Enterobacteria counts in MacConkey Agar plates. Then, 1.7 ± 0.64 L of colostrum were fed to calves, and 6 h after the first colostrum consumption another blood sample was harvested. Colostrum IgG concentration from the third colostrum sample, and serum IgG concentration at 0 and 6 h after the colostrum was fed were determined to calculate IgG absorption 6 h after the first colostrum consumption. Total bacteria and Enterobacteria counts increased ($P < 0.001$) from the udder to the milking bucket (from 3.66 to 5.39 ± 0.209 log total bacteria counts, and from 2.45 to 4.69 ± 0.231 log total Enterobacteria counts), but they did not increase from the milking bucket to calf bucket. Furthermore, a negative relationship was observed between log total bacteria counts in colostrum from calf buckets and IgG absorption 6 h after colostrum was fed ($R^2 = 0.26$; $P = 0.05$). However, there was no relationship between log total Enterobacteria counts and IgG absorption 6 h after colostrum consumption. Although there exist many factors that affect IgG absorption (time elapsed from birth to colostrum consumption, IgG colostrum quality) keeping colostrum with low bacteria contamination may help to improve IgG absorption and calf health.

Key Words: Calves, Colostrum, IgG Absorption

W6 Comparison of growth, feed intake, and feed efficiency of female calves fed aureomycin plus lasalocid or monensin. G. E. Higginbotham*[1], R. C. Chebel[2], and L. Pereira[3], [1]*University of California*, *Fresno*, [2]*University of California-Davis*, *Tulare*, [3]*California State University*, *Fresno*.

Objectives were to evaluate growth, feed intake, and feed efficiency of female Holstein calves fed aureomycin and lasalocid (AL) compared to those fed monensin (M). Holstein females calves from a commercial dairy herd located in the central valley of California were enrolled in the study within 12 h after birth. At enrollment, blood was sampled for evaluation of concentration of total proteins and calves were weighed and allotted randomly into 1 of 2 treatments: monensin (M) or aureomycin plus lasalocid (A+L). Feed supplements were mixed into their respective grain starters to provide 60 g/T of monensin and 350 g/T of aureomycin and 60g/T of lasalocid for M and A+L treatments, respectively. During the first 3 wk of life, calves were fed reconstituted commercial non-medicated milk replacer. After 3 wk of age, calves were fed pasteurized waste milk in addition to or as a replacement for milk replacer. From birth to 12 wk of age, calf starter was fed once daily and no hay was offered, feed intake was measured and feces were scored for its consistency (1 = firm, 2 = soft, 3 = runny) daily, and calves were weighed weekly. Feed analysis demonstrated that the amounts of monensin, aureomycin and lasalocid added to the grain starters were actually 44.2, 222.8, and 42.7g/T, respectively. Treatment did not affect average daily weight gain (M = 0.66 ± 0.03, A+L = 0.68 ± 0.03 kg/d; P = 0.59) or average body weight (M = 60.20 ± 0.90, A+L = 60.38 ± 0.92 kg; P = 0.88) during the study. Similarly, there was no effect of treatment on grain intake (M = 648.2 ± 0.04, A+L = 663.4 ±0.04 g/d; P = 0.79) or feed efficiency (M = 0.76 ± 0.06, A+L = 0.72 ± 0.06; P = 49). Fecal score during the study period also was not affected (P = 0.25) by treatment (M = 1.73 ± 0.04, A+L = 1.66 ± 0.04). Treatment did not affect the proportion of calves diagnosed with at least one event of diarrhea (M = 79.5, A+L = 65.0%; P = 0.16) or pneumonia (M = 30.8, A+L = 25.0%; P = 0.53). Supplementation with aureomycin and lasalocid did not improve performance of calves compared to those supplemented with monensin.

Key Words: Calves, Aureomycin, Lasalocid

W7 An international survey on the occurrence of mycotoxins in dried distillers grains with solubles (DDGS). U. Hofstetter*[1] and E. Pichler[2], [1]*Biomin GmbH*, *Herzogenburg, Austria*, [2]*Quantas Analytics GmbH*, *Tulln, Austria*.

Bioethanol production is booming especially in North America. The inclusion of the resulting by-product DDGS – dried distillers grains with solubles – is becoming popular in the global raw material market. However the mycotoxin menace is not eliminated by the fermentation processes during ethanol production. Mycotoxins are toxic metabolites formed by fungi species that colonize crops and thus pose a potential threat to animal health. Mycotoxin contamination of crops may cause economic losses at all levels of food and feed production. Raw material contamination is augmented during the bioethanol production. This study was initiated to provide customers insights in the occurrence of mycotoxins in DDGS samples worldwide thereby enabling better feed management. A total number of 191 samples were analyzed for the major mycotoxins of interest (aflatoxins, zearalenone, deoxynivalenol or vomitoxin, T-2 toxin and fumonisins). The tests have been conducted by Quantas Analytics, Austria, and Romer Labs, Singapore. Aflatoxins, ZON and total FUM were analyzed by HPLC (High Pressure Liquid Chromatography) whereas DON values were obtained by TLC (Thin Layer Chromatography). From all samples analyzed, zearalenone accounted for a 87% contamination rate; 70% of tested DDGS were positive for vomitoxin and 88% for fumonisins. The presence of so-called field mycotoxins (ZON, DON, FUM) produced by different *Fusarium* sp. which – despite Good Agricultural Practice – cannot be avoided totally is very frequent. Almost no aflatoxins and T-2 toxin were found in the DDGS samples collected. Only 13% of the samples were positive for aflatoxin with an average contamination level of 1 µg/kg and only 12% for T-2 toxin with an average contamination level of 11 µg/kg. 96% were tested positive for at least one mycotoxin whereas only 8 samples (4%) of the analyzed DDGS didn't show mycotoxin levels above the detection limit. More interesting was the fact that 97% of the positive samples have shown a co-occurrence of 2 or more mycotoxins. This study confirmed previous literature stating the high levels of mycotoxins in distillers grains.

Table 1. Occurrence of mycotoxins in a total number of 191 DDGS samples

	AfB1	ZON	DON	FUM	T-2
% positive	13	87	70	88	12
Avg. level [µg/kg]	1	208	1504	767	11
Max. level [µg/kg]	89	8107	12000	9042	226

Key Words: DDGS, Mycotoxins

W8 Incubation temperatures affect secretion of TNF-alpha and IL-6 by peripheral blood mononuclear cells from Brown and Holstein cows. N. Lacetera*[1], M. Amadori[2], U. Bernabucci[1], and A. Nardone[1], [1]*Dipartimento di Produzioni Animali*, *Viterbo, Italy*, [2]*Istituto Zooprofilattico Sperimentale Lombardia-Emilia Romagna*, *Brescia, Italy*.

This study aimed at evaluating spontaneous and concanavalin A (ConA)-stimulated secretion of tumor necrosis factor alpha (TNF-alpha) and interleukin 6 (IL-6) by peripheral blood mononuclear cells (PBMC) from Brown (Br) and Holstein (Ho) cows exposed to different treatments (T). PBMC from 7 Br and 7 Ho cows were alternatively subjected to each of the following T: T39) 39°C continuous, T40) 40°C for 39 h and 39°C for 26 h, T41) 41°C for 39 h and 39°C for 26 h, T42) 42°C for 39 h and 39°C for 26 h, and T43) 43°C for 39 h and 39°C for 26 h. Under T40, 41, 42 and 43, three 13 h cycles at 40, 41, 42 or 43°C were alternated with two 13 h cycles at 39°C. T39 mimicked normothermia; T40, 41, 42 and 43 mimicked conditions of hyperthermia alternated with normothermia, which may occur in dairy cows in hot seasons. TNF- alpha and IL-6 were evaluated in supernatants collected at the end of the incubation period by MTT biological assays on WEHI164 and 7TD1 cells, respectively. In both breeds, compared to T39, cultivation of PBMC under T40, 41, 42 and 43 reduced both spontaneous and ConA-stimulated secretion of TNF-alpha. Furthermore, spontaneous secretion of TNF-alpha under T39, was higher in Ho compared to Br cows. In both breeds, IL-6 tended to be higher in PBMC cultured under T40, 41 and 42 compared to T39. Only in Ho cows, IL-6 secretion was reduced in PBMC cultured under T43 compared to T39. Finally, under T39, secretion of IL-6 in ConA-stimulated PBMC was higher in Ho compared to Br cows. Differential regulation of proinflammatory cytokines has been already reported for mammalian cells exposed to stimuli other than temperature. Changes of both TNF-alpha and IL-6 reported

herein may be conducive to a successful adaptation to the perturbation caused by high temperatures. Different responses of the two breeds to temperatures simulating normothermia may reflect differences of the steady state endogeneous inflammatory response associated with different levels of production stress.

Key Words: Temperature, Peripheral Blood Mononuclear Cells, Cytokines

W9 Association of tumor necrosis factor-α *(TNF-α)* gene promoter polymorphisms with TNF-α response to endotoxin (LPS) in calves. S. Kahl*, M. Proszkowiec-Weglarz, E. E. Connor, and T. H. Elsasser, *USDA, Agricultural Research Service*, *Beltsville, MD, USA*.

Attenuation of *TNF*-α gene expression is a NF-κB-mediated regulatory process essential to avoid deleterious effects of excessive or prolonged synthesis of TNF-α, especially in response to gram-negative bacterial infection or LPS. An uncommon G to A transition polymorphism in the promoter region of *TNF*-α gene (designated the TNF-α2 allele) was shown to be highly associated with excessive TNF-α production and TNF-α-mediated pathologies in humans. We performed a preliminary survey to determine if similar polymorphisms exist in Angus × Hereford calves that might suggest a potential for particular animals to have excessive TNF-α responses to LPS challenges. A 574-bp *TNF*-α gene promoter fragment was generated by PCR from bovine genomic DNA and evaluated by bi-directional automated fluorescent sequencing. Two linked single nucleotide polymorphisms were located between NF-κB binding sites at positions -701 (C/T) and -526 (A/G). Calves (n=17; 279 ± 10 kg) were assigned to groups by genotype (4 TT-AA, 5 CT-AG, 8 CC-GG), fed a TMR diet (15% CP) to appetite, and challenged with two consecutive LPS injections 4 d apart (LPS1, LPS2; 0.2 μg *E. coli* 055:B5/kg BW, i.v.). Jugular blood samples were obtained at 0, 1, 2, and 4 h relative to each LPS injection. Plasma TNF-α was measured by RIA and TNF-α response was calculated as area under the time × concentration curve (AUC; ng/mL × h). After LPS1, mean TNF-α responses were greater in TT-AA than CT-AG and CC-GG calves (4.9, 2.2, and 3.0, respectively; $P < 0.05$). While for each calf the TNF-α response to LPS2 was numerically lower than that calculated for LPS1 (indicating LPS tolerance attenuation was achieved), mean TNF-α responses to LPS2 were still greater in TT-AA than CT-AG and CC-GG calves (3.3, 1.0, and 1.1, respectively; $P < 0.01$). The magnitude of the attenuation was less in TT-AA than in CC-GG calves ($P < 0.05$). The results suggest that polymorphisms in the *TNF*-α gene promoter may play a role in the intensity of the TNF-α response to proinflammatory stimuli in cattle.

Key Words: Cattle, SNP, Tumor Necrosis Factor-α

W10 Efficacy of a polyclonal antibody preparation against respiratory disease pathogens on cattle morbidity and performance during the step-up period. C. R. Dahlen*, N. DiLorenzo, and A. DiCostanzo, *University of Minnesota*, *St. Paul*.

A polyclonal antibody preparation (PAP) against respiratory pathogens including *Mycoplasma bovis*, *Haemophilus*, *Pasteurella multocida* and *Mannheimia haemolytica* reduced morbidity and mortality during the first 32 d on feed in lightweight, high morbidity (212 kg and 29%, respectively) calves. However, it is not known whether PAP reduces morbidity in heavier, lower risk (> 15% morbidity) calves, or its effects on intake and gains during the step-up period. Thus, the current study was designed to determine the efficacy of PAP in heavier, lower risk calves. One hundred thirty six Angus and Angus crossbred steer calves (276 kg) were randomly assigned to one of two treatments (Control or intranasal dosing 1.5 mL PAP/nostril on arrival and 7 d later) on arrival at the NWROC research feedlot. Within treatment, calves were then allocated (9 or 10/pen) to one of each of 12 pens for a 27-d diet step-up period. On arrival, at d 7 and 27, rectal temperatures were measured. Calves were considered morbid if rectal temperature recorded > 39.7°C. Body weights, pen and intakes were measured from d 7 to d 27 of the step-up period. Dosing cattle on arrival and 7 d later with PAP reduced ($P = 0.01$) morbidity (5% vs 14%) detected 7 post-arrival. Rectal temperatures did not differ on arrival or at day 27 (38.8 vs 38.9°C and 38.6 vs 38.7°C for Control and PAP, respectively). At day 7 rectal temperatures were lower ($P < 0.05$) for cattle dosed with PAP (39.0 vs 38.8°C for control and PAP, respectively). No effects ($P > 0.10$) of PAP dosing were observed on DMI, ADG or feed conversion during the step-up period. A reduction in morbidity of 9 percentage units represents economic savings in medication and labor costs.

Key Words: Antibodies, Health, Cattle

W11 Effect of rubber flooring on leukocyte activation during the periparturient period. K. O'Driscoll[1,2], M. M. Schutz[3], and S. D. Eicher*[4], [1]*Teagasc*, *Fermoy, Ireland*, [2]*NUI Dublin*, *Dublin, Ireland*, [3]*Purdue University*, *West Lafayette, IN*, [4]*USDA-ARS*, *West Lafayette, IN*.

This study aimed to evaluate the effect of 2 dairy cow housing systems on innate immune status during the peri-parturient period. Leukocyte counts, phagocytic ability and neutrophil and monocyte differentiation were examined. Cows were assigned to free-stall housing with either rubber (RUB; n=13) or concrete (CON; n=14) at the feed-face immediately after their first calving, and managed on this system during all subsequent lactations. Between lactations cows remained in a straw bedded-pack dry cow pen. A year-round calving system was utilized. Cows entered the experiment at the end of either their 1st (n=16) or 2nd (n=11) lactations. Blood samples were obtained approximately -60, -30, 0, +7 and +14 d relative to calving. Differential leukocyte counts were obtained using an automated cell counter. Phagocytic activity, and cells positive for CD14 and CD18 expression were measured by flow cytometry using labelled micro-beads and antibodies. Treatment effects were determined using repeated measures ANOVA. An interaction of treatment and d ($P<0.05$) on neutrophil and lymphocyte counts ($P<0.05$) was found. RUB cows had higher neutrophil and lower lymphocyte numbers post calving than CON. Neutrophil to lymphocyte ratio tended ($P=0.1$) to be higher for RUB than CON cows post calving. There was no effect of treatment on phagocytosis or percentage of cells positive for CD14 or CD18 However, d tended ($P=0.1$) to have an effect on phagocytic events, with the highest value at d -60. Cells positive for CD14 were greatest on d 0 ($P<0.05$), and a treatment by d effect was found for cells positive for CD14. CD14 percentages were greater for RUB than CON cows post calving. A high neutrophil to lymphoctye ratio is associated with physiological stress, but suppressed leukocyte function is associated with peri-partuient period. Thus, the ability of RUB cows to activate neutrophils and monocytes is indicative of an improved immune response.

Key Words: Rubber Flooring, Cow Locomotion, Innate Immune Activation

W12 Functional evaluation of polymorphisms in the bovine IL-8 gene promoter. S. Kandasamy*, K. L. Haddock, and D. E. Kerr, *University of Vermont*, *Burlington*.

An early event in the response of the host to infection is the release of chemokines to attract neutrophils and other immune cells to the site of infection. An early robust response may be critical in containing and eliminating the pathogen, but the potential exists for an exaggerated response leading to collateral tissue damage. Our objectives were to determine if SNPs exist in the 5′-regulatory region of the bovine IL-8 gene and if so to determine if they affected functionality of the gene in response to LPS treatment. We located 5 SNP sites through individual sequencing of PCR products (extending 1 kb upstream from the translation start site) from DNA of 28 Holstein cattle. In all cases the 5 SNPs were linked resulting in two haplotypes (A or B). We have now genotyped an additional 10 animals by PCR-RFLP giving a total of 14 AA, 16 AB, and 6 BB genootypes (61%A, 39%B). The two haplotypes were cloned into luciferase expression vectors (pGL-3 basic), with subsequent transfection into bovine mammary epithelial cells (Mac-T). Cells were also co-transfected with a GFP expression plasmid (pCMV-GFP) as a transfection control. Following LPS exposure (100ng/ml, 24h), cell extracts were prepared and assayed for fluorescence then combined with Bright-Glo Reagent (Promega) and assayed for luminescence. Substantial levels of luciferase activity were recorded from both haplotypes under control and LPS-stimulated conditions. However, the A haplotype generated more luciferase activity (1.25 vs 0.85 relative units) although there was no direct effect of LPS nor an LPS*haplotype interaction in this model. In a second experiment, heparinized whole blood from homozygous AA or BB animals (n=3) was stimulated with LPS (1, 10, and 100 ng/ml, or vehicle) for 3h or 6h. The concentration of IL-8 in the subsequently obtained plasma was highest following 6 h exposure to 100 ng/ml dose of LPS (157±13 pg/ml vs 42±14 in control). Overall the concentration of IL-8 was significantly ($P<.01$) affected by LPS, by exposure time, and was greater in blood from AA animals. It remains to be determined if differences exist between AA and BB animals in their response to infectious pathogens.

W13 Genomic response of immune associated genes to LPS challenge in bovine mammary gland and epithelial cells. D. E. Kerr*, M. Latshaw, and R. Parik, *University of Vermont*, *Burlington*.

The innate immune response to bacterial entry into the mammary gland is critical in determining the outcome of mastitis. Our goal was to profile the transcriptional response of mammary tissue and epithelial cells to an LPS challenge to further our understanding of the bovine innate immune system. Sources of RNA applied to Affymetrix GeneChips included biopsy samples from LPS-challenged (1 ug/gland) and contralateral control mammary glands of 3 lactating cows 4 h post-LPS challenge (COW); and from LPS-stimulated (100 ng/ml) or control cultures of primary mammary epithelial cells from different cows 3 h (C3), 8 h (C8), and 24 h (C24) post-LPS exposure. Filtering the data at a fold change ≥2.0 or ≤-2.0, and $P<.05$ revealed differential expression of 3.0%, 0.6%, 1.5%, and 1.6% of the 24,128 probe sets contained on the chip for COW, C3, C8, and C24, respectively. A common core of 47 induced probe sets included 3 of 26 genes on the GeneChip associated with the TLR4 signaling pathway (NFKB1, NFKBIA, and NFKBIZ), 4 members of the neutrophil attracting, ELR positive CXC chemokines (CXCL1, CXCL2, CXCL6, and IL-8), 2 additional chemokines (CX3CL1, CCL2) and inflammatory associated proteins (IL6, LTF, SAA3, PLAU, SOD2, S100A8). Key differences between cells and biopsies in the TLR4 signaling pathway included induction of CD14 by cells and of TLR4 in the tissue. Additional differences between cells and tissue included marked induction (>5 fold) of IL1B, CCL5, and CCL20 in the cells and marked induction of CCL4, CCL8, CCL23, and IL1RN in the tissues. Notable time dependent changes in the cell response included a continual increase ($P<.01$) in the fold change response of SAA3 and S100A8 and the delayed induction of interferon regulated proteins MX1, MX2, IFI6, and ISG15. These studies have revealed a rapid, robust response of the bovine mammary gland and epithelial cells to LPS. The genomic response includes a core of common genes and distinct time and source differences, yet appears dominated by activation of the NF-kB complex leading to upregulation of inflammatory cytokines and multiple members of the chemokine gene family.

W14 Genetic analysis of dairy calf health traits and survival. L. Henderson*[1], F. Miglior[2,3], D. Kelton[1], J. Robinson[4], J. Wormuth[5], A. Sewalem[2,3], and K. Leslie[1], [1]*University of Guelph*, *Guelph, ON, Canada*, [2]*Dairy and Swine Research and Development Centre, Agriculture and Agri-Food Canada*, *Sherbrooke, QC, Canada*, [3]*Canadian Dairy Network*, *Guelph, ON, Canada*, [4]*University of Guelph*, *Guelph, ON, Canada*, [5]*CY Heifer Farms*, *Batavia, NY*.

Genetic selection for improved health and longevity is a major initiative of dairy cattle breeding programs. Recently, extensive efforts have been made to improve selection indices for calf survival at birth in Canadian dairy cattle. To date, little effort has been put into exploring the genetic components of measures of calf health, survival and performance from birth until the post-weaning period. The objective of this study is to evaluate the heritability and genetic correlations of calf health traits based on measures of passive transfer of immunity, disease occurrence, survival and growth from birth to weaning for a large population of Holstein calves. Health and performance records were available from approximately 10,000 dairy heifer calves from a commercial heifer raising facility in western New York. Data was recorded from arrival of the calf at 2-5 days of age for the duration of stay at the facility. At enrollment, calves were weighed and evaluated for passive transfer of immunoglobulins from colostrum feeding. A standard protocol was followed for health management practices, disease recording and therapy throughout the growing period. All disease occurrences, treatments, management events and weight measurements were recorded in DairyComp 305 to create a complete record for each animal. In a subset of these data, 650 calves from 20 Holstein sires have been analyzed. The number of calves per sire ranged from 16 to 82, with an average of 35 per sire. The average serum total solids in calves by specific sire group ranged from 6.2 to 7.2 g/dL. The average daily gain for the growing period by sire group ranged from 650 to 900g/day. These data along with mortality rates suggest that there may be significant genetic differences among Holstein calves for health status in the early neonatal period, susceptibility to neonatal disease problems, and for survival to weaning.

Key Words: Genetics, Calf-Health, Survival