W16 Hair whorls locations of dairy heifers affects their growth, but not behavior. J. Broucek*[1], S. Mihina[1], M. Uhrincat[1], C. W. Arave[2], P. Kisac[1], and A. Hanus[1], [1]*Research Institute of Animal Production*, *Nitra, Slovakia*, [2]*Utah State University*, *Logan*.

We tested hypothesis that growth, time solving the maze (TSM) and number of grid crossings (GC) in open-field tests (OFT) are affected by the height location of facial whorl in heifers. 58 Holstein heifers were used. They originated from 2 sires. Differences between sire lineage's were not significant in any trait. Whorl placement was recorded by one person as each heifer entered the scale as hair whorl (HW) high (if the whorl was above the top of eyes), middle (if the whorl center was located between the top of the eyes and the bottom of the eyes) and low (if the center was located below the bottom of the eyes). Heifers were kept in hutches and fed 6 kg milk replacer (0.6 kg powder) per d until 8 wks. After weaning all heifers were kept in loose housing pens according to age and size, regardless the HW positions. Equal conditions of nutrition were ensured. Experimental conditions were as follows: The maze tests were performed in the indoor space at the age of 15 wks. Animals were deprived of concentrate prior to maze tests. A bucket with 1 kg of concentrate was placed at the exit. The heifers had to solve 2 tasks on two consecutive days. On the first day, the passage was open on the left side, and on the right side on the second day. Before the first test was one training run. Each day, the heifers were tested 4 times, TSM was measured from video tape. OFTs (one 5-min test, morning) were conducted at 16 wks and 18 months in an inside arena, visually and acoustically isolated from other animals. Number of GC were recorded. The data were analyzed using a GLM/ANOVA. We did not find any significant differences in behaviors. Heifers with a high hair whorl were the fastest during the maze tests and they had the highest GC at the both ages. Heifers with a high HW had the highest BW at days 360 ($P<0.05$) and 540 ($P<0.01$) and ADG from birth to 21 months ($P<0.001$) and from the 6th to 21st months ($P<0.01$) of age. We found that the growth was influenced in dairy cattle by height of their facial whorl, but the time of solving the maze and the locomotive activity in open-field testing was not.

Key Words: Dairy heifers, Hair whorl, Growth

W17 Effect of transport for up to 24 hours followed by twenty-four hours recovery on liveweight, physiological and hematological responses of bulls. B. Earley*, D. J. Prendiville, and E. G. O' Riordan, *Teagasc, Grange, Beef Research Centre*, *Dunsany, Co. Meath, Ireland*.

The objective of the study was to investigate the effect of road transport on liveweight, physiological and hematological responses of bulls after journeys of 0, 6, 9, 12, 18 and 24h. Eighty-four continental x bulls (mean weight (s.d.) 367 (35) kg) were randomly assigned to one of six journey (J) times of 0 (0km), 6 (280km), 9 (435km), 12 (582km), 18 (902km) and 24h (1192km) at a spatial allowance of 1.02m^2/bull. Blood samples were collected by jugular venipuncture before, immediately after and at 1, 2, 4, 6, 8, 12 and 24h. Bulls were weighed before, immediately after, and at 4, 12 and 24h. Blood samples collected into heparinized tubes were centrifuged and the plasma separated for subsequent analysis of: globulin, albumin, total protein, and creatine kinase. The hematological variables including red blood cell number (RBC), hemoglobin (Hb), hematocrit (packed cell volume (PCV)), mean cell volume (MCV), white blood cell (WBC) count, number of lymphocytes and neutrophils were determined for unclotted (K_3EDTA) whole blood. There were no differences ($P\geq0.05$) in rectal body temperature, pre- and post-transport, or liveweight among treatments on days 0 (pre-transport). Bulls traveling for 6, 9, 12, 18 and 24h lost 4.7, 4.5, 5.7, 6.6 and 7.5 percentage liveweight compared with the -24h baseline. There was no change ($P\geq0.05$) in globulin, albumin, total protein, or creatine kinase concentrations before or after transport. Neutrophil numbers (mean ± s.d) were greater ($P\leq0.01$) in all transported animals post-transport (J6,55±6.7; J9,60±10.1; J12, 48±16.8; J18,46±10.9, J24, 48±6.9) and counts returned to baseline by 24 hours for the J6 (30±15.0), J12 (34±9.3), J18 (36±12.1) and J24 (43±11.3) treatments. Control animals had greater ($P\leq0.01$) neutrophil numbers at the 6, 8, 12, and 24h sampling time periods as transported animals. Transport of bulls from 6 to 24h did not impact negatively on animal welfare. In conclusion, liveweight, physiological and hematological responses of bulls returned to pre-transport levels within 24h with animals having had access to feed and water.

Key Words: Transport, Physiology, Immune response

Animal Health III

W18 Maternal stress: Effect on the stress response and immune function of the progeny. M. Reyna*[1], S. Martinez[1], T. H. Welsh, Jr.[2], J. A. Carroll[3], and J. C. Laurenz[1], [1]*Texas A&M University*, *Kingsville*, [2]*Texas A&M University and Texas Agriculture Experiment Station*, *College Station*, [3]*USDA-ARS Livestock Issues Research Unit*, *Lubbock, TX*.

This study examined the effects of maternal stress on the stress response and immune function of the pig. Pregnant sows were assigned by parity to one of two treatments and either managed per current industry standards (Control; n=4) or subjected to a daily 5 min acute restraint stress from d 85 to 110 of gestation (Stressed; n=4). Following farrowing, pigs (n=37 from Control sows; MC; and n=31 from Stressed sows; MS) were weighed and tattooed. Pigs were subsequently reweighed at weekly intervals and average daily gain (ADG) calculated. At day 21, pigs were weaned and allowed 14 days to adapt to the new environment. Pigs were subjected to an acute restraint stress (3 min) and blood samples collected. Plasma concentrations of cortisol (C), epinephrine (E), norepinephrine (NE), and dopamine (D) were determined. To assess immune function, pigs were immunized against keyhole limpet hemocyanin (KLH) and serum samples obtained prior to immunization (d=0), and at 3, 7, 14, 21, 28, and 35 d post-immunization. Total immunoglobulin G (IgG) and KLH-specific IgG were determined. ADG during the pre-weaning period (d 1 to 21) was lower ($P < 0.05$) in MS vs. MC pigs (222 ± 8 vs. 247 ± 7 g/d, respectively). Gender affected C, with female pigs having greater ($P < 0.05$) C then male pigs (72 ± 6 vs. 50 ± 4 ng/mL) during an acute restraint stress. There was a maternal treatment by gender interaction, with male MS pigs having C concentrations lower then MC males and similar ($P > 0.05$) to female pigs. Regardless of gender, MS pigs had lower ($P < 0.05$) levels of E, NE and D. Immunization against KLH resulted in time-dependent increases ($P < 0.05$) in both total and KLH-specific IgG, with peak concentrations occurring at d 21 and 28 post-immunization, respectively. Although not affecting the temporal pattern, MS pigs had reduced ($P < 0.05$) total and KLH specific-IgG in response to immunization. These results indicate that maternal stress can dramatically impact the stress response of the progeny with an associated detrimental effect on immune function.

Key Words: Maternal stress, Immune function, Pig

W19 Maternal stress modulates the acute stress response and immune function of the pig. N. C. Burdick*[1], T. H. Welsh, Jr.[2], J. A. Carroll[3], and J. C. Laurenz[1], [1]*Texas A&M University*, *Kingsville*, [2]*Texas A&M University*, *College Station*, [3]*USDA-ARS Livestock Issues Research Unit*, *Lubbock, TX*.

This study examined the effects of maternal stress on the response of the pig to acute restraint stress and in vitro measures of immune function. Pregnant sows were assigned by parity to one of two treatments and managed per current industry standards (Control; n=2) or subjected to a daily 5 min acute restraint stress from d 85 to 110 of gestation (Stressed; n=2). After farrowing, pigs (n= 12 from control sows; MC; and n=15 from stressed sows; MS) were weighed and tattooed for permanent identification and managed similarly throughout the remainder of the study. At 35 d of age, pigs were restrained and blood collected initially (t = 1.5 ± 0.1 min), and at 3 and 6 min. Plasma was collected and analyzed for cortisol (C), epinephrine (E), norepinephrine (NE) and dopamine (D). To assess immune function, lymphocytes were isolated using density gradient centrifugation. Cells were plated in DME/F12 media containing Concanavalin A (ConA; 0 to 10 ug/mL) and cultures incubated for 96 hours (37C and 5% CO2). Following incubation, IgM production and the extent of proliferation were determined. Plasma C did not differ ($P > 0.05$) between MS and MC pigs, and increased ($P < 0.01$) with duration of restraint (40±5 vs. 75±5 ng/mL for 1.5 vs. 6 min). Plasma E and NE increased with duration of restraint, ($P < 0.05$) and MS pigs had lower ($P < 0.05$) E and NE than MC pigs. In MC pigs, D increased ($P < 0.05$) with duration of restraint. In contrast, in MS pigs D was not affected ($P > 0.05$) by restraint, and D was lower in MS relative to MC (1.6 ± 0.2 vs. 2.9 ± 0.3, respectively). ConA induced dose-dependent increases ($P < 0.01$) in lymphocyte proliferation and IgM production. The extent of proliferation was not affected ($P > 0.05$) by duration of restraint. In contrast, IgM production by cultures decreased ($P < 0.05$) with increasing time of restraint. Regardless of duration of restraint, cultures established from MS pigs had a reduced ($P < 0.05$) proliferative and IgM response to ConA than MC pigs. These results indicate that maternal stress affects the stress response of the progeny which may have a negative impact on immune function.

Key Words: Acute restraint stress, Immune function, Reprogramming

W20 Non-nutrient additives alter the weaned pig's stress response to a *Mycoplasma hyponeumoniae* vaccination. J. Carroll*[1] and K. Haydon[2], [1]*Livestock Issues Research Unit, Agricultural Research Service-USDA*, *Lubbock, TX*, [2]*Prince Agri Products, Inc.*, *Quincy, IL*.

Previously we demonstrated that the acute phase response of weaned pigs following a lipopolysaccharide challenge can be altered with non-nutrient additives. The current objective was to evaluate three non-nutrient additives as potential modulators of the stress and immune responses of pigs following vaccination for *Mycoplasma hyponeumoniae*. Pigs (n=32; 6.3 ± 0.1 Kg) were weaned at 21.4 ± 0.3 d and moved to an off-site nursery where they were weighed, blocked by BW, and assigned to one of four treatment groups: 1) Control pigs (Cont; n=8) fed a non-medicated starter ration, 2) Pigs supplemented with 0.4% of experimental blend B (Exp B, n=8), 3) Pigs supplemented with 0.4% of experimental blend C (Exp C, n=8), and 4) Pigs supplemented with 0.4% NeutroMAX (NM, n=8). NM is a proprietary blend (patent pending) with proven immune enhancing properties. Exp B and Exp C are experimental 'next generation' NM blends. Pigs were individually housed and fed *ad libitum* for 10 d. Feed intake and BW were collected on d 5 and 10. On d 10, all pigs were non-surgically fitted with an indwelling jugular catheter. On d 11, all pigs received an i.m. dose (2 mL) of a *Mycoplasma hyponeumoniae* vaccine (RESPISURE-ONE®) at time 0 and blood samples collected at 30-min intervals from -2 h until 6 h, and then at 24 h. Catheters were removed and the pigs maintained on their respective diets for an additional 13 d. Blood samples were collected on d 7 and 14 post-vaccination via venipuncture. Whole blood samples were utilized for hematological measurements and serum samples were analyzed for cortisol. ADG prior to vaccination was greater ($P < 0.04$) in the NM and Exp B groups compared to the Cont group. However, post-vaccination, growth was similar in all groups. Prior to vaccination, lymphocyte ($P < 0.08$) and neutrophil ($P < 0.01$) cell counts were higher in the Exp B and Exp C groups compared to the Cont group. During the first 24 h post-vaccination, serum cortisol was greater ($P < 0.02$) in the Cont group compared to all other groups. These data suggest that non-nutrient additives can alter the stress response associated with a *Mycoplasma hyponeumoniae* vaccination.

Key Words: Pig, Stress response

W21 Three strategies to counteract the negative impact of mycotoxins on piglets. U. Hofstetter*[1], D. Schatzmayr[1], G. Schatzmayr[1], and E. M. Binder[2], [1]*Biomin GmbH*, *Herzogenburg, Austria*, [2]*Erber AG*, *Herzogenburg, Austria*.

Mycotoxins are toxic chemical products formed by fungi species that colonize crops and pose a potential threat to human and animal health as many of these toxins are acutely toxic, immunosuppressive, genotoxic, and show estrogenic effects. The purpose of this study was to investigate the impact of deoxynivalenol (DON) and zearalenone (ZON) on growth performance, blood biochemistry and immune response of pigs and the alleviating effects of a detoxifying feed additive (Mycofix Plus) based on the following three different strategies. A strictly anaerobic bacterium belonging to *Eubacterium sp.* (BBSH 797) is capable of detoxifying trichothecenes by enzymatic reduction of the toxic 12,13-epoxy-group and the newly discovered yeast strain *T. mycotoxinivorans* detoxifies ochratoxins and zearalenone. As all mycotoxins are known to damage the liver and to cause immunosuppression in animals, plant and algae extracts were selected to overcome these negative influences. A total of 48 weaning piglets were randomized allotted to four treatments including a negative control group which got neither mycotoxins nor feed additive, a toxin group (1 mg/kg DON and 250 µg/kg ZON), a trial group (1 mg/kg DON, 250 µg/kg ZON and 1.5 kg/t feed additive) and a positive control group which received the feed additive alone for 6 weeks with two replicates per treatment. The results of different evaluated parameters including growth performance, serum biochemistry parameters, alveolar macrophages activity, antibody titers for PR vaccine and cytokines secretion profile showed that DON and ZON caused an impairment in piglets after 6 weeks of exposure. Histopathological findings and blood biochemistry suggest that the combination of DON and ZON causes a multi-organ toxicity in pigs. All these detrimental effects were overcome by addition of the new feed additive. This study also suggests that levels below the critical value of DON and ZON for farm animals published by BML (1 mg/kg DON and 250 µg/kg ZON in starting and finishing pig diets) still have adverse and toxic effects.

Key Words: Deoxynivalenol (DON), Zearalenone (ZON), Immune function

W22 Successful detoxification of ochratoxin A in weaning piglets. U. Hofstetter*[1], D. Schatzmayr[1], G. Schatzmayr[1], and E. M. Binder[2], [1]*Biomin GmbH*, *Herzogenburg, Austria*, [2]*Erber AG*, *Herzogenburg, Austria*.

Mycotoxins are secondary metabolites produced by fungi in certain stress periods. They can cause insidious losses, ill thrift and reduced disease resistance. While the use of products based on aluminosilicates gave good results in counteracting aflatoxins the adsorptive deactivation of other toxins failed under field conditions. A novel yeast strain with the capability of degrading ochratoxin A (OTA) was isolated and characterized. A trial with weaning piglets was conducted to prove the efficacy of the feed additive *T. mycotoxinivorans* in pig diets contaminated with ochratoxin A. 48 weaning piglets were randomly assigned to 4 groups. A positive control group (no product, no toxin), a negative control group (no toxin but 1x10 ^{5} CFU *T. mycotoxinivorans* /g feed), a toxin group (500 ppb OTA, no product) and a trial group(500 ppb OTA and 1x10 ^{5} CFU *T. mycotoxinivorans* /g feed). At the end of week 2 all animals showed mild symptoms of diarrhea for 2 days. The animals were weighed separately on day 1, 14 and 42. Analysis of the data revealed differences between the negative control group and the toxin group, which could be improved by the addition of *T. mycotoxinivorans* so that the difference between toxin group and trial group was improved about +10.2%. For daily weight gain the same results could be obtained as for live weight. Daily weight gain was significantly reduced in the toxin group compared to both control groups. With the addition of *T. mycotoxinivorans* daily weight gain could be improved. Feed intake was reduced clearly in the toxin group and was improved in the trial group. Feed conversion rate (FCR) was much higher in the toxin group compared to all other groups. Feedstuff with 500 ppb OTA caused a clear depression in performance in the toxin group. *T. mycotoxinivorans* could compensate these effects and increase daily weight gain, improve feed consumption and thus improve feed conversion in rearing piglets.

Key Words: Mycotoxins, Biotransformation, Growth performance

W23 The effect of butyrate on cytokine production and proliferation by porcine monocytes. T. E. Weber*[1], C. G. Chitko-McKown[2], and B. J. Kerr[1], [1]*USDA/ARS, National Swine Research and Information Center*, *Ames, IA*, [2]*USDA/ARS, Meat Animal Research Center*, *Clay Center, NE*.

Although butyrate modulates the immune system in some species, the role of butyrate as a regulator of immune function in the pig has not been studied. Therefore, the primary objective of this study was to determine whether butyrate influences the proliferation, cytokine secretion and mRNA expression by porcine immune cells in vitro. For experiments using peripheral blood mononuclear cells (PBMC), blood was collected from healthy pigs (n = 6), and PBMC were isolated to test the effect of sodium butyrate (0, 0.2, or 2.0 mM) on the blastogenic response to concanavilin A (Con A; 5 μg/mL) and cytokine expression and secretion. Cytokine mRNA abundance was determined using real-time reverse transcriptase PCR, and cytokine secretion was measured via enzyme-linked immunoassay (ELISA). Butyrate at 2.0 mM, but not 0.2 mM, suppressed ($P < 0.05$) Con A-induced PBMC proliferation and led to a paradoxical increase ($P < 0.05$) in interleukin-2 (IL-2) mRNA expression. The secretion and mRNA expression of interferon-γ (IFN-γ) by Con A-activated PBMC was increased several-fold ($P < 0.05$) by butyrate at 2.0 mM. Treating activated PBMC with butyrate at 2.0 mM decreased ($P < 0.05$) the secretion of IL-10. In contrast, butyrate at 0.2 mM increased ($P < 0.05$) both IL-10 secretion and mRNA expression. To test the effect of butyrate on cytokine expression by porcine macrophages, cells from a porcine monocyte-derived macrophage cell-line were cultured with E. coli. lipopolysaccharide (LPS;10 μg/mL) in the presence or absence of sodium butyrate (2.0 mM). Activating the macrophages with LPS increased ($P < 0.05$) the mRNA expression of tumor necrosis factor-∝ (TNF-∝) at 2 h post treatment and IL-6 at 2 h and 4 h post treatment. Treating the activated-macrophages with sodium butyrate tended ($P < 0.07$) to decrease the expression of TNF-∝ at 2 h and partially reversed ($P < 0.05$) the induction of IL-6 by LPS at 4 h post treatment. These data indicate that the effect of butyrate on proliferation and cytokine production by porcine PBMC is dose-dependent, and provide evidence that butyrate decreases the expression of inflammatory cytokines by porcine macrophages.

Key Words: Butyrate, Pig, Immune system

W24 Expression of an active Colicin E1 in the yeast pichia pastoris. S. A. Cutler* and C. H. Stahl, *Iowa State University*, *Ames*.

Escherichia coli infections, causing post-weaning diarrhea or edema disease, are one of the most commonly reported disease problems in young pigs in this country, causing substantial losses to the swine industry due to both mortality and morbidity. With worldwide concern over the use of prophylactic antibiotics in animal agriculture, the development of new products to protect swine from E. coli infections is urgently needed. We have previously shown that Colicin E1 is highly effective against the E. coli strains (F4 and F18) responsible for post-weaning diarrhea and edema disease in pigs. In order to make a colicin product more cost-effective for use in swine diets, we recombinantly expressed Colicin E1 in the yeast Pichia pastoris. The Colicin E1 gene was amplified by PCR and ligated into a yeast expression vector, pPICZαC, under control of the methanol inducible AOX1 promoter. The construct was then chromosomally integrated into P. pastoris X33 by electroporation. Transformants were selected by Zeocin resistance. Both the supernatant and cell extract of the transformed yeast were screened for colicin activity by spot testing onto lawns of E. coli DH5α. Yeasts demonstrating the highest colicin activity were selected for batch fermentation studies. Time course studies demonstrated that maximum Colicin E1 levels were obtained in the cell extract after 4d of methanol induction. No detectable colicin activity was found in the supernatant. The level of expression obtained in the yeast was comparable to that obtained with Mitomycin C induction of the native Colicin E1 producing E. coli, approximately 100U/mL of culture. Expressing an active Colicin E1 as an intracellular protein in P. pastoris is advantageous because both purification and processing costs would be dramatically reduced because the yeast may be directly fed to the piglets post-weaning. The production of Colicin E1 by a yeast system holds promise as an alternative to conventional antibiotics for the treatment/prevention of E. coli disease in pigs.

Key Words: Swine, Diarrhea, Yeast

W25 Polymorphisms within the *lactoferrin* gene promoter in various cattle breeds. M. Daly[1], O. Casey[1], F. Buckley[2], P. Ross[1], and L. Giblin*[1], [1]*Moorepark Food Research Centre*, *Teagasc, Fermoy, Co. Cork, Ireland*, [2]*Moorepark Dairy Production Research Centre*, *Teagasc, Fermoy, Co. Cork, Ireland*.

Lactoferrin is an iron binding glycoprotein known for its antimicrobial properties. It is expressed in a species–, tissue– and cell type–specific

manner. In milk, this protein provides protection to infant mammals and plays a key role in defence of the maternal mammary gland against infection. The aim of this study was to increase our knowledge of polymorphic variation in the bovine *lactoferrin* promoter. Oligonucleotide primers were designed to amplify and sequence this region in a total of 58 cattle from 5 different cattle breeds (Holstein Friesian, New Zealand Holstein, Montebéliard, Normande and Norwegian Red). In total 15 different single nucleotide polymorphisms (SNP) were identified, 9 of which were novel and located at positions –765, –610, –599, –585, –457, –271, –255, –190 and –132 respectively. In general, the identified SNPs were widespread throughout the various breeds. However, 3 of the novel SNPs only occurred in a Montebéliard at positions –457, –255 and –132 and one was only present in a Normande at position –765. The most frequently encountered polymorphism (52%), found in all breeds was at position –28, which is immediately proximal to the TATA box of the promoter. The most variable base position was –131, which included three heterozygote and three homozygote variants. This polymorphism occurs in a putative transcription factor binding site, for the Nuclear factor of activated T cells. Norwegian Red cattle, which have been selected for mastitis resistance, displayed fewer polymorphisms than other breeds with most nucleotide changes occurring at positions –190, –156, –131 and –28. These unique SNP profiles may contribute to their low somatic cell count averages and/or their inherent resistance to udder pathogens. Individual SNPs or SNP combinations may result in the identification of stronger *lactoferrin* promoters. Higher levels of Lactoferrin could contribute to improved health of the mammary gland by lowering the severity and/or incidence of mastitis.

Key Words: Bovine, Lactoferrin

W26 Using microarray analysis to decipher gene expression in mastitis causing *Escherichia coli* exposed to bovine whey. M. Worku*, J. Bowman-Simpson, and P. Matterson, *North Carolina Agricultural and Technical State University*, *Greensboro*.

Escherichia coli cause mastitis upon entry into the mammary gland where exposure to milk components such as whey, occurs. Infection with *Escherichia coli*, release of endotoxin and the resulting inflammation is associated with changes in milk composition, loss of production and has consequences for animal health. Exposure to immune factors in whey are important in combating infection through immunomodualtion and can impact bacterial pathogenesis. The objective of this study was to evaluate the effect of host immune factors in whey on gene expression in *E.coli* using microarray analysis. A mid-log culture of *E.coli* isolated from an acute case of clinical mastitis was grown. Whey samples were prepared from clinically healthy cows. The samples were heat inactivated (56°C, 30 min.). Six samples of *E. coli* (109) were incubated in RNase free Phosphate Buffered Saline (PBS) as negative controls. Six samples were incubated with a 1:1 dilution of the inactivated whey (10 min., 37°C). RNA from control and treated samples was isolated using the RNeasy (Quaigen) kits. The integrity and size distribution of total purified RNA was checked on ethidium bromide stained denaturing agarose gels and using a bioanlyzer. Two *E. coli* K12 Starter V2 array chips consisting of 2 identical grids with a total of 192 spots (MWG Biotech, High Point) were used for expression profiling of *E. coli*. Data were analyzed using MicroArray Genome Imaging and Clustering Tool (MAGIC Tool) Version 1.0 an open source program. Exposure of *E. coli* cultures to whey components resulted in transcriptional up regulation of all heat shock related *E. coli* genes when compared to samples maintained in PBS. Following log transformation three genes were markedly up-regulated as indicated by values greater than 3 for the expression ratio. The gene encoding 2-oxoglutarate dehydrogenase was down regulated (- 2). The differential expression of these genes may serve to identify pathways for the control of *E. coli* mastitis and indicate targets for intervention.

Key Words: *E. coli*, Microarray, Whey

W27 Microarray analysis of bovine blood neutrophils exposed to *E. coli* endotoxin. M. Worku*, P. Matterson, and Z. Li, *North Carolina Agricultural and Technical State University*, *Greensboro*.

Polymorphonuclear leukocytes (PMNs) are key players in the inflammatory response to bacterial products such as endotoxin (LPS). Endotoxins are components of the outer cell wall of gram negative bacteria. Few studies have addressed the effects of LPS on global gene expression in bovine blood PMNs. This study aims to explore the utility of microarray analysis for evaluation of the effects of LPS on global gene expression in bovine PMN. Blood PMN (8 million) isolated from a clinically healthy cow were exposed to LPS (10 ng/million cells). Total RNA was isolated from control and treated samples. RNA quality and quantity were evaluated using a Bioanlayzer. RNA was provided to Paradigm Array labs (Icoria) where following quality and quantity assessment cRNA was produced labeled and hybridized to GeneChip bovine arrays with approximately 23,000 bovine transcripts (Affymetirx). Comparison expression analysis compared the cell intensity data of the LPS treated samples to a baseline GeneChip® expression probe array (of control samples). This comparison analysis identified the relative change in the expression level of each transcript represented on the probe array. The procedure for selecting robust changes between control and experimental GeneChip probe arrays was based upon Affymetrix GCOS guidelines, using default parameters for probe detection, comparison analysis between experimental and baseline arrays, and signal log ratios. The final dataset resulted in all probe sets with at least either a two-fold increase or two-fold decrease in expression. Thus, in the LPS treated sample 12,874 genes were detected. In the control sample 13,263 genes were detected. Changes in gene expression were observed in 540 genes. At least a two fold increase in expression was observed in 111 genes. A two fold decrease in expression was observed in 429 genes. The types of transcripts impacted are being characterized. Global gene expression in bovine PMN was differentially impacted by exposure to LPS. Microarray analysis proved to be a useful tool for evaluation of the effects of LPS on global gene expression in bovine PMN.

Key Words: Neutrophil, Endotoxin (LPS), Microarray

W28 Increased pulmonary arterial pressure (PAP) and maternal undernutrition induces differential gene expression in right ventricle of steers. B. Berg*[1], B. Hess[1], S. P. Ford[1], K. McInnerney[2], W. Means[1], T. Hansen[3], and H. Han[1], [1]*University of Wyoming*, *Laramie*, [2]*Montana State University*, *Bozeman*, [3]*Colorado State University*, *Fort Collins*.

Brisket disease, characterized by elevated pulmonary arterial pressure (PAP) and right ventricular hypertrophy, is primarily observed at altitudes over 1500m, and is due to decreased levels of atmospheric oxygen. We hypothesized that maternal undernutrition programs right ventricular gene expression and sensitivity to high altitude stress (2200m). Forty AngusXGelbvieh cows were grouped by BW from 30 to 125 days of gestation. On day 30 of gestation, cows were divided in equal numbers and fed either to meet NRC requirements (control; C) to

gain weight (average = +4.25% BW) or fed below NRC requirements (nutrient restricted; NR) to lose weight (average = -6.8% BW) from day 30-125 of gestation. On day 126 of gestation NR cows were realimented so as to achieve the same BW and BCS as controls as d250 of gestation. Parturition occurred naturally. Pulmonary arterial pressure of 15-mo-old steers from C or NR cows were measured before slaughter (values ranged from 40-114 mmHg). Hearts were collected from steers, separated into right and left ventricles, atria, and septa and weighed. Ventricle thickness was recorded. Right ventricle mRNA from high PAP (n=4; 2 C and 2 NR) and low PAP (n=4; 2 C and 2 NR) were used for Affymetrix bovine gene chips (contains 25mer probes per gene) screening. Gene chip data was analyzed by two-way ANOVA. Right ventricular weight (corrected by total body weight; r^2=0.76; $P < 0.05$) and thickness (r^2=0.53) were correlated with increased PAP. Screening of steer right ventricles from low PAP and high PAP control fed steers revealed that 177 genes were differentially expressed. Right ventricles from NR low PAP steers revealed 42 differentially expressed genes (≥2 fold) when compared to C steers. Our study suggests that maternal NR programs gene expression in the fetal heart possibly affecting sensitivity of the steer heart to stress by 15 months of age. Differential programming of right ventricular gene expression in the fetus during early gestation may be detrimental to animal health, particularly at high altitude. Supported by NIH INBRE 1P20RR16474.

Key Words: Brisket disease, Gene expression, Undernutrition

W29 - See abstract number 77.

Dairy Foods: Cheese, Products, and Processing

W30 Probiotic properties of the *Candida kefyr* isolated from kefir. S. J. You[1], J. K. Cho[1], C. G. Ha[2], C. H. Kim[1], and K. C. Heo*[1], [1]*Hankyong National University*, *Anseong, Gyonggi, Republic of Korea*, [2]*Hanyang University*, *Ansan, Gyonggi, Republic of Korea*.

In this study, *Candida* sp. was isolated from Kefir grains and tested as a potential probiotic. The isolated strain was identified as *Candida kefyr* with 99.8% identity to the species of *C. kefyr* by a sugar fermentation test kit. The yeast strain was higher in amylase activity compared with its phytase, cellulase and xylanase activities. The growth curve of the isolated strain reached a peak at 30h incubation with 1.4×10^{10} CFU/ml. Because probiotic organisms should be acid and bile tolerant, qualitative analyses were carried out using the isolated strain. After exposure to acidic condition(pH2), the strain was able to grow in PD medium up to $1x10^8$ CFU/ml compared with 8×10^9 CFU/ml at pH 5. Irrespective of the presence of bile acid, growth was observed in the strain cultured in medium containing 1.0% bile salt. Especially, *C. kefyr* showed high heat stability in which the microbial counts of the strain was 37.5% at 60°C incubation compared with those at 30°C incubation. *Candida kefyr* was grown in PD medium containing 13 antibiotics with 5 different addition levels and it was mostly not inhibited by 11 antibiotic agents which belong to tetracycline groups. The results indicated that the isolated *C. kefyr* from Kefir grains could be a useful probiotic for animal production due to its strong resistance in acid and thermal conditions and antibiotics.

Key Words: Kefir, *Candida Kefyr*, Probiotics

W31 Volatile fraction of Sicilian Pecorino cheese: Comparison of raw and pasteurized milk cheese. T. Rapisarda[1], S. Carpino*[1], G. Azzaro[1], and G. Licitra[1,2], [1]*CoRFiLaC, Regione Siciliana*, *Ragusa, Italy*, [2]*D.A.C.P.A. Catania University*, *Catania, Italy*.

SPME coupled to gas chromatography/mass spectrometry/olfactometry was used to identify and compare the relative amounts of the volatile compounds of raw (RM) and pasteurized Pecorino (PM) cheese from animal on pasture. Cheese samples were analyzed at 4 days, 1, 3, 6, 9 and 12 months of ripening. The majority of volatile compounds were more abundant in RM cheeses. Volatile compounds related to the families of free fatty acids, fatty acid esters, aldehydes, alcohols, ketones and sulfur compounds were detected in RM and PM Pecorino cheese profiles. Acetic acid and hexanoic acid, 2-butanol, 2,3-butanediol and ethoxy propanol, diethyl acetal, phenyl ethyl alcohol and ethyl dimethyl thiazole, hexanoic acid 1-methylpropyl ester and methyl nonanoate, 1-octen-3-one, diethyl methyl pyrazine and sulfur compounds like thiophene and dimethyl trisulfide were exclusively detected in RM cheeses likely due to the pasture diet and to the wild microbial communities presented in raw milk. Only a few exclusive compounds were detected in PM cheeses: benzaldehyde, benzaldehyde-4-methoxy, 2-undecanone, showing that milk pasteurization might determine lower levels of volatile compounds. Other relevant volatile compounds: (E)-2-nonenal, (Z)-2-nonenal and decadenal derived from oxidation of insaturated fatty acids in plants and monoterpenes: (Z)-linalool oxide, nerol oxide, (E)-limonene oxide and isogeraniol derived from secondary plant metabolites, were detected only in RM cheeses. The greater presence of these volatile compounds in RM cheeses suggests that the influence of pasture and indigenous microflora of milk was reduced by the pasteurization process. In general, raw and pasteurized Pecorino cheeses volatile profiles increased for intensity and number of compounds with aging, with RM cheeses always showing richest volatile profiles at all different ages. Peculiar odor notes for raw milk Pecorino cheeses were green, hay, mushroom, nutty, garlic and floral, produced, respectively, by aldehydes, ketone, pyrazine, sulfur compound and terpene.

Key Words: Pecorino cheese, Raw/pasteurized milk, Volatile compounds

W32 Characteristics of reduced fat milks as influenced by the incorporation of folic acid. K. Achanta, C. A. Boeneke*, and K. J. Aryana, *Louisiana State University Agricultural Center*, *Baton Rouge*.

Milk and milk products serve as a beneficial source for folic acid fortification due to the presence of folate binding proteins which seem to be involved in folate bioavailability. Folic acid fortification plays an important role in the prevention of neural tube defects such as spina bifida and ancencephaly, heart defects, facial clefts, urinary abnormalities and limb deficiencies. Though milk is not a good source of folic acid, fortification could help in the prevention of the above mentioned defects. The objective of this study was to examine the physico-chemical characteristics of reduced fat milks fortified with folic acid. Reduced fat milks were prepared using 25, 50, 75 and 100% of the recommended dietary allowance of 400 micrograms of folic acid. Treatments included addition of folic acid at these levels before and after pasteurization. Color, pH, fat , protein, viscosity, folic