Our objective was to evaluate the effect of decreasing progesterone (P4) before initiation of an Ovsynch protocol on luteal regression and fertility. Hormonal manipulation of progesterone before initiation of an Ovsynch protocol to increase ovulatory response to the first GnRH treatment in Holstein cows. P D Carvalho*, M C Willbank, and P M Fricke, Department of Dairy Science, University of Wisconsin-Madison, Madison, WI.

Lactating Holstein cows (n = 800) were synchronized using a Double Ovsynch protocol [Pre-Ovsynch protocol (GnRH; 7 d, PGF2α; 3 d, GnRH) followed 7 d later by an Ovsynch-56 protocol (G1; 7 d PGF2α; 24 h, PGF2α; 32 h, GnRH)] to receive first timed artificial insemination (TAI; 80 ± 3 DIM) 16 h after the last GnRH treatment. Cows were randomly assigned to receive a half-dose of PGF2α (12.5 mg dinoprost tromethamine) 2 d before G1 (TRT) or serve as untreated controls (CON). Data were analyzed by logistic regression using GLIMMIX and ANOVA with MIXED procedures of SAS. Overall, CON cows had greater (P < 0.01) P4 than TRT cows at G1 (4.2 vs. 2.1 ng/mL). Ovulatory response to G1 was greater (P < 0.01) for TRT vs. CON cows (81.9% [90/110] vs. 60.9% [70/115], respectively). Luteal regression during the second Ovsynch protocol did not differ (P = 0.33) between treatments [15.2% (15/99) vs. 10.6% (11/104); TRT vs. CON]. At 32 d after TAI, P/AI did not differ (P = 0.34) between treatments [56.2% (223/397) vs. 52.8% (209/396); TRT vs. CON]. At 67 d after AI, P/AI also did not differ (P = 0.56) between treatments [50.8% (190/374) vs. 48.6% (179/368); TRT vs. CON]. Pregnancy loss from 32 to 67 d after TAI did not differ [10.0% (21/211) vs. 9.6% (19/198); TRT vs. CON; P = 0.90]. Overall, cows that ovulated to G1 had greater (P = 0.02) P/AI compared with cows that did not ovulate [58.2% (89/153) vs. 41.5% (27/65), respectively]. The increase in P/AI in ovulating cows (16.7%) and observed increase in ovulation (21%; TRT – CON) produced an expected increase of 3.5% in P/AI in TRT vs. CON; similar to the observed 3.4% difference. Thus, administration of a half-dose of PGF2α 2 d before G1 during a Double Ovsynch protocol decreased P/AI at G1 and increased ovulatory response. Larger studies are needed to determine if this modified protocol increases P/AI. Supported by USDA Hatch project 231440.

Key Words: Ovsynch, progesterone, fertility
Effect of a second dose of prostaglandin F2α during Double-Ovsynch on successful luteolysis and fertility. Giovanni M. Baeza1, Rafael V. Barletta1, Alessandro Ricci1, Eduardo Trevisol1, Jerry N. Guenther1, Alvaro Garcia-Guerra1, Beatriz O. Cardoso1, Mateus Z. Toledo1, João P. Ferreira2, and Milo C. Wittbank1, 1University of Wisconsin-Madison, Madison, WI, 2São Paulo State University, Botucatu, SP, Brazil.

Lack of complete regression of the corpus luteum (CL) after prostaglandin F2α (PGF) treatment may reduce fertility during timed AI (TAI) protocols. A total of 373 lactating Holstein cows (172 primiparous; 201 multiparous) were synchronized with Double-Ovsynch starting at 53 ± 3 DIM (GnRH-7d-PGF-3d-GnRH-7d-GnRH-7d-PGF-56d-GnRH-16h-TAI). At the final PGF, cows were randomized to 1 of 2 treatments: 1PGF = No additional PGF treatment; 2PGF = Second PGF treatment 24h after first PGF. Blood samples were collected at the final PGF and GnRH treatments (72 and 16 h before timed AI). Only cows with P4 above 2.0 ng/ml before PGF (n = 344) were further analyzed. Fisher’s exact test and t-test were used to analyze categorical and continuous variables respectively, and logistic regression analysis was used to calculate probabilities of CL regression and P/AI. Primiparous cows had greater P4 than multiparous cows (7.7 ± 0.22 vs. 6.5 ± 0.18; P = 0.0001) before treatment. At 56 h after PGF, P4 was greater (P = 0.005) for 1PGF (0.4 ± 0.04) than 2PGF (0.2 ± 0.05) cows. The percentage of cows with complete CL regression (<0.5 ng/ml at 56 h after PGF) was increased by second PGF for primiparous (81.2% vs. 97.5%; 1PGF vs. 2 PGF; P = 0.001) or multiparous (84.4% vs. 96.7%; P = 0.006) cows. Cows with lower P4 at time of PGF had a reduced probability of complete CL regression with 1PGF by logistic regression (P = 0.02) or by comparing (P = 0.0016) quartile 1 (lowest P4; 2.0 to 4.8 ng/ml; 66.7%; 28/42) to the other 3 quartiles (88.1%; 118/134) which did not differ. In contrast, 2PGF cows had elevated CL regression (>95%) regardless of P4 at time of PGF (P = 0.60). Nonetheless, 2PGF increased CL regression for cows in both quartile 1 (66.7% vs. 95.1%; P = 0.0016) or quartiles 2–4 (88.1% vs. 97.6%; P = 0.0034). Interestingly, there was increasing P/AI with increasing P4 before PGF treatment for 2PGF (P = 0.02), but not 1PGF cows (P = 0.13). Cows with lower P4 at the time of PGF (Quartile 1) had similar P/AI for 1PGF (31.0%; 13/42) or 2PGF (31.7%; 13/41). In contrast, for quartiles 2–4, there was a tendency for decreased P/AI (P = 0.10) in 1PGF (44.0%; 59/134) vs. 2PGF (52.8%; 67/127) cows. Thus, treatment with a second PGF during Double-Ovsynch reduced inadequate CL regression and tended to increase P/AI, particularly in cows with greater P4 at the time of PGF treatment.

Key Words: prostaglandin F2α, fertility, luteolysis

Liver metabolism in dairy cows during repeated short-term feed-restrictions and LPS induced systemic inflammation. Josef J. Gross1, Emmanouil Kalaitzakis2, Olga Wellnitz1, Heiner Bollwein2, and Rupert M. Bruckmaier1, 1Veterinary Physiology, Vetsuisse Faculty University of Bern, Bern, Switzerland, 2Clinic of Reproductive Medicine, Vetsuisse Faculty University of Zurich, Zurich, Switzerland.

Body fat mobilization during a negative energy balance (NEB) requires metabolic adaptations on the part of the liver. We investigated if responses of hepatic mRNA abundancies of genes involved in metabolism and immune system to an energy deficiency differ between lactational stages. Holstein dairy cows (n = 14) (control (CON) and restricted (RES) group) were fed with grass and additional concentrate from wk 3 ap until wk 12 pp, except the RES group receiving only grass during wk 1-wk feed-restrictions in wk 2, 5, 8, and 11 pp. At the end of the first restriction period, LPS from E. coli was infused intravenously (0.5 µg/kg BW) to induce an inflammatory status. Energy balance (EB) was calculated on a weekly basis. Blood was obtained weekly and liver tissue was collected for biopsy before and after restriction periods and at 8h after the systemic LPS challenge. Blood samples were analyzed for metabolic adaptations on the part of the liver.
glucose, NEFA, and BHBA concentrations. Hepatic gene expression of 3-hydroxybutyrate dehydrogenase (BDH) 2, carnitine palmitoyltransferase (CPT) 1A and 2, mitochondrial glycerol-3-phosphate-acyltransferase (GPAM), 3-hydroxy-3-methylglutaryl-CoA synthase (HMGCS) 2, cytosolic phosphoenoxypruvate carboxykinase (PEPCKc), growth hormone receptor (GHR) 1A, insulin-like growth factor (IGF) 1, Hsp (haptoglobin), serum amyloid A (SAA), and tumor necrosis factor (TNF) α were measured. Data were analyzed using a mixed model including group and wk as fixed effects. During restriction periods, RES had a more distinct negative EB (wk 2: Δ17 MJ NEL/d; wk 5: Δ19 MJ; wk 8: 6 MJ; wk 11 Δ13 MJ) and in wk 5 higher NEFA (0.64 mmol/L) and BHBA (0.65 mmol/L) concentrations compared with CON (0.39 and 0.37 mmol/L, resp.; P < 0.05). Hepatic mRNA abundances showed expression patterns depending on the lactational stage. During feed-restriction periods, expression of IGF-1 was upregulated in RES compared with CON (based on ratios between RES and CON: +11.1 in wk 2, +14.7 in wk 5, +2.9 in wk 8, +7.3 in wk 11; P < 0.05). At 8h after the initiation of the systemic LPS challenge, SAA, TNFα and Hp were downregulated in RES and CON, while GPAM, HMGCS2, GHR1A, CPT1A and 2, PEPCKc, and BDH2 were upregulated (P < 0.05). In conclusion the experiment showed that hepatic metabolism was clearly affected by feed-restrictions and systemic LPS-challenge.

Key Words: feed restriction, metabolism, dairy cow

681 Prediction of portal and hepatic blood flow in cattle.
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An integral part of linking a multi-organ post-absorptive model is the prediction of nutrient fluxes between organs via blood flow. This paper reports a multivariate meta-analysis approach to model portal vein blood flow (PORBF) and hepatic venous blood flow (HEPBF) simultaneously. The developmental database consisted of 296 measurements (pAH dilution) for growing and lactating cattle with 55 treatments from 17 studies, and a separate evaluation database with 31 treatment means from 8 studies. Both databases had information on feed intake, bodyweight and diet composition. Blood flows predicted with DMI or metabolizable energy intake (MEI) was tested with both linear and quadratic equations using the NLINMIX macro of SAS. Cow(study) and study were treated as random effects and blood flow location (PORBF or HEPBF) as a repeated effect. Equations based on DMI rather than MEI typically resulted in higher concordance correlation coefficient (CCC) values, indicating better predictions. Quadratic equations did not out-perform their linear counterparts (CCC analysis), and quadratic equation terms were frequently non-significant. The best predictive equations were: PORBF (L/d) = 4855(±1097) + 2007(±145.5) × DMI (kg/d) and HEPBF (L/d) = 4463(±1094) + 2492(±74.5) × DMI (kg/d), with CCC values of 0.887 and 0.922, respectively. The residuals (predicted – observed) for PORBF were expressed as a fraction of HEPBF (PORBF/HEPBF), and hepatic arterial blood flow (ARTBF (L/d) = HEPBF – PORBF) were affected by the proportion of forage in the diet, and thus equations for PORBF and HEPBF based on forage and concentrate DMI were developed: PORBF (L/d) = 5043(±1186) + 1989(±148.8) × Forage (kg DM/d) + 1989(±141.4) × Concentrate (kg DM/d), and HEPBF (L/d) = 4416(±1177) + 2223(±145.5) × Forage (kg DM/d) + 2741(±137.5) × Concentrate (kg DM/d), where CCC values were 0.886 and 0.912, respectively. The CCC for ARTBF improved from 0.877 to 0.904 and PORBF/HEPBF from 0.115 to 0.447 with forage and concentrate DMI separation. Developed equations predicted blood flow well, and also suggest different sensitivity of PORBF and HEPBF to the downstream effects of DMI composition.

Key Words: blood flow, liver, meta-analysis

682 Effects of reducing dietary cation-anion difference level on plasma Ca concentration and VDR expression level in gastrointestinal tract of transition mice. Wen-xuan Wu*, Hai-liang Xin, Yi Yang, and Ruo-yu Liu, College of Animal Science, Guizhou Province, Guiyang, Guizhou Province, China.

The mechanism of reducing dietary cation-anion difference (DCAD; Na–K–Cl/S, mmol/kg DM) to prevent hypocalcemia is not completely known. Therefore, this study was conducted to clarify the mechanism why reducing DCAD was effective for increase in plasma Ca concentration and thus for hypocalcemia prevention by detecting plasma Ca concentration and vitamin D receptor (VDR) expression level in gastrointestinal tracts (GIT) of transition mice. One hundred twenty transition mice were randomly allocated to 3 blocks with each of 40 individuals and were fed 3 diets with varying DCAD level at +300 (treatment 1, HD), +150 (control, CON), and −150 (treatment 2, LD), respectively. Ten mice for each treatment were killed to collect blood sample for plasma Ca concentration analysis and harvest GIT tissues (stomach, duodenum, jejunum, ileum, cecum, and colon) samples for VDR expression level detection at 4 time points: day of 20 (−20) and 5 (−5) before kidding, day of kidding (0), and day of 3 after kidding (+3). Data on plasma Ca was analyzed using SAS 9.3 with Proc MIXED and VDR mRNA with Proc NPAR1WAY. Plasma Ca concentration (mg/dL) in LD mice (6.37) was higher than that in HD (4.43) and CON (4.98) mice for the whole and individual blood sampling time (P < 0.05). On d −20 diet LD resulted in higher VDR mRNA expression level in jejunum, ileum, and colon over diet HD (P < 0.05). On d −5 mice fed LD diet had more VDR mRNA expression level in jejenum and colon relative to HD and CON (P < 0.05). On d 0 feeding of treatment 2 had the highest VDR mRNA expression level in duodenum and colon, which was statistically higher than HD and CON (P < 0.05). On d 3 duodenum, jejenum, and colon were observed to show increased VDR mRNA expression level for LD compared with HD and CON (P < 0.05). These results indicated that reducing the DCAD upregulates VDR mRNA expression in GIT of transition mice and increases plasma Ca concentration, which explains some of the benefits of low DCAD on prevention of hypocalcemia.

Key Words: dietary cation-anion difference, plasma Ca, gastrointestinal VDR expression