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395 ASAS Early Career Award Presentation: Placental programming: How the maternal environment can impact placental growth and function. K. A. Vonnahme*, C. O. Lemley, L. E. Camacho, L. A. Lekatz, D. A. Redmer, L. P. Reynolds, and J. S. Canton, *Center for Nutrition and Pregnancy, Department of Animal Sciences, NDSU, Fargo.*

As placental growth and vascularity precedes exponential fetal growth, not only is proper establishment of the placenta important, but a continual plasticity of placental function throughout gestation. Inadequate maternal environment has been documented to alter fetal organogenesis and growth, thus leading to improper postnatal growth and performance in many livestock species. The timing and duration of maternal nutritional restriction appears to influence the capillary vascularity, angiogenic profile, and vascular function of the placenta in cattle and sheep. Moreover, upon realimentation, it appears as if the placenta may try to “overcompensate” allowing for enhanced blood flow and nutrient delivery. In environments where fetal growth and/or fetal organogenesis are compromised, potential therapeutics may augment placental nutrient transport capacity and improve offspring performance. Supplementation of specific nutrients, including selenium and protein, as well as hormone supplements, such as indolamines during times of nutrient restriction may assist placental function. Current use of Doppler ultrasonography has allowed for repeated measurements of uterine and umbilical blood flow including assessment of uteroplacental hemodynamics in cattle and sheep. Moreover, these variables can be monitored in conjunction with placental capacity and fetal growth at specific time points of gestation. Elucidating the consequences of inadequate maternal intake on the continual plasticity of placental function will allow us to determine the proper timing and duration for intervention.

396 Blood metabolites and hormones as potential markers of body reserves dynamic and energetic balance in ruminants. E. González-García*¹, N. Debus¹, P. Hassoun¹, S. Camous², M.-R. Aurel³, F. Bocquier¹, and F. Barillet⁴, ¹INRA UMR⁸⁶⁸, *Systèmes d'Élevage Méditerranéens et Tropicaux (SELMET), Montpellier, France*, ²INRA UMR¹¹⁹⁸, *Biologie du Développement et Reproduction (BDR), Domaine de Vilvert, Jouy-en-Josas Cedex, France*, ³INRA UE⁰³²¹, *Domaine Expérimental de La Fage, Roquefort-Sur-Soulzon, France*, ⁴INRA UR⁰⁶³¹, *Station d'Amélioration Génétique des Animaux (SAGA), Chemin de Borde Rouge, Auzeville, BP 52627, Castanet-Tolosan Cedex, France.*

Under strict controlled conditions, and throughout a whole lactation period, we evaluated the consistence of some plasma metabolites and hormones as potential markers of body reserves status (mobilization or accretion) in ruminants. Forty-eight confined primiparous (PRIM; n = 48) and multiparous (MULT; n = 48) dairy Lacaune ewes were monitored from late pregnancy to late lactation in a 2 × 2 × 2 factorial design. Parity (PRIM or MULT), litter size (singletons –SING– or twins –TWIN) and energetic balance (milked once –ONE– or twice –TWO) were the fixed effects. NEFA, glucose (GLUC) and triglycerides (TRIG) plasma metabolites, and leptin (LEPT), insulin (INSU) and tri-iodothyroidine (T3) hormones were monitored. Animals received a 70:30 hay:concentrate TMR diet. Blood samples (10 mL) were individually collected (≈biweekly) early morning by jugular venipuncture in EDTA or heparin tubes. Plasma was harvested from blood samples that were centrifuged immediately after collection. After centrifuga-

tion, samples were transferred to 5-mL tubes and frozen at –20°C until analyses. Energy restriction (i.e., TWO higher energy expenditure than ONE) resulted in higher concentrations of NEFA (PRIM, $P < 0.001$; MULT, $P < 0.05$); in contrast, concentrations of INSU (PRIM, $P < 0.05$; MULT, $P < 0.001$) decreased until 1 mo after ONE; in MULT ewes, LEPT consistently decreased in TWO when compared with ONE (11.15 ± 0.571 vs. 14.31 ± 0.676 , $P < 0.05$). However, LEPT was affected ($P < 0.05$) by litter size × number of milking interaction in PRIM, SING × ONE and SING × TWO ewes showing the highest (12.33 ± 1.04) and lowest (7.36 ± 0.989 ng.mL⁻¹) values, respectively. Ewes with TWIN had higher NEFA and lower INSU or LEPT than SING from before lambing until weaning. T3 results showed contradictory variability. Either for parity or number of milking, no differences at all were found for TRIG. For GLUC, differences (ONE > TWO) appeared just 1 wk after passing to ONE. Even when differences in BW or BCS were not found, NEFA, LEPT and INSU showed the higher sensitivity as potential markers of body reserves mobilization under the conditions of this experiment.

Key words: metabolites, hormones, markers of body reserve status

397 Metabolic gene expression in bovine ruminal tissue in response to age and pre and postweaning plane of nutrition. A. Naeem*, J. Stamey, J. K. Drackley, and J. J. Loor, *University of Illinois, Urbana.*

We evaluated expression of 22 genes encoding enzymes involved in ketogenesis, cholesterogenesis, TCA cycle flux, long-chain fatty acid (LCFA) oxidation, and transcriptional regulation in ruminal tissue of male Holstein calves fed a conventional milk replacer (20% CP, 20% fat; 1.25% of birth BW as solids) and starter (19.6% CP, DM basis; control) or enhanced milk replacer (28.5% CP, 15% fat; 2% of BW; ENH) and enhanced starter (25.5% CP, DM basis). All calves were weaned on d 42. Groups of calves in control and ENH were harvested after 43 d (wk 5) and 71 d (wk 10) of feeding. There was marked upregulation of HMGCS2, the rate-limiting enzyme of hepatic mitochondrial ketogenesis in non-ruminants, between wk 5 and 10 regardless of diet. This response paralleled an increase in plasma BHBA concentration (0.09 vs. 0.24 mmol/L) between wk 5 and 10. Expression of other ketogenic (BDH1, HMGCL), cholesterogenic (HMGCS1), and TCA cycle-related enzymes (LDHA, GOT2, PCCA) also increased by wk 10 regardless of diet. A higher expression of CPT1A and ACADVL at wk 5 in calves fed ENH vs. control suggested greater LCFA oxidation potentially driven by the greater intake of LCFA from milk replacer. This suggestion is supported by the greater concentration of plasma NEFA (128 vs. 95 μEq/L) at wk 5 due to ENH vs. control. Expression of peroxisome proliferator-activated receptor-δ increased ~8-fold between wk 5 and 10 regardless of diet, suggesting a role for this nuclear receptor in postweaning ruminal tissue development. In conclusion, several metabolic enzymes were upregulated at wk 10 regardless of diet suggesting a coordinated response to support ruminal tissue development. The mRNA of HMGCS2 accounted for ca. 50% of total genes measured (e.g., HMGCS1 was 0.2%), suggesting this enzyme is key for regulating ketogenesis in ruminal epithelium as in liver. Enhanced nutrition during the first 5 wk of life had minor effects on the selected genes.

Key words: ketogenesis, nuclear receptor, dairy calf