Maternal Recognition of Pregnancy in the Mare: What is Needed to Make Progress in our Understanding of This Complex Issue.
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Abstract: Maternal recognition of pregnancy (MRP) resulting in prolonged luteal lifespan is crucial to maintenance of pregnancy. Mechanisms underlying MRP differ in between species, whereat the precise mechanism by which luteolysis is prevented has yet to be described for equine pregnancy. Transcriptional profiling studies entailing analysis of endometrial and embryonic tissues have shed light into the wider context of maternal recognition of pregnancy. Our own studies revealed the secretion of fibrinogen by preimplantation equine embryos, which is a peculiar finding as fibrinogen synthesis almost exclusively occurs in the liver. Conceptus-derived fibrinogen likely contributes to cell adhesion during fixation and underlines the helpfulness of transcriptome studies in identifying species-specific aspects of early pregnancy. Despite all our advances, we yet have to decipher the signaling pathways leading to reduced endometrial production of prostaglandin F2alpha during MRP. We recently analyzed samples from mares undergoing spontaneous pregnancy loss in the face of high progesterone in comparison to samples collected from mares at Day 20 of intact pregnancy. No differentially expressed transcripts could be detected. It appears that after maternal recognition of pregnancy and consequent suppression of luteolysis, progesterone, not the presence of a viable conceptus, is the driving force of gene expression. This finding underlines the importance of understanding the events surrounding luteostasis. We propose that a standardized approach in vitro cell culture model is needed to address mechanistic questions pertaining to MRP. Approaches currently underway such as CRISPR/Cas9-mediated targeted integration of TERT and TERC to immortalize equine endometrial stromal fibroblasts will be discussed.

MEAT SCIENCE AND MUSCLE BIOLOGY

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Abstract: Research has established that muscle fiber hyperplasia is complete during mid gestation; therefore, skeletal muscle fiber hypertrophy is responsible for the increase in muscle mass observed during late gestation and postnatal growth periods. Our research is investigating key times points during muscle fiber hypertrophy and the role of miRNA and mRNA transcriptome in this process. Two studies were conducted to examine changes in muscle mass, muscle fiber hypertrophy, and gene expression from gestational d (gd) 85 to market weight in Suffolk or Texel cross lambs. Longissimus muscle (LM) samples were taken for muscle fiber histology at the following time points: gd85, gd110, gd133, and market (d243) in study one and at postnatal d2, d14 and d203 in study two. microRNA (miRNA) and mRNA sequencing of the LM were conducted in study one and included biopsies at d 42 and 65. Type I and Type II muscle fiber area increased (P < 0.05) at each stage of growth evaluated. Type I muscle fiber area increased by 26.7-fold and Type II muscle fiber area increased by 37.4-fold from gd85 to market (d243). mRNA sequencing identified a total of 9360 unique genes differentially expressed (DEGs; P < 0.05) in LM during hypertrophic growth but the majority of DEGs were observed in the prenatal (51%) and early postnatal (54%) periods. There were 142 unique miRNAs differentially expressed (P < 0.05) during hypertrophic growth of LM but the majority (62%) were observed in the transition period from prenatal to postnatal growth. Overall, muscle fiber hypertrophy is dynamic from late gestation through postnatal growth, but transcriptomic changes indicate key time periods during development in which mechanisms underlying hypertrophic growth may be altered.

Keywords: lamb, muscle fiber hypertrophy, miRNA, mRNA