Public Abstract First Name:JIN-GEOL Middle Name: Last Name:KIM Adviser's First Name:JONATHAN Adviser's Last Name:GREEN Co-Adviser's First Name:RANDALL Co-Adviser's Last Name:PRATHER Graduation Term:WS 2007 Department:Animal Sciences Degree:MS Title:COMPARATIVE TRANSCRIPTIONAL PROFILING OF THE UTERUS ACCORDING TO STAGE OF

In most mammals, female reproductive organs including the ovary, oviduct and uterus undergo extensive tissue remodeling throughout the estrous cycle and during pregnancy. These changes, which are reflective of temporal and spatial specific gene expression, are required to promote successful embryonic development and fetal growth, particularly during the early pregnancy where early embryonic loss during the first 30 days of gestation is approximately 20 to 30%. The uterine endometrium nourishes the embryo by providing an environment conducive to gamete maturation, fertilization, placental attachment and the continued growth of the conceptus. A better understanding of these developmental events arbitrating conceptus-endometrial interactions will have important applications for understanding prenatal loss and improving domestic animal productivity.

This study has investigated the expression patterns of genes during the estrous cycle and pregnancy, and led to the identification of numerous differentially transcribed transcripts by using cDNA microarray and qRT-PCR. Not unexpectedly, many of these genes are estrogen- and/or progesterone-responsive and, presumably, play key roles in establishing and maintaining the pregnancy. Moreover, a number of uterus-specific transcripts analyzed and identified in this study are very helpful for a thorough understanding of uterine physiology throughout how such transcripts change during the estrous cycle and pregnancy.