COMPARATIVE TRANSCRIPTIONAL PROFILING OF THE UTERUS ACCORDING TO STAGE OF THE ESTROUS CYCLE AND PREGNANCY STATUS IN GILTS

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ABSTRACT

In most mammals, female reproductive tracts undergo extensive tissue remodeling throughout the estrous cycle and during pregnancy that arise in response to an array of endocrine, paracrine, and autocrine signals. These changes, which are reflective of temporal and spatial specific gene expression, help create the microenvironment required for movement of gametes, capacitation of sperm, fertilization, successful embryonic development and subsequent fetal growth.

During the first 30 days of gestation, early embryonic loss 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. 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. 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.