

MicroRNA in Bovine Corpus Luteum during Early Pregnancy

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Abstract : The maintenance of corpus luteum (CL) during early pregnancy in cattle is a critical and multifarious process. A luteotrophic mechanism originating from the embryo is widely accepted as the triggering signal for the CL maintenance. In the cattle, it is the interferon-tau (IFNT) secretion from conceptus that prevents CL regression and ensures progesterone production for the establishment of pregnancy. In addition to endocrine and paracrine signals, microRNA (miRNA) can also support CL sustainability during early pregnancy. MiRNAs are small non-coding nucleic acids that regulate gene expression post-transcriptionally and are shown to be involved in the modulation of CL function. However, the examination of miRNAs in corpus luteum function at the early pregnancy still remains largely uncovered. This study aims at profiling the expression of miRNA in CL during the early pregnancy in cattle by comparing it with the CL from late cycle and with the regressed CL. Corpora lutea were assigned in two different groups during the cycle (C13 group, late CL: days 13-18 and C18, regressed CL group: day >18) and during the early pregnancy (group P: 1-2 month). The estrous cycle was determined by macroscopic examination and to age the fetus crown-rump length measurement was applied. A total of 9 corpora lutea from individual animals were included in the study, three corpora lutea for each group. MiRNAs population was profiled using small RNA next-generation sequencing and biologically significant miRNAs were evaluated for their differential expression using the DESeq2-methodology. We show that 6 differentially expressed miRNAs (bta-mir-2890, -2332, -2441-3p, -148b, -1248 and -29c) are common to both comparisons, P vs C13 and P vs C18. While for each stage individually we have identified unique miRNAs differentially expressed only for the given comparison. bta-miR-23a and -769 were unique miRNAs differentially expressed in P vs C13, whereas forty-four unique miRNAs were identified as differentially expressed in P vs C18. These data confirm that miRNAs are highly abundant in luteal tissue during early pregnancy and potentially regulate the CL maintenance at this stage of fetus development.

Keywords : bovine, corpus luteum, microRNA, pregnancy, RNA-Seq

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