Granulosa cell tumors (GCTs) are the most common ovarian tumor of the horse and can result in suppression of folliculogenesis, stallion-like behavior, and/or continuous estrus. Circulating microRNAs (miRNAs) in women with ovarian cancer are found to change expression patterns in the presence of disease. The objective of our study was to evaluate serum miRNAs expression via quantitative real-time PCR (qRT-PCR) and determine if levels differed in normal cycling mares vs. mares with GCTs.

Serum samples from nine normal cycling mares (estrous, day of ovulation, and seven days post-ovulation), and 15 mares with histologically confirmed GCTs were evaluated. Relative expression of 383 miRNAs was performed initially profiling five normal mares at all sample time points and five GCT mares (n=20 samples total). Based on preliminary data a modified list of 127 miRNAs was used to profile remaining samples (normal mare n=12; GCTs mare n=10). Data were analyzed using the comparative Ct method.1

Evaluation of serum samples from normal mares and mares with GCTs revealed significant differences in expression level for at least 15 miRNAs. These include: miR-19a, miR-92b, miR-124, miR-302a, miR-432, and miR-501-3p. Results of this study demonstrated changes in the expression of specific circulating miRNAs in mares with GCTs compared to normal cycling mares and additional research is needed to determine the clinical diagnostic potential of these identified findings.

Keywords: Granulosa cell tumor, microRNA, mare

Reference