The micro RNA expressions of cultured myometrial and leiomyoma cells stimulated with prostaglandins and sex-steroids

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MicroRNAs (miRNAs) are short non-coding single-strand RNAs, key posttranscriptional regulators and, they play a central role in various aspects of cell proliferation, differentiation, apoptosis, and inflammation. MicroRNA analyses are useful tools for tumor classification and target gene identification. Leiomyomas are benign uterine tumors considered to arise from transformation of myometrial cells, which develop during the reproductive years. It is clear that ovarian steroids are essential for leiomyoma growth, and expression of many autocrine/paracrine mediators. Estrogen and progesterone are considered as promoters of leiomyoma growth, and growth factors, cytokines, and chemokines are thought to be as potential effectors of estrogens and progesterone. We evaluated the expression of 8 miRNAs on treated E2, P4, PGE2 and PGF2α by quantitative reverse transcription-polymerase chain reaction (qRT-PCR) using primary leiomyoma cell and matched myometrial cell. Internal control for U6 small nuclear RNA (U6) was performed in all samples. The expression patterns of 2 groups of miRNAs - inflammation (miR-29b, miR-93, miR-106b, and miR-100b) and proliferation (let 7a, miR-21, miR-26a, and miR-200a)- were involved in growth of leiomyoma, which was compared with the cells stimulated with sex steroids. The miRNA expressions in the cells treated with prostaglandins were very comparable to the expressions of cells treated with sex steroids. Although it is unclear that leiomyoma growing is a consequence of inflammatory response occurred during menstruation, this result may implicate that anti-inflammatory substances could be alternative agents for controlling the leiomyoma growth.

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