J Tissue Sci Eng 2018, Volume: 9
DOI: 10.4172/2157-7552-C1-046

MicroRNA expression profile of *in vitro* engineered endometrial cells depending on treated hormone concentrations

Seung-Yup Ku[1], **Kim Y J**[2], **Kim Y Y**[1], **Kim H**[1] and **Suh C S**[1]
[1]Seoul National University Hospital, South Korea
[2]Korea University Guro Hospital, South Korea

In vitro endometrial cell culture is critical in artificial uterus engineering. Especially the use of uterine endometrium implant engineered as cell sheet can be a novel treatment option for sub-fertile patients with intractable endometrial dysfunction. During early pregnancy, the endometrial cell function for communication between embryo and maternal reproductive system is indispensable. The profile of microRNA (miR) expression in endometrial cells according to treated hormone concentrations such as progesterone provides important data for *in vitro* endometrial cell culture strategy that is useful for engineering artificial uteri, since these hormones play direct important roles in pregnancy maintenance. The authors attempted to assess the miR expression profile of in vitro cultured endometrial cells under various hormonal milieus that simulate that of early pregnancy period. Murine uterine endometrial cells, immortalized human uterine endometrial cells, and human uterine endometrial carcinoma cells were cultured at various sex steroid hormone concentrations. The expression of miRs critical for early pregnancy was analyzed. The tested expression of miRs such as miR-20, -21, and -200 was characteristically differently modulated depending on sex hormone concentration in different endometrial cell types. of Candidate target gene analysis revealed that the MUC1, progesterone receptor, matrix metallopeptidase-9 was significantly altered by hormone treatment, differently in human and murine endometrial cell lines. Conclusively, physiological concentration range (e.g., 10^{-7} and 10^{-9} M) of specific sex steroid hormones seems to affect the survival and target gene expression via regulating miR expression (2016R1D1A1A02937287 and 2016R1E1A1A01943455).

jyhsyk@snu.ac.kr