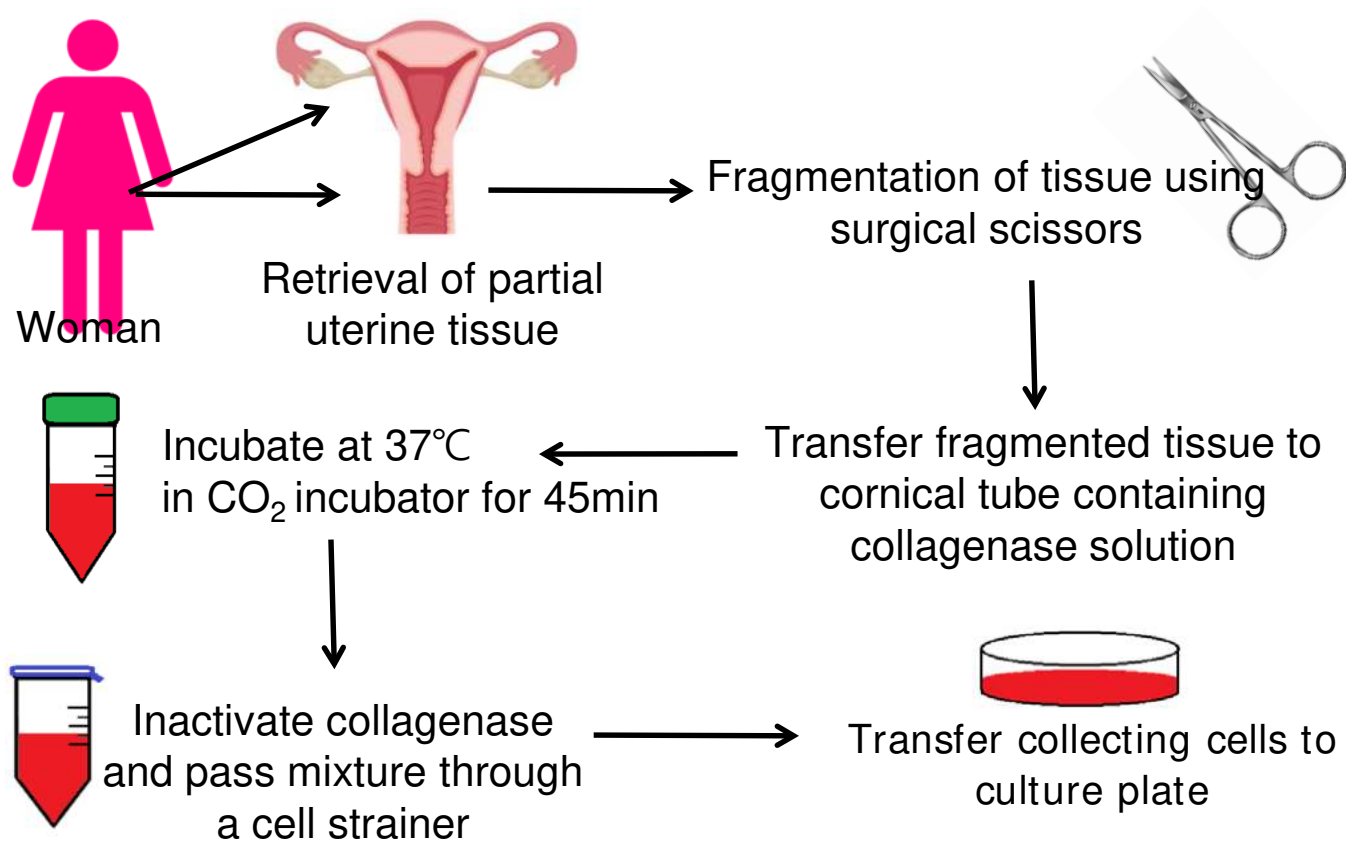


Introduction

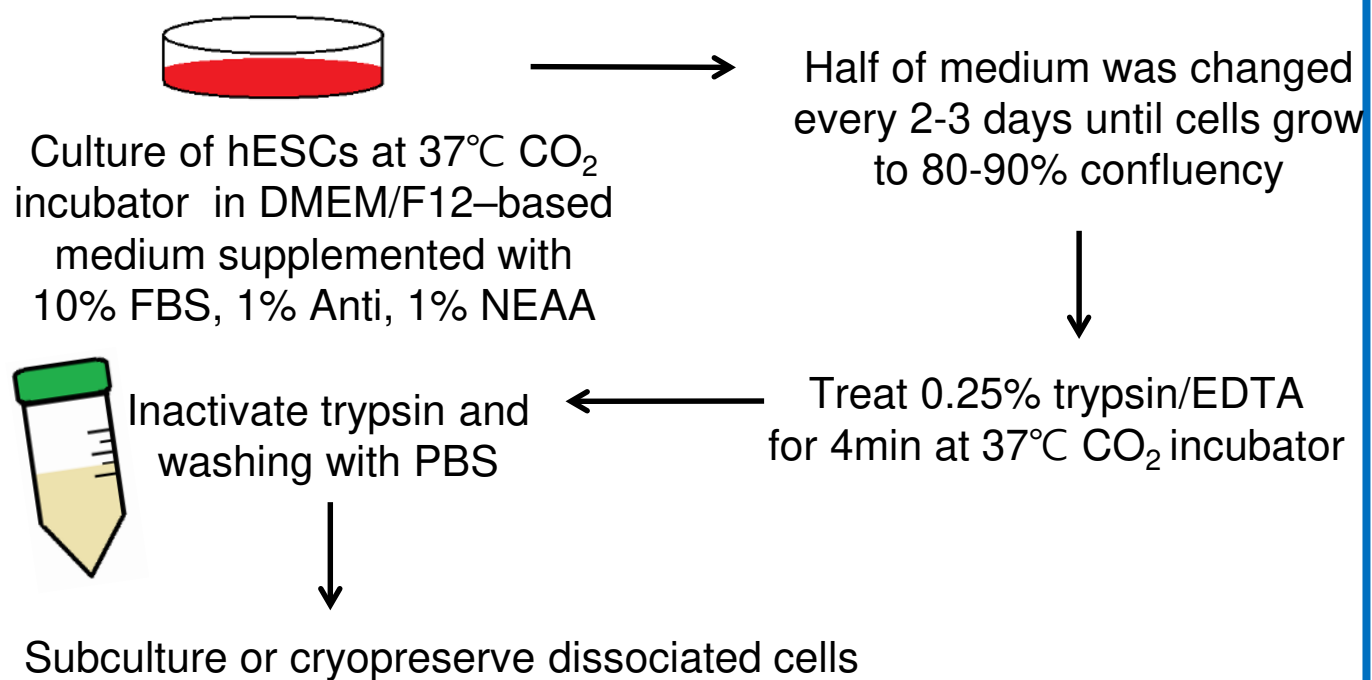
In *in-vivo* endometrium, endometrial cells experience dramatic alterations during the menstrual cycle by a variety of hormones secreted from sexual organs. These hormonal regulation make it difficult to study physiological and pharmacological aspects of endometrial biology. Therefore, organization of artificial uterine tissues through construction of non-cellular niche mimicking microenvironment enclosing endometrium is important for eliminating chaotic treatment effects detected in the implantation-related studies. Accordingly, as a step towards constructing a precisely defined three-dimensional microenvironment engineering extracellular signaling to regulate physiological characteristics of endometrial cells derived from human uterus, information on microenvironment factors presented in the extracellular space of human endometrial stromal cells (hESCs) should be requested

Materials and Methods

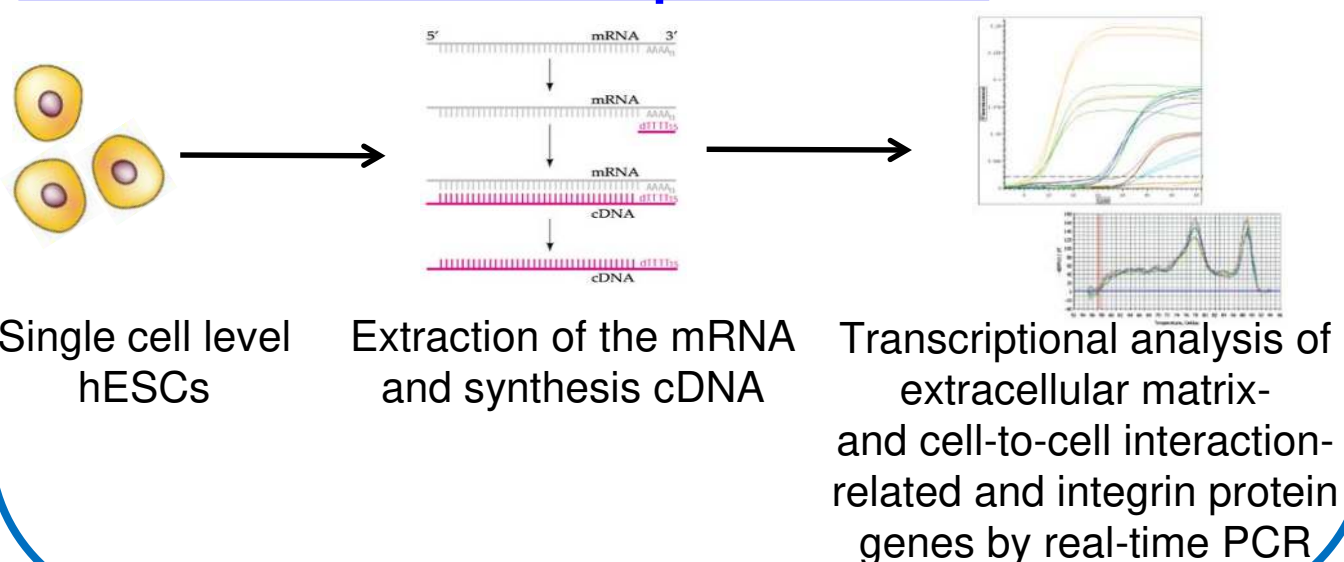
Isolation of hESCs from Endometrium



Culture of hESCs



Measurement of Transcriptional levels



Results

Figure 1. Transcriptional levels of the extracellular matrix- and cell-to-cell interaction-related protein genes in the hESCs. The hESCs were isolated by enzymatic method and mRNA level was measured by real-time PCR. Total 12 extracellular matrix-related protein genes were quantified, and *COL1* and *COL3* showed significantly higher expression levels than other genes. By contrast *FN*, *NID*, *LN*, *TN*, *ELN*, *COL4* and *COL5* were weakly transcribed (A). Among 11 cell-to-cell interaction-related protein genes, *CDH2* showed significantly the strongest transcription compared to the other genes. By contrast *CDH1*, *CDH3*, *DSG2*, *ICAM1*, *HSPG2*, *VCAN* and *SDC1* were weakly transcribed (B). All data shown are means \pm SD of 3 independent experiments. $^{***}p < 0.05$. ND=not detected.

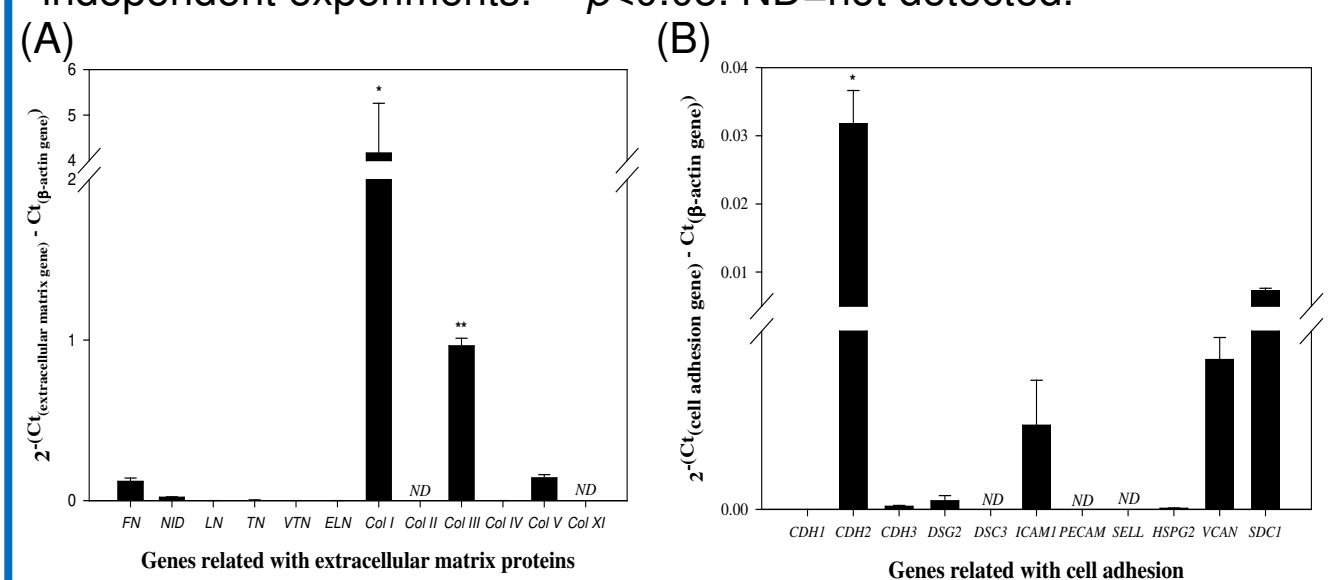
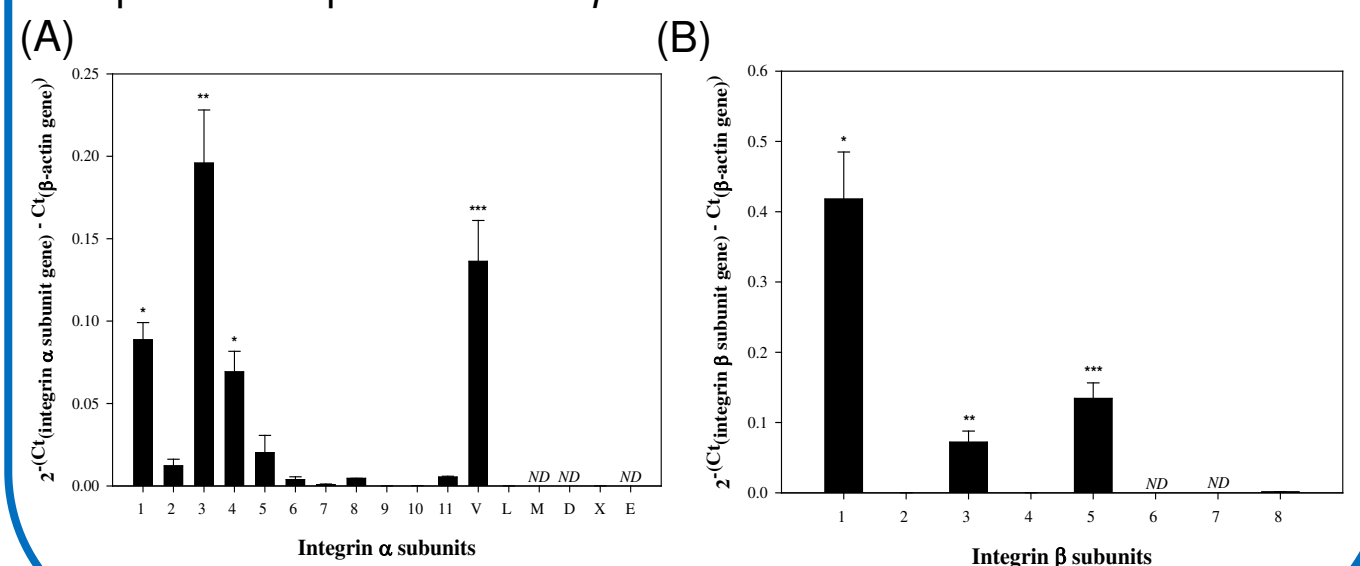


Figure 2. Transcriptional levels of the integrin α and β subunit genes in the hESCs. The hESCs were isolated by enzymatic method and mRNA level was measured by real-time PCR. Total 25 integrin subunit genes were quantified and integrin α_1 , α_3 , α_4 , and α_v (A) and integrin β_1 , β_3 , and β_5 (B) subunit genes showed significantly higher expression levels than other subunits. By contrast, integrin α_2 , α_5 , α_6 , α_7 , α_8 , α_9 , α_{10} , α_{11} , α_L , and α_X (A) and integrin β_2 , β_4 , and β_8 (B) subunit genes were weakly transcribed. All data shown are means \pm SD of 3 independent experiments. $^{***}p < 0.05$. ND=not detected.



Conclusion

In conclusion, we could identify types of extracellular matrix- (*COL1* and *COL3*), cell-to-cell interaction- (*CDH2*), and integrin-related (*ITGA1*, *ITGA3*, *ITGA4*, *ITGAV*, *ITGB1*, *ITGB3* and *ITGB5*) protein genes significantly up-regulated transcriptionally in hESCs. Moreover, these results will contribute greatly to develop non-cellular niche mimicking endometrium

Acknowledgement

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