Exploring key genes and pathways underlying metastasis endometrial cancer based on gene expression microarray.

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Abstract

Purpose: To reveal the key genes and pathways involved in the metastasis of endometrial cancer.

Methods: Microarray data GSE29436 consisting of 4 progressive endometrial cancer samples and 4 non-progressive controls were downloaded from Gene Expression Omnibus database. Differentially Expressed Genes (DEGs) were screened out using Limma package in R, followed by hierarchical clustering. Gene Ontology and pathway enrichment analysis were performed for DEGs.

Results: Bioinformatic analysis revealed a total of 65 DEGs between progressive and non-progressive samples. Functional annotation showed that those genes were mainly enriched in functions of cell proliferation, MAPK and TGF-beta signaling pathways, which involved with up-regulated genes pleiomorphic adenoma gene 1 (PLAG1), Insulin-Like Growth Factor 2 (IGF2), and down-regulated genes Fibroblast Growth Factor 20 (FGF20) and Thrombospondin 4 (THBS4).

Conclusion: Sixty-five identified genes in progressive endometrial cancer samples were mainly associated with tumor metastasis possibly by enhancing cell proliferation and affecting MAPK and TGF-beta signaling pathways. High expression of PLAG1, IGF2 and low expression of FGF20, THBS4, therefore, appear to play an important role in tumorigenesis and progression of endometrial cancer.

Keywords: Endometrial cancer, Differentially expressed genes, Pathways, Microarray.