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ASPM, CDC20, DLGAP5, BUB1B, CDCA8, and NCAPG May Serve as Diagnostic and Prognostic Biomarkers in Endometrial Carcinoma

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Abstract

Uterine Corpus Endometrial Carcinoma (UCEC), the most common gynecologic malignancy in developed countries, remains to be a major public health problem. Further studies are surely needed to elucidate the tumorigenesis of UCEC. Herein, intersecting 203 differentially expressed genes (DEGs) were identified with the GSE17025, GSE63678, and The Cancer Genome Atlas-UCEC datasets. The Gene Ontology/Kyoto Encyclopedia of Genes and Genomes functional enrichment analysis and protein-protein interaction (PPI) network were performed on those 203 DEGs. Intriguingly, 6 of the top 10 nodes in the PPI network were related to unfavorable prognosis, that is, ASPM, CDC20, DLGAP5, BUB1B, CDCA8, and NCAPG. The mRNA and protein expression levels of the 6 hub genes were elevated in UCEC tissues compared to normal tissues. Higher expression of the 6 hub genes was associated with poor prognostic clinicopathological characteristics. The receiver operating characteristic curve suggested the significant diagnostic ability of the 6 hub genes for UCEC. Then, underlying pathogeneses of UCEC including promoter methylation level, TP53 mutation status, genomic genetic variation, and immune cells infiltration were analyzed. The mRNA expression level of the 6 hub genes was also higher in cervical squamous cell carcinoma and endocervical adenocarcinoma, uterine carcinosarcoma, and ovarian serous cystadenocarcinoma tissues than in corresponding normal tissues. In conclusion, ASPM, CDC20, DLGAP5, BUB1B, CDCA8, and NCAPG may be considered diagnostic and prognostic biomarkers in UCEC.

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