ANALYSIS OF ENDOMETRIAL CARCINOGENESIS
AND PROGNOSTIC-RELATED GENES IDENTIFIES
ECT2 AS A POTENTIAL TARGET

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Abstracts

Introduction Based on bioinformatics analysis and clinical tissue sample verification, this study sought potential targets for prediction and diagnosis in uterine corpus endometrial carcinoma (UCEC).

Methods The DEGs in endometrial carcinoma cohorts of GEO and TCGA were analyzed by R and the series test of cluster was performed by STEM software. GO and KEGG analysis and PPI analysis were performed to screen for Hub genes. The expression level and prognostic analysis of these genes were verified in the online database. The expression of ECT2 was validated by immunohistochemistry in local clinical endometrial samples.

Results There are 763 common DEGs (368 up-regulated genes and 395 down-regulated genes) and 530 genes of endometrial carcinogenesis related cluster. 13 Hub genes were selected for further analysis, 9 significantly differential genes were selected as follow: ASPM, ATAD2, BUB1B, ECT2, KIF14, NUF2, HELLS, NCAPG and SPAG5. The ROC curves of candidate genes revealed that ECT2 had the best diagnostic efficacy for UCEC. The expression level of ECT2 was significantly higher in endometrial carcinoma than that in normal endometria and differently among different FIGO stages and pathological grades in UCEC. The level of ECT2 in local endometrial samples, including normal endometria (30 cases), simple hyperplasia (30 cases), atypical hyperplasia (52 cases), and endometrial carcinoma (83 cases) revealed an increase gradually trend from normal to cancer. ECT2 can significantly distinguish and help diagnose normal endometrium, simple hyperplasia, atypical hyperplasia and endometrial cancer.

Conclusion/Implications ECT2 is expected to become a potential marker for the screening and diagnosis of endometrial carcinoma.

THE EFFECT OF TCGA MOLECULAR TYPING
AND IMMUNOHISTOCHEMICAL MARKERS ON
THE PROGNOSIS OF ENDOMETRIOD
CARCINOMA WITH FERTILITY-SPARING
TREATMENT

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Abstracts

Introduction For early young and non-pregnant patients with endometrioid carcinoma, drug treatment can reverse the carcinoma. But there are several problems: (1) there is a significant individual difference in reaching complete regression (CR) after 3-month treatment. (2) The recurrence rate after CR is high. The purpose of this study is to investigate the correlation between TCGA molecular typing and immunohistochemical markers with 3-month CR and recurrence in patients with conservative treatment.

Methods The paraffin pathological specimens of 71 patients with stage IA and G1-G2 endometrioid carcinoma who underwent conservative treatment in Peking University Third Hospital from January 2010 to October 2022 were collected retrospectively for TCGA molecular typing and immunohistochemical staining (including PTEN, PIK3CA, β-catenin, ARID1A, ER, PR) to explore the influencing factors of 3-month CR and recurrence.

Results There were 2 MSI-H subtypes, 1 high copy-number subtype, 68 low copy-number subtypes and no POLE mutations. Univariate and multivariate logistic analysis showed those PTEN-positive, ER and PR high-expression were more likely to achieve 3-month CR (OR=24.811, P=0.034; OR=9.428, P=0.025; OR=29.178, P=0.011). Univariate and multivariate COX regression analysis showed that patients with high-expression PIK3CA were more likely to recurrence (OR=2.705, P=0.017).

Conclusion/Implications Patients with PTEN positive, ER and PR high-expression are more likely to achieve 3-month CR after treatment. Individuals with high expression of PIK3CA are more likely to relapse after CR. Further expansion of sample size is needed to confirm the impact of TCGA molecular typing on the prognosis of endometrioid carcinoma with fertility-sparing treatment.