

Prognostic significance of UBE2C mRNA expression in high-risk early breast cancer. A Hellenic Cooperative Oncology Group (HeCOG) Study.

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Source

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Abstract

BACKGROUND:

The ubiquitin-proteasome system (UPS) plays a pivotal role in tumorigenesis. Components of the UPS have recently been implicated in breast cancer progression. In the present study, we sought to explore the prognostic and/or predictive significance of UBE2C messenger RNA (mRNA) expression on disease-free survival (DFS) and overall survival (OS) in high-risk operable breast cancer patients.

METHODS:

Five hundred and ninety-five high-risk breast cancer patients were treated in a two-arm trial evaluating postoperative, dose-dense sequential chemotherapy with epirubicin followed by CMF (cyclophosphamide, methotrexate and 5-fluorouracil) with or without paclitaxel (Taxol). RNA was extracted from 313 formalin-fixed primary tumor tissue samples followed by one-step quantitative RT-PCR for assessment of mRNA expression of UBE2C.

RESULTS:

High UBE2C mRNA expression was associated with poor DFS (Wald's $P = 0.003$) and OS (Wald's $P = 0.005$). High tumor grade, as well as high Ki67 protein expression, was more frequent in the high-expression group of UBE2C. Results of the Cox multivariate regression analysis revealed that high UBE2C mRNA expression remained an independent adverse prognostic factor for relapse ($P = 0.037$) and death ($P = 0.05$).

CONCLUSIONS:

High UBE2C mRNA expression was found to be of adverse prognostic significance in high-risk breast cancer patients. These findings need to be validated in larger cohorts.