

## **Evaluation of the prognostic and predictive value of HER family 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**

The aim of the study was to evaluate the prognostic ability of the transcriptional profiling of the HER family genes in early breast cancer, as well as to investigate the predictive value of HER2 mRNA expression for adjuvant treatment with paclitaxel. RNA was extracted from 268 formalin-fixed paraffin-embedded (FFPE) tumour tissue samples of high-risk breast cancer patients enrolled in the randomised HE10/97 trial, evaluating the effect of dose-dense anthracycline-based sequential adjuvant chemotherapy with or without paclitaxel. The mRNA expression of all four HER family members was assessed by kinetic reverse transcription-polymerase chain reaction (kRT-PCR). The overall concordance between kRT-PCR and IHC/FISH for HER2 status determination was 74%. At a median follow-up of 8 years, multivariate analysis showed that EGFR and HER2 mRNA expression was associated with reduced overall survival (OS). HER3 and HER4 mRNA level had a favourable prognostic value in terms of OS and disease-free survival (DFS), respectively. Adjusting for HER2 mRNA expression, OS and DFS did not differ between treatment groups. These data indicate that EGFR as well as HER2 are prognostic factors of worse clinical outcomes, whereas HER3 and HER4 gene transcription is associated with better prognosis in high-risk early breast cancer. However, HER2 mRNA expression did not predict clinical benefit from paclitaxel. Kinetic RT-PCR represents an alternative method for evaluating the expression of HER family members in FFPE breast carcinomas.