Abstract

Purpose: Patients with residual diseases (RD) usually have poor prognoses after neoadjuvant chemotherapy for breast cancer. The aim of this study was to explore therapeutic targets and potential additional adjuvant treatments for patients with RD after standard neoadjuvant chemotherapy.

Materials and Methods: We retrieved publicly available cDNA microarray data from 399 human epidermal growth factor 2 negative primary breast cancer samples from patients undergone standard neoadjuvant chemotherapy. We analyzed the mRNA expression levels of key breast cancer markers and therapeutic target genes based on residual cancer burden (RCB) classification: RCB-0/I, RCB-II, and RCB-III.

Results: Among hormone receptor (HR) -positive samples, there were more luminal A tumors by PAM50 in RCB-III than in RCB-0/I and RCB-II ($P < 0.01$). The mRNA expressions of *ESR1* and *PGR* were significantly higher and that of *MKI67* was lower in RCB-II and RCB-III than in RCB-0/I. The mRNA expression of *cyclin D1* was upregulated in RCB-III and that of *CDKN2A* was down-regulated in RCB-III ($P = 0.027$ and < 0.01). Among triple negative (TN) samples, RCB-III had higher clinical Stage and more lymph node-positive samples than RCB-0/1 and RCB-II ($P < 0.01$). In both subtypes, *VEGF-C* expression was significantly higher in RCB-III than in RCB-0/I and RCB-II.

Conclusion: In HR-positive breast cancer, biological features such as luminal A were associated with RCB; this trend was not observed in TN breast cancer. Further, some targeted therapies should be tested as new strategies after standard neoadjuvant chemotherapy in future clinical trials.