Abstract

Purpose: To evaluate whether tumor androgen receptor (AR) expression has various prognostic roles in breast cancer depending on joint hormone receptor (HR) status and to explore the association between an integrated AR and BRCA1 signature and survival outcome in patients with triple negative breast cancer (TNBC).

Methods: An immunohistochemistry screen for AR and BRCA1 was performed on a tissue microarray containing 450 pathologically verified breast cancer samples collected from female patients in the Fudan University Shanghai Cancer Center between August 2001 and January 2008. Associations between immunohistochemical AR expression and tumor characteristics were analyzed. The effect of AR status on disease-free survival (DFS) was evaluated alone or in combination with HR status. Moreover, a new prediction model for DFS incorporating AR and BRCA1 status was constructed to improve the accuracy of prognostic predictions in TNBC.

Results: ER-positive tumors were more likely than ER-negative tumors to have high AR expression (56.0% vs. 28.1%,$P < 0.001$). AR was positively associated with increased DFS in patients with luminal breast cancer ($P < 0.001$) but negatively associated with DFS in patients with TNBC ($P = 0.014$). When AR and HR status were combined, $HR^{+}AR^{low}$ tumors were associated with the worst prognosis of all receptor status combinations. In TNBC patients, the prediction capability of the model combining AR and BRCA1 surpassed that of the traditional model (area under the curve comparison, $P < 0.001$).

Conclusions: AR had distinct prognostic value depending on HR status. TNBC prognostic predictions were improved by combining AR and BRCA1 status.