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Extended Abstract

A predictive model for serous epithelial ovarian cancer chemo-response using clinical characteristics

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Objectives

One of the prognostic factors most highly associated with ovarian cancer survival is response to initial chemotherapy. Current prediction models of chemo-response built with comprehensive molecular datasets, like The Cancer Genome Atlas (TCGA), could be improved by including clinical and outcomes data designed to study response to treatment. The objective of this study was to create a prediction model of ovarian cancer chemo-response using clinical-pathological features, and to compare its performance with a similar TCGA clinical model.

Methods

We first performed a retrospective case-control study of 359 patients with primary, high-grade, advanced-stage serous ovarian cancer treated at a single academic institution. Responders were defined as those patients whose disease disappeared after standard chemotherapy and did not recur for 6 months. Non-responders were defined as those with persistent disease or recurrence within 6 months of completing chemotherapy. A prediction model was created using a lasso (least absolute shrinkage and selection

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operator) regression analysis and included clinical variables associated with chemo-response. Performance was evaluated using the area under the curve (AUC) of the receiver operating curve and its 95% confidence interval (CI). This prediction model was compared to a similar model derived using clinical variables available in TCGA dataset for serous ovarian cancer.

Results

As expected, the strongest predictor of survival in the single-institution cohort was chemo-response (p=2x10-16). Factors independently associated with chemo-response were age, grade, optimal surgery, residual disease after surgery, and receipt of neoadjuvant chemotherapy. The performance of the prediction model yielded an AUC of 0.72 (95% CI of 0.69, 0.75). A similar clinical model from TCGA had an AUC of 0.53.

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