Predicting response to neoadjuvant therapy in esophageal cancer with p53 genotyping: A fortune-teller’s crystal ball or a viable prognostic tool?

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EDITORIAL COMMENTARY

Ideally, predictive biomarkers with associated targeted therapies would be available for individualized treatment of esophageal cancer, optimizing outcome and minimizing chemotherapy-associated risks. Unfortunately, clinically relevant biomarker identification for esophageal cancer has been elusive, more often resembling predictions from a fortune-teller’s crystal ball than proving to be valid, clinically useful prognostic tools. The quest continues, however, and the p53 (TP53) gene appears promising. One of the most frequently mutated cancer-associated genes and a critical tumor suppressor gene involved in programmed cell death,1 multiple studies show a relationship between TP53 mutation and response to chemotherapy, including that of esophageal cancer. A recent meta-analysis of 28 studies with 1497 patients by Zhang and colleagues2 showed high response rates to chemotherapy-based treatment regimens in tumors with low p53 protein expression or wild-type p53. Despite statistically significant findings, however, the conclusions were limited by tremendous heterogeneity across studies with respect to assessment of therapeutic response, chemotherapy regimens (dose and type), and the p53 (TP53) mutation and response to chemotherapy in advanced non-small cell lung cancer. J Thorac Cardiovasc Surg. 2008;135:1036-41.


See related article on pages 2280-6.
and use of radiation. Zhang and colleagues\(^2\) cautioned that immunohistochemistry interpretation is highly susceptible to interobserver differences and may have limited usefulness because of the instability of the wild-type protein. There were also discrepancies between p53 protein levels and p53 gene mutations when assessed with reverse transcription polymerase chain reaction. They concluded that predicting response to chemotherapy in esophageal cancer may be possible by assessing pretreatment p53 status but could not make a definitive statement.

To investigate further the prognostic capabilities of TP53, the current study of Kandioler and colleagues, published in this issue of the *Journal of Thoracic and Cardiovascular Surgery*, sought to determine whether mutations in TP53 were associated with differential survival outcomes after neoadjuvant cisplatin and 5-fluorouracil chemotherapy followed by esophagectomy. TP53 genotyping identified 18 patients with TP53 mutations and 18 with normal TP53 genotype. All patients were evaluated on an intention-to-treat basis, although only 27 patients underwent esophagectomy; 8 patients had disease progression on chemotherapy and 1 had a complete response and declined esophagectomy. Overall and tumor-specific survivals were stratified by TP53 status and compared; patients with TP53 mutation had significantly worse survival (median, 8.6 vs 26.2 months) and were twice as likely to be dead at each follow-up interval than patients with normal TP53. The study results suggest a lack of response in the population with TP53 mutation, but Kandioler and colleagues conclude that further validation is needed.

Several study strengths warrant highlighting. First, all patients were treated with cisplatin and 5-fluorouracil. Both agents rely on induction of DNA damage, a potent trigger for activation of the TP53 gene, for therapeutic effect. In the setting of a TP53 mutation, DNA damage would not activate TP53, providing a biologically plausible explanation for lack of treatment response. Second, p53 status is assessed at a genomic rather than at a protein level, eliminating the potential biases noted by Zhang and colleagues\(^3\) in their meta-analysis. The analysis is also correctly based on intention-to-treat regardless of esophagectomy, allowing close examination of the relationship between TP53 mutation and response to treatment. All 8 patients with progression (no esophagectomy) had TP53 mutations, as did 6 of 7 patients with radiographically stable disease who underwent esophagectomy (\(P < .0001\)). The 3 patients with complete response had normal TP53. Additional strengths include complete patient follow-up of long duration (median, 87.4 months) and appropriately circumspect study conclusions that take into account the study limitations.

The weaknesses of the study of Kandioler and colleagues include small study size, relatively high perioperative mortality (11\%), mixed histologic tumor types (squamous cell and adenocarcinoma), and inadequate clinical staging. The limitations of computed tomographic scanning for depth of tumor invasion and nodal metastasis are well described; tumor-stage misclassification is as high as 58\%.\(^3\) Misclassification can be either overstaging or understaging, and at a minimum endoscopic ultrasonographic and positron emission tomographic testing should be included in the pretreatment clinical staging assessment. Some surgeons also recommend routine laparoscopic staging before neoadjuvant therapy to lessen the significant rate of misclassification.\(^1,5\)

In summary, these findings have potentially significant implications for pretreatment decision making for patients with esophageal cancer. If validated, phenotyping of the TP53 gene with pretreatment tumor biopsies may allow tailored therapy. Whether this means primary esophagectomy, an alternate chemotherapeutic regimen, or palliative definitive chemoradiation, the potential benefit lies in optimizing outcomes while reducing the morbidity and mortality of treatments without measurable, proven benefit to the individual patient. Definitive conclusions regarding the prognostic role of TP53 remain to be established, but the study of Kandioler and colleagues suggests a potential prognostic role that warrants further study. Toward this end, enrollment of 168 patients in the p53 Adapted Neoadjuvant Chemotherapy for Operable Esophageal Cancer (PANCHO) trial was recently completed. If the study design addresses the weaknesses of the current study of Kandioler and colleagues, particularly with regard to the issues of clinical staging and histologic subtypes, more definitive assessment of the classification accuracy and positive and negative predictive values of p53 for response to chemotherapy may be possible. Although a single crystal ball for predicting response to chemotherapy may not even exist, mutations of the p53 gene may prove to be an important tool for stratifying patients into appropriate treatment regimens.

References