Secrets of Drug Resistance in NSCLC Exposed by New Molecular Definition of EMT

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In this issue of Clinical Cancer Research, Byers and colleagues report a gene expression signature of epithelial-to-mesenchymal transition (EMT) that can classify non–small cell lung cancers (NSCLC) as either epithelial or mesenchymal and show its use as a biomarker of response to some targeted therapies used in patients with NSCLC (ref. 1; Fig. 1).

The management of patients with NSCLC has changed dramatically over the past decade because of the identification of molecular drivers of NSCLC and the development of targeted therapies that act against many of these key oncogenic drivers (2, 3). Molecularily targeted therapies used in many patients with NSCLC are less toxic and more effective than conventional chemotherapy. This is because NSCLCs that harbor a driver oncogene depend on its activity for their growth such that targeted inhibition of it causes tumor regression with minimal effect in normal cells lacking its expression. Indeed, in approximately 10% to 15% of patients with NSCLC with advanced disease, whose tumors harbor activating mutations in the kinase domain of the EGF receptor (EGFR), the EGFR tyrosine kinase inhibitor (TKI) gefitinib or erlotinib is standard first-line therapy (3, 4). However, EGFR-mutant patients with NSCLC respond variably to initial EGFR TKI treatment and those who initially respond invariably relapse because of the development of drug resistance (5, 6). In addition, some patients whose NSCLCs harbor wild-type EGFR also benefit from EGFR TKI treatment. Developing more effective molecular biomarkers of response and resistance to EGFR TKI treatment in both EGFR mutant and EGFR WT NSCLCs is essential to optimize the use of EGFR TKIs in patients with NSCLC.

Byers and colleagues shed light on this issue by further investigating the relationship between EMT and drug sensitivity in NSCLC. EMT is a phenotypic manifestation of complex changes in gene expression that include decreased expression of epithelial markers (e.g., E-cadherin) and increased expression of mesenchymal markers (e.g., vimentin; ref. 7). EMT, as defined by the analysis of a limited set of epithelial or mesenchymal markers, has been observed in several epithelial cancers, including NSCLCs. EMT has been associated with increased tumor cell proliferation, invasion, migration, and metastasis and in some cases with resistance to EGFR inhibitor treatment in NSCLCs (7, 8). Yet, a robust and comprehensive gene expression signature capturing the molecular elements underlying EMT and its association with drug resistance in NSCLC had not been developed. Thus, the relationship between EMT and drug response and the molecular events driving the observed clinical manifestations of EMT in NSCLC have remained incompletely characterized.

Through gene expression profiling in a large panel of NSCLC lines, Byers and colleagues defined a signature consisting of 76 genes whose expression most closely correlated with several established markers of EMT, including E-cadherin and vimentin. The authors found that the gene expression classifier composed of the differential expression of these 76 genes could reliably cluster the NSCLC lines into either an epithelial or mesenchymal group. The authors found that cell lines in the mesenchymal group expressed increased levels of EMT markers, such as MMP2, vimentin, and ZEB1. Among the genes increased in mesenchymal lines was the kinase AXL that had been linked previously to EMT in some breast and pancreatic cancers (9, 10). The authors then used a high-throughput proteomics approach to identify differences in protein expression between the cell lines classified by the EMT gene expression signature as either epithelial or mesenchymal. An unsupervised analysis of the proteomic data clustered the cell lines into either the epithelial or mesenchymal group and also confirmed overexpression of AXL in the mesenchymal class. Together, the integrated gene expression and proteomic analysis showed the robust discriminative power of the novel EMT classifier in the NSCLC models.
In a series of elegant in vitro experiments, the authors showed that the EMT gene expression signature could be used as a predictive biomarker of resistance to erlotinib and inhibitors of phosphoinositide-3 kinase (PI3K), AKT, and mTOR signaling in a panel of NSCLC cell lines derived from treatment-naive patients. The cell lines classified by the EMT signature as mesenchymal were more resistant to erlotinib and the PI3K pathway inhibitors, but not other targeted agents or cytotoxic chemotherapies, than the cell lines in the epithelial group. In some of the erlotinib-resistant mesenchymal cell lines that had increased expression of EMT markers including AXL, pharmacologic inhibition of AXL was synergistic with erlotinib both in vitro and in vivo. These effects of combined AXL and EGFR inhibition were observed in some cell lines expressing WT EGFR, suggesting that AXL is a promising therapeutic target to enhance EGFR TKI response in selected EGFR WT NSCLC patients.

The authors clinically validated their preclinical observations by examining whether the EMT signature was a predictive biomarker of erlotinib response in patients with NSCLC enrolled in the Biomarker-integrated Approaches of Targeted Therapy for Lung Cancer Elimination (BATTLE-1) trial. Indeed, erlotinib was more effective at controlling the disease in those patients whose NSCLCs were classified by the EMT signature as epithelial compared with mesenchymal, in which increased expression of AXL and its ligand GAS6 was observed. This correlation between the EMT signature and clinical outcomes was predictive and not merely prognostic because there was no association between the EMT signature and outcomes in all clinically evaluable patients enrolled on all treatment arms of the BATTLE-1 trial. These results raise the exciting possibility that the EMT gene signature could be used to predict response to erlotinib in a broad spectrum of patients with NSCLC and suggest that inhibition of AXL may enhance responses to erlotinib in some patients with EGFR WT NSCLCs.

The data reported by Byers and colleagues compliment recent work that showed that AXL causes acquired EGFR TKI resistance in some EGFR-mutant NSCLCs, in some cases in association with an EMT, and that AXL inhibition overcomes resistance to erlotinib in this setting (11). Together, these studies highlight a previously unappreciated and important role for AXL and EMT in regulating response to...
EGFR inhibitor treatment in patients with NSCLC. Prospective clinical studies aimed at validating the use of the EMT signature and AXL as predictive biomarkers of drug response and therapeutic targets in patients with NSCLC are warranted.

The report by Byers and colleagues significantly increases our understanding of the importance of EMT in the response of NSCLCs to targeted therapy and provides a rationale for further studies. Though the data show that increased AXL expression is associated with the mesenchymal signature, this study does not directly address the potential mechanisms underlying AXL upregulation. Are there epigenetic alterations that regulate AXL expression in the setting of EMT, and could such epigenetic events be potential therapeutic targets? Are there genomic alterations that contribute to EMT or AXL upregulation in NSCLCs that remain undefined? Furthermore, Byers and colleagues found evidence of EMT and increased AXL expression in cells obtained from treatment-naïve patients, whereas other work showed that AXL upregulation can occur during treatment with EGFR TKIs (11). Is the mechanism of AXL overexpression and the biologic functions of AXL identical or different in these distinct contexts? As emerging data have implicated AXL and EMT in both innate and acquired resistance to erlotinib, how could EMT be prevented or reversed in NSCLC? Uncovering the answers to these questions should enable us to develop strategies to optimize the efficacy of mechanism-based therapies that enhance outcomes for patients with NSCLC broadly.

Disclosure of Potential Conflicts of Interest
T.G. Bivona is a consultant/advisory board member of the Cancer Therapeutics Innovation Group. No potential conflicts of interest were disclosed by the other author.

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Conception and design: T.G. Bivona
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Grant Support
This study was supported by funding from the following sources: NIH Director’s New Innovator Award, Howard Hughes Medical Institute, Doris Duke Charitable Foundation, American Lung Association, National Lung Cancer Partnership, Uniting Against Lung Cancer, and Sidney Kimmel Foundation for Cancer Research (to T.G. Bivona).

Received October 31, 2012; accepted November 9, 2012; published OnlineFirst November 21, 2012.

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Clinical Cancer Research

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doi:10.1158/1078-0432.CCR-12-3232

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