In this issue of *Cancer Discovery*, Hammerman and colleagues (1) report that mutations in the gene encoding the discoidin domain receptor 2 (DDR2) kinase identify a novel therapeutic target in squamous cell lung cancer.

Lung cancer is the leading cause of cancer-related death in the United States and worldwide. Until the last decade, treatment decisions for patients were largely based on histologic considerations. Those with small-cell lung cancer (SCLC; now ~10% of cases) were treated in one way and those with non–small cell lung cancer (NSCLC) in another. In major trials, investigators studied patients with NSCLC as one disease entity regardless of whether they had adenocarcinoma (50% of lung cancers), squamous cell carcinoma (SCC; 30%), or large-cell carcinoma (10%). However, recent clinical and translational studies have demonstrated that this approach is no longer applicable. First, the antiangiogenesis agent bevacizumab was approved for use in nonsquamous NSCLC; use in SCC was restricted because of increased bleeding risks (2). Second, the multitargeted antifolate pemetrexed was approved for use in only nonsquamous NSCLC; in several studies (2), pemetrexed did not show a benefit in patients with squamous cell tumors. Third, most targetable mutant kinases, such as epidermal growth factor receptor (EGFR), anaplastic lymphoma kinase (ALK), and HER2, were found in lung adenocarcinomas and only rarely in other histologic subtypes (3). Such advances seem to have left SCC as the “odd man out.”

Although the lung adenocarcinoma genome has been characterized extensively (4), less is known about specific genetic alterations, especially “driver mutations,” in SCC of the lung. Large-scale genomic studies in the latter have been hampered by difficulty obtaining samples with high tumor content and minimal necrosis. Nevertheless, some efforts are beginning to bear fruit. SCC of the lung may be categorized into distinct subsets based on mRNA expression patterns (5). Recent molecular analyses have identified genes that may play important roles in lung squamous cell tumorigenesis (e.g., *SOX2, p63, BRF2, GRM8, BAI*). Perhaps more clinically applicable, some potentially targetable alterations in genes encoding kinases have been identified in lung SCC, including *FGFR1*, *EGFReIII*, and *PIK3CA* (Table 1). Whereas *EGFReIII* and *PIK3CA* mutations are relatively uncommon, focal *FGFR1* amplification occurs in up to 22% of SCC cases. Importantly, cells with *FGFR1* amplification may be dependent on fibroblast growth factor receptor (FGFR) signaling for survival and are sensitive to FGFR inhibitors, many of which are in clinical development (6).

Hammerman and colleagues (1) describe driver mutations involving another kinase in SCC of the lung. Using dideoxynucleotide-based re-sequencing, they screened 201 genes (including those that encode the tyrosine kinome) in 20 primary lung SCC samples and matched normal controls, and identified somatic missense mutations in 25 genes, including 2 in *DDR2*. In a secondary screen of 48 SCC samples that included 13 cell lines, they found 4 additional *DDR2* mutations. They then sequenced *DDR2* in a validation cohort of 222 primary lung SCC samples and identified another 5 samples with mutation, resulting in an overall frequency of 3.2% (9 of 227) in primary lung SCC samples. In total, 11 novel *DDR2* mutations were found throughout the entire gene, not just in exons encoding the kinase domain. Mutations did not correlate with amplification or overexpression of the gene. *DDR2* mutations also had no correlation with gender or smoking history.

*DDR2* is the second member of the DDR kinase family, which possess a motif in their extracellular domains with homology to the *Dictyostelium discoideum* protein discoidin-I. DDR kinases are widely expressed in human tissues, are activated by collagens, and have roles in cell adhesion. *DDR1* and *DDR2* mutations have been reported previously in multiple tumor types including lung cancer (7), but they are rare and have not been functionally characterized. In the study by Hammerman and colleagues (1), the mutants that were studied biologically had transforming ability. Tumor cell lines harboring activating *DDR2*...
mutations displayed increased sensitivity in vitro and in vivo to multiple tyrosine kinase inhibitors, including the 3 small molecules dasatinib, nilotinib, and AP24534, which are more commonly known for their ability to inhibit ABL kinase activity but appear to have “off-target” anti-DDR2 activity. Interestingly, the authors identified one patient with lung SCC whose tumor harbored a DDR2 mutation and responded significantly to treatment with dasatinib and erlotinib. The patient’s tumor did not have any EGFR kinase domain mutation associated with sensitivity to erlotinib, suggesting that the tumor responded to dasatinib because of its dependency on mutant DDR2.

The new findings raise many questions. Are DDR2 mutations specific to SCC of the lung, or will they also be found in other cancer types? In lung cancer, will ethnic differences be found in the frequency of DDR2 mutations, as for EGFR, KRAS, and LKB1 mutations in lung adenocarcinoma? Are DDR2 mutations overlapping with FGFR1 amplification, EGFRvIII mutations, and/or PI3KCA mutations? Are all DDR2 mutants equally sensitive to dasatinib? What signaling pathways are activated by DDR2 mutants? A previous phase II study of dasatinib in NSCLC showed only 1 partial response among 34 patients (8); was this result negative due to lack of studying the appropriate molecularly enriched cohort of patients (i.e., patients with DDR2 mutant tumors)? Because dasatinib induces pleural effusion as a problematic toxicity, do more potent DDR2 inhibitors with fewer side effects exist?

The findings by Hammerman and colleagues (1) offer a promise of the translational knowledge that may soon emerge from the ongoing Cancer Genome Atlas project on SCC of the lung (9). Whereas this study used targeted dideoxynucleotide-based re-sequencing of only 201 genes, future efforts will deliver portraits of whole exomes and/or whole genomes. We look forward to a more comprehensive picture of the lung SCC genome, so that SCC of the lung no longer is the odd man out in terms of therapeutic options.

Disclosure of Potential Conflicts of Interest

W. Pao received consulting fees (Astra-Zeneca, Bristol-Myers Squibb, Symphony Evolution, and MolecularMD) and grant support (Xcovery, Astra-Zeneca, and Enzon). K. Ohashi disclosed no potential conflicts of interest.

Table 1. Potential targetable driver mutations in squamous cell carcinoma of the lung

<table>
<thead>
<tr>
<th>Gene</th>
<th>Frequency (%)</th>
<th>Drug</th>
<th>Reference</th>
</tr>
</thead>
<tbody>
<tr>
<td>FGFR1 amplification</td>
<td>22</td>
<td>FGFR TKIs</td>
<td>Weiss et al. (6)</td>
</tr>
<tr>
<td>EGFRvIII mutations</td>
<td>5</td>
<td>EGFR TKIs</td>
<td>Ji et al. (10)</td>
</tr>
<tr>
<td>PIK3CA mutations</td>
<td>3.6</td>
<td>PI3K inhibitors</td>
<td>Yamamoto et al. (11)</td>
</tr>
<tr>
<td>EGFR kinase domain mutations</td>
<td>3.4</td>
<td>EGFR TKIs</td>
<td>Miyamae et al. (12)</td>
</tr>
<tr>
<td>DDR2 mutations</td>
<td>3.2</td>
<td>Dasatinib, nilotinib</td>
<td>Hammerman et al. (1)</td>
</tr>
</tbody>
</table>

Abbreviation: TKI, tyrosine kinase inhibitor.

REFERENCES

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