Missense Mutations of the BRAF Gene in Human Lung Adenocarcinoma

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INTRODUCTION

Lung carcinoma is the leading cause of cancer death in the United States and worldwide, claiming more than 150,000 lives each year in the United States alone (1). Current therapies for lung carcinoma remain inadequate; only an average of 15% of patients survive as long as 5 years from diagnosis. The development of targeted therapy for cancer-specific molecular alterations has led to significant clinical advances, such as the use of the c-Abl tyrosine kinase inhibitor, imatinib mesylate, for treatment of chronic myelogenous leukemia (2). Genome-wide screens for gene alterations in lung carcinoma should provide new therapeutic opportunities for this disease.

Adenocarcinoma is the most common histological class of lung carcinoma, and its relative incidence is increasing (3). Activating mutations of the KRAS proto-oncogene are known to occur in roughly 30% of human lung adenocarcinomas (4, 5). The pathway linking receptor tyrosine kinases to the Ras family to the Raf serine-threonine kinase to the mitogen-activated protein kinase cascade is critical for cell proliferation and is frequently activated in human cancers (6). Thus it is important to look for mutations of other members of this pathway in lung adenocarcinoma, in addition to KRAS.

A recent study revealed activating mutations in the BRAF kinase gene in over 60% of melanomas and a broad range of other human cancers (7). In particular, Davies et al. (7) found BRAF missense mutations in 4 of 35 lung adenocarcinoma cell lines tested (11%), but not in 14 primary lung cancers analyzed. Because of the possibility of therapeutic inhibition of the BRAF kinase in lung cancer, it is important to determine the frequency of BRAF mutations in primary lung adenocarcinomas.

We have recently analyzed a set of 127 human lung adenocarcinomas by gene expression profiling and unsupervised clustering (8). Here we report 2 cases with BRAF missense mutations of 127 lung adenocarcinomas tested.

MATERIALS AND METHODS

Specimens and RNA. Lung adenocarcinoma samples and RNA preparation methods have been described previously (8). We used 127 of 139 samples from the previous report, excluding 12 samples suspected to be metastases of extrapulmonary origin.

RT-PCR, Genomic DNA PCR, and DNA Sequencing. Total RNA from lung cancer specimens was used to generate cRNA by in vitro transcription (8). cRNA samples were amplified by RT-PCR of BRAF exon 11 and exon 15 using specific primers [exon 11, TACCTGGCTCACAATACAAGGTG (forward) and CACATGTCGTGTTTCTCGAG (reverse); exon 15, ACT GCACAGGCGATGATTAC (forward) and AATTCATACAGAACACATC- CAAA (reverse)]. PCR primers were designed to amplify target exons plus approximately 50-bp flanking exonic sequences in both upstream and downstream directions.

RT-PCR was performed using Superscript One-Step RT-PCR with Platinum Taq kit (Life Technologies, Inc., Gaithersburg, MD). A single 50-μl RT-PCR reaction mix contained 1 μg of cRNA, 3 mM MgSO4, 100 pmol of each primer, and 1 μl of reverse transcriptase/Platinum Taq mix. RT-PCR was carried out in a GeneAmp PCR system 9700 (Applied Biosystems) as follows: after 30 min of cDNA synthesis at 50°C and 2 min of denaturation at 94°C, samples were subjected to 35 cycles of amplification, consisting of 15 s at 94°C, 30 s at 61°C, and 1 min at 72°C, with a final additional extension step at 72°C for 7 min.

We also analyzed KRAS codon 12, 13, and 61 mutations using cRNA samples with RT-PCR. Amplification was done using specific primers (forward, CGGGAGAGAGGCCTGCTGA; reverse, CCACTTGTACTAGTATGTG). PCR primers were designed to amplify BRAF exons 11 and 15 from genomic DNA (7), 100 ng of genomic DNA were amplified using standard PCR protocol.

RT-PCR and PCR products were visualized by 2% agarose gel electrophoresis and purified using QIA quick purification kit (Qiagen) according to the manufacturer’s instructions. Using primers designed to amplify BRAF exons 11 and 15 from genomic DNA (7), 100 ng of genomic DNA were amplified using standard PCR protocol.

RT-PCR and PCR products were visualized by 2% agarose gel electrophoresis and purified using QIA quick purification kit (Qiagen) according to the manufacturer’s instructions. Purified products were subjected to primer extension sequencing (9) in both forward and reverse directions, by either the Molecular Biology Core Facility at Dana-Farber Cancer Institute or Seqwright Inc. (Houston, TX). Sequences were examined using Sequencer software (Gene Codes Corp., Inc.).

As positive and negative controls, we sequenced the BRAF gene in four lung carcinoma cell lines. We detected the missense mutations that were reported previously (7). The NCI-H1395 cell line has a G1403C (G468A) mutation in exon 15, whereas the NCI-H2087 cell line has a C1786G (L596V) mutation in exon 15. The other two cell lines, CaLu1 and NCI-H1437, did not have BRAF mutations in these exons.

Expression Analysis. Gene expression values were compared between the two BRAF mutant adenocarcinomas and the 57 lung adenocarcinomas known to be wild-type for BRAF and KRAS sequence, using the dChip program (10). We used the following criteria to select genes specific for the BRAF mutant tumors: (a) minimum fold change (BRAF mutant versus wild-type) >2.0; (b) minimum lower bound of fold change (90% confidence bound) >1.25; and (c) minimum mean difference in arbitrary Affymetrix expression units (8) >100.
RESULTS AND DISCUSSION

To detect mutations in the \textit{BRAF} gene in primary lung adenocarcinomas, we sequenced exons 11 and 15 from the 127 lung adenocarcinomas characterized by gene expression analysis (8). These exons were chosen because all reported \textit{BRAF} mutations were within them (7).

Among the primary lung adenocarcinomas, we detected a lower frequency of \textit{BRAF} mutations than had been reported in the cell lines: 2 of 127 adenocarcinomas (1.6%). One human lung adenocarcinoma (AD210) has the missense mutation G1394T (G465V) in exon 11 (Fig. 1A); no mutation was detected in the corresponding normal lung tissue (Fig. 1B). In a second human lung adenocarcinoma (AD238), we found the missense mutation T1787G (L596R) in exon 15 (Fig. 1C); again, this sequence is wild-type in the uninvolved lung from the same patient (Fig. 1D). Both of these mutations had been previously reported in human cancer, G465V in a lung adenocarcinoma cell line and L596R in a primary ovarian cancer (7).

Because \textit{KRAS} is frequently mutated in lung adenocarcinoma, we compared the frequency of \textit{BRAF} mutations with \textit{KRAS} mutations and with gene expression-defined tumor classes (8) for the same samples (Table 1). The frequency of \textit{KRAS} mutations in the 89 samples sequenced for \textit{KRAS} was 33.7%, similar to that reported in the literature; in these samples, \textit{BRAF} and \textit{KRAS} mutations were not present in the same tumor specimen.

Comparison with gene expression patterns revealed that both tumors with \textit{BRAF} mutants were clustered in group I of our expression analysis (Fig. 2). Histologically, both tumors showed moderately differentiated adenocarcinoma, and both patients had stage I tumors. Whereas this clustering is intriguing, the sample size is too small at present to deter-

<table>
<thead>
<tr>
<th>Table 1</th>
<th>\textit{BRAF} and \textit{KRAS} mutations in lung adenocarcinoma</th>
</tr>
</thead>
<tbody>
<tr>
<td>No. of cases</td>
<td>\textit{BRAF} mutation$^a$</td>
</tr>
<tr>
<td>---------</td>
<td>-------------------------------</td>
</tr>
<tr>
<td>Total 127</td>
<td>2/127 (1.6%)</td>
</tr>
<tr>
<td>\textit{BRAF} mutants 1</td>
<td>G1394T WT</td>
</tr>
<tr>
<td>1</td>
<td>T1787G WT</td>
</tr>
<tr>
<td>1</td>
<td></td>
</tr>
<tr>
<td>\textit{KRAS} mutants 30</td>
<td>WT MUT$^e$</td>
</tr>
<tr>
<td>1</td>
<td>C1 1/8 (13%)</td>
</tr>
<tr>
<td>2</td>
<td>C2 5/7 (71%)</td>
</tr>
<tr>
<td>3</td>
<td>C3 5/11 (45%)</td>
</tr>
<tr>
<td>4</td>
<td>C4 3/11 (27%)</td>
</tr>
<tr>
<td>Others 57</td>
<td>WT WT</td>
</tr>
</tbody>
</table>

$^a$ Exons 11 or 15.
$^b$ Codons 12, 13, or 61.
$^c$ Clusters defined in Ref. 8.
$^d$ WT, wild-type sequence.
$^e$ MUT, mutant sequence.

Fig. 1. Mutations in the \textit{BRAF} gene. A and B, a point mutation was identified in exon 11 of one human lung adenocarcinoma sample, AD210T (G1394T/G465V), which is not present in a normal lung tissue sample from the same patient, AD210N. C and D, a point mutation was identified in exon 15 of sample AD238T (T1787G/L596R), which is not present in the corresponding normal lung tissue sample, AD238N.

Fig. 2. Dendrogram of lung adenocarcinoma with reference to \textit{BRAF} mutation. A, expression-defined adenocarcinoma subclasses (8). There are four major clusters (C1–C4) and three groups with weaker association (group I–III). Samples of colon metastasis (CM) and normal lung (NL) were not included in this \textit{BRAF} mutation search. B, enlarged view of group I. The two samples with \textit{BRAF} mutation (AD210 and AD238) were both included in group I. Please note that this figure is adapted from Ref. 8.

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mine whether BRAF-mutant tumors represent a distinct subset of lung adenocarcinomas. It is worth noting that analysis of oligonucleotide array gene expression data did not reveal any significant differences in BRAF expression between mutant and wild-type tumors. However, the BRAF-mutant tumors are characterized by high relative expression levels of multiple genes in this sample set (Table 2); these include the adenosine A2a receptor, several B lymphocyte and/or plasma cell genes, and cyclin D1. It is interesting to note that cyclin D1, itself a transforming oncoprotein, has been reported to be downstream of oncogenic Raf signaling pathways in several independent studies (11–15). Obviously, the sample size is small, and any conclusions about expression correlates of BRAF mutation must remain tentative.

In summary, we have found 2 cases with BRAF missense mutation in 127 human lung adenocarcinomas. Although the percentage of lung adenocarcinomas with BRAF mutation in lung cancer patients is relatively low compared with melanomas and colon carcinomas (7, 16), if BRAF inhibitors are found to be effective in these tumors, they should be also considered for treatment of BRAF-mutant lung adenocarcinomas. Furthermore, even 1.6% of lung adenocarcinoma would represent well over 1,000 patients per year in the United States, a significant group in terms of public health importance. Several Raf inhibitors have been recently discovered and entered into clinical trials (17–19).

Furthermore, the presence of both KRAS and BRAF mutations in lung adenocarcinomas suggests that other members of the receptor tyrosine kinase/Ras/Raf/mitogen-activated protein kinase cascade should be evaluated for mutations in these tumors.

REFERENCES

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