BRAF and RAS Mutations in Human Lung Cancer and Melanoma

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ABSTRACT

BRAF encodes a RAS-regulated kinase that mediates cell growth and malignant transformation kinase pathway activation. Recently, we have identified activating BRAF mutations in 66% of melanomas and a smaller percentage of many other human cancers. To determine whether BRAF mutations account for the MAP kinase pathway activation common in non-small cell lung carcinomas (NSCLCs) and to extend the initial findings in melanoma, we screened DNA from 179 NSCLCs and 35 melanomas for BRAF mutations (exons 11 and 15). We identified BRAF mutations in 5 NSCLCs (3%; one V699 and four non-V599) and 22 melanomas (63%; 21 V599 and 1 non-V599). Three BRAF mutations identified in this study are novel, altering residues important in AKT-mediated BRAF phosphorylation and suggesting that disruption of AKT-induced BRAF inhibition can play a role in malignant transformation. To our knowledge, this is the first report of mutations documenting this interaction in human cancers. Although >90% of BRAF mutations in melanoma involve codon 599 (57 of 60, 8 of 9 BRAF mutations reported to date in NSCLC are non-V599 (89%; P < 10−6), strongly suggesting that BRAF mutations in NSCLC are qualitatively different from those in melanoma; thus, there may be therapeutically different between lung cancer and melanoma in response to BRAF inhibitors. Although uncommon, BRAF mutations in human lung cancers may identify a subset of tumors sensitive to targeted therapy.

INTRODUCTION

Identification of gene mutations in human cancers can lead to the development of effective targeted therapies (1). We reported recently that activating BRAF mutations are present in 66% of melanomas and a small percentage of NSCLC cell lines (2). In melanoma, most BRAF mutations involved codon 599 in the activation segment of the kinase domain (exon 15; Fig. 1); however, four of four BRAF mutations found in NSCLCs were non-V599 (exons 11 and 15). Interestingly, none of the 3 of 43 cancer cell lines with both BRAF and RAS mutations had a codon 599 BRAF mutation [one each in NSCLC (NRAS and Q61K), colorectal (KRAS and G13D), and ovarian cancer lines (KRAS and G13D; Ref. 2)]. This (2) and a subsequent report (3) provide evidence that BRAF kinase mutations are present in 10% of colon cancers overall and in 31% of mismatch repair-deficient tumors (P < 10−6; Ref. 3). In the latter series of colon cancers, KRAS and BRAF mutations were mutually exclusive (P < 10−6); our current and previous series have inadequate power to evaluate this interaction. ERK1 and ERK2, downstream effectors of the RAS-RAF-MEK-ERK-MAP kinase pathway, are constitutively active in many NSCLCs and melanomas (4, 5). MAP kinase pathway activation in these tumors has not been associated with mutations in ERK1/2 or MEK but rather is attributable to constitutive phosphorylation of these proteins. Thus, activating mutations in BRAF could explain activation of MEK and ERK1/2 in both melanoma and NSCLC. To follow up on the observation that NSCLCs (particularly adenocarcinomas) may have an inverted ratio of V599/non-V599 BRAF mutations as compared with melanoma (2) and to investigate the role of BRAF mutations in the unexplained activation of the MEK-ERK-MAP kinase pathway in lung cancer, we evaluated the frequency of BRAF kinase domain mutations in primary NSCLCs and early passage melanoma cell lines. On the basis of the initial observation that one NSCLC cell line with a BRAF mutation had an NRAS mutation (2), we also screened the NSCLCs and melanomas for codon 61 NRAS and codon 12/13 KRAS mutations, which may be found in these tumors.

MATERIALS AND METHODS

DNA Isolation. DNA was obtained from 35 early passage melanoma cell lines, 2 snap-frozen metastatic melanomas, and 139 snap-frozen lung tumors (>40% tumor) using the Wizard Genomic Purification Kit (Promega). DNA from 165 paraffin-embedded lung tumor specimens was prepared from 10 × 30-μm sections after macrodissection, resulting in selection of ≥90% tumor cells. DNA was isolated after xylene extraction and proteinase K digestion as described previously (6).

Mutation Screening and Confirmation. Genomic DNA was screened for mutations using conformation-sensitive capillary electrophoresis as described previously (2). The following intron-based PCR primers were designed to amplify the exons of interest and the associated splice junctions: KRAS exon2:F-GTGTGACATGTTCTAATATAGTC. KRAS exon2:R-CAAATGTTGCGAGAGATGAA.

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Received 10/3/02; accepted 10/15/02.

1 Supported by funding from the Abramson Family Cancer Research Institute (to B. L. W.) and Lung Cancer SPORE P50 CA70907 (to J. M.). M. Brose is a General Motors Cancer Research Scholar.

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3 The abbreviations used are: NSCLC, non-small cell lung cancer; SCC, squamous cell carcinoma.
and optimized run conditions (2). Data were captured using GeneScan to identify samples with a shift in peak migration relative to a wild-type control, indicating the presence of a putative sequence variation. PCR products selected by the presence of a heteroduplex shift were gel purified and sequenced on the ABI 3100 to confirm the presence of a mutation.

DNA was prepared from 292 NSCLCs, 12 neuroendocrine lung cancers, and 35 melanomas. Amplicons of all four exons (BRAF exons 11 and 15, KRAS exon 2, and NRAS exon 3) were obtained from 158 NSCLCs, 10 neuroendocrine lung cancers, and 33 melanomas (Table 1). Data on both BRAF exons were available for 179 NSCLCs, 11 neuroendocrine lung cancers, and 35 melanomas (Table 1). Mutation frequencies did not vary significantly when tumors lacking data on one BRAF exon were included in the analysis (“All results” versus “Complete Sets”; Fig. 2). Tumor DNA from failed reactions was repurified, and a minimum of three attempts was made to amplify the exon. Success rates using DNA from frozen tissue and cell lines were almost 100%, but amplification of DNA from archival material was inconsistent. Of the 165 paraffin-embedded lung tumors, 30 failed to yield any amplifiable DNA, and 54 yielded DNA that could not be amplified using at least one primer pair. In only three paraffin-embedded lung cancers, neither BRAF exon, but both RAS exons, amplified, suggesting that frequent large genomic deletions involving BRAF are an unlikely explanation for these results. PCR failures were not consistently attributed to a specific primer pair, suggesting they are a result of random cross-linking during fixation that interferes with primer annealing.

**RESULTS AND DISCUSSION**

BRAF mutations were identified in 5 NSCLCs (3%), KRAS mutations in 14 of 147 adenocarcinomas (10%), and NRAS mutations in none (0%; Fig. 2). No NSCLC had both a BRAF and a RAS mutation, but the number of mutations identified in either gene is too small to evaluate a genetic interaction. BRAF mutations were identified in 22 of 35 (63%) melanomas, 1 in exon 11, and the remaining 21 in exon 15 (Fig. 2 and Table 2). Twenty of 21 exon 15 mutations involved codon 599. One NRAS mutation of uncertain significance (S65C) was identified in a melanoma that also had a BRAF mutation (V599E); no KRAS mutations were identified in the melanomas.

In our previous study, the initial analysis of six NSCLC cell lines yielded two BRAF mutations (neither V599), one in exon 15 and one in the exon 11 G-loop (2). That prompted analysis of 125 additional NSCLC cell lines and 14 primary lung tumors. Two more BRAF mutations were identified in the second analysis, for a total of 4 of 131 mutations in NSCLC cell lines but none in the primary tumors. Interestingly, zero of four BRAF mutations identified in NSCLC cell lines were V599 mutations (2). These data were in contrast to that from melanomas, where 100% of the melanoma cell lines and 91% of primary melanoma mutations involved V599, raising the possibility that BRAF mutations in NSCLC are qualitatively different from those in melanoma. Additionally of interest, all four BRAF mutations identified in NSCLC cell lines were in cell lines derived from adenocarcinomas, with none identified in those from SCCs. Given these findings, we evaluated data from the present study for codon mutation frequency between NSCLC and melanoma and for differences between adenocarcinomas and SCCs of the lung.

In this series, we identified five NSCLCs with mutations in BRAF, only one of which involves V599. Taken together with data from the previous study (2), we have identified nine BRAF mutations in NSCLCs, eight of which are non-V599 (P < 10^-7). These data provide a high level of statistical support to the hypothesis that BRAF-related tumorigenesis in NSCLC is qualitatively different from that in melanomas with codon 599 mutations, raising the possibility that therapeutic response to RAF inhibitors may be different in these two tumor types, despite the presence of activating BRAF mutations in both.

Of the 104 adenocarcinomas evaluable for both BRAF exons, two

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<table>
<thead>
<tr>
<th>Tissue type</th>
<th>Total DNA prepared</th>
<th>BRAF exons 11 and 15</th>
<th>Complete sets BRAF exons 11 and 15, KRAS, NRAS</th>
</tr>
</thead>
<tbody>
<tr>
<td>Non-small cell lung cancers (n = 292)</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>adenocarcinoma</td>
<td>171</td>
<td>104</td>
<td>89</td>
</tr>
<tr>
<td>SCC</td>
<td>117</td>
<td>72</td>
<td>67</td>
</tr>
<tr>
<td>Poorly differentiated adeno/squamous carcinoma</td>
<td>4</td>
<td>3</td>
<td>2</td>
</tr>
<tr>
<td>Total</td>
<td>292</td>
<td>179</td>
<td>158</td>
</tr>
<tr>
<td>Neuroendocrine lung tumors</td>
<td>12</td>
<td>11</td>
<td>10</td>
</tr>
<tr>
<td>Melanoma primary cell lines</td>
<td>35</td>
<td>35</td>
<td>33</td>
</tr>
</tbody>
</table>
had novel mutations in exon 11. V458L is five codons upstream of the first glycine in the G-loop (Fig. 1). It is possible that this leucine residue changes the conformation of the adjacent G-loop (2), resulting in activation; however, this remains speculative. The second mutation, K438T, alters the basic residue next to a threonine phosphorylated by AKT (Fig. 1). BRAF has three AKT phosphorylation sites: (a) Thr439 is one of two unique to BRAF; (b) the other being Ser428; and (c) Ser364 is conserved in RAF1 (Ref. 7; Fig. 1). In vitro alanine substitution at Thr439 leads to BRAF activation through loss of AKT-induced inhibition (7), with progressively increased BRAF activity as the additional two sites are mutated. The inhibitory effect of AKT-induced phosphorylation on RAF1 also has been demonstrated (8). Thus, K438T, as well as K438Q found in a melanoma as described below, is likely to inhibit AKT-dependent phosphorylation of the adjacent Thr439, as adjacent basic residues are commonly required in AKT Ser/Thr phosphorylation consensus sequences (9). These data suggest that transformation-related BRAF activation may occur through multiple mechanisms and that mutations of Thr439, as well as the two additional AKT consensus sites (Ser364 and Ser428; Fig. 1; Ref. 10), could play a role in tumorigenesis. Although AKT-BRAF cross-talk has been documented in vitro, to our knowledge, this is the first report of mutations involving this interaction in human cancers.

Fourteen of 147 lung adenocarcinomas had KRAS mutations (Fig. 2), all but one in codon 12, the exception being A18T, the significance of which is unknown. Constitutional DNA was not available from this patient; thus, a germ-line polymorphism cannot be excluded. The overall KRAS mutation frequency in this series of lung adenocarcinomas is 10%, lower than the 17% detected in NSCLCs in the previous series (2) and lower than the frequently cited rate of 30% (11, 12). Multiple studies suggest that the frequency of KRAS mutations in nonsmokers (and dogs) is in the range of 10% (11, 13–15). We have no information on the smoking status of the patients whose tumors were evaluated in our studies, but a bias toward young nonsmokers might occur because of various factors related to selectivity of referrals to a tertiary care hospital.

Table 2: BRAF and RAS mutations identified in lung cancers and melanomas

<table>
<thead>
<tr>
<th>Lung cancer</th>
<th>BRAF exon 11</th>
<th>BRAF exon 15</th>
<th>KRAS exon 2</th>
<th>NRAS exon 3</th>
</tr>
</thead>
<tbody>
<tr>
<td>Lung adenocarcinoma</td>
<td>V458L (1)</td>
<td></td>
<td>G12R (1)</td>
<td>S65R (1)</td>
</tr>
<tr>
<td></td>
<td>K438T (1)</td>
<td></td>
<td>G12A (3)</td>
<td></td>
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<tr>
<td></td>
<td></td>
<td></td>
<td>G12L (1)</td>
<td></td>
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<td></td>
<td>G12D (1)</td>
<td></td>
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<td></td>
<td>G12S (2)</td>
<td></td>
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<td></td>
<td>G12F (1)</td>
<td></td>
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<td></td>
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<td></td>
<td>G12C (4)</td>
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<td></td>
<td></td>
</tr>
<tr>
<td>Lung SCC</td>
<td>T439P (1)</td>
<td></td>
<td>G12L (1)</td>
<td></td>
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<tr>
<td>Lung poorly differentiated</td>
<td></td>
<td></td>
<td></td>
<td>S65C (2)</td>
</tr>
<tr>
<td>carcinoma</td>
<td>L596V (1)</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Lung neuroendocrine cancer</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Malignant melanoma</td>
<td>K438Q (1)</td>
<td></td>
<td>V599E (19)</td>
<td>S65C (1)</td>
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<tr>
<td></td>
<td></td>
<td></td>
<td>V599D (1)</td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>K600E (1)</td>
<td></td>
</tr>
</tbody>
</table>
In the 117 SCC, we identified one novel mutation in exon 11 (T439P) and two mutations in exon 15 (L596V and V599E). As expected based on the existing literature, we did not identify RAS mutations in SCCs. The exon 15 BRAF mutations are both in the activation segment and cause BRAF activation (2). However, the exon 11 mutation is novel. This mutation alters Thr439, an AKT phosphorylation site (described above), further supporting the suggestion that transformation-related BRAF activation may occur through multiple mechanisms.

No BRAF or KRAS mutations were identified in the 12 neuroendocrine lung cancers, but two had codon 65 NRAS mutations (20%). Analysis of this mutation in a melanoma (described below) suggests this mutation may not be transforming. There are few data in the literature on the prevalence of NRAS mutations in neuroendocrine lung cancers, and our series is small as well, but additional investigation may be warranted.

Data from the 35 early passage primary melanoma cell lines confirm our previous report that the majority of melanomas have BRAF mutations (63% in this series), predominantly V599 (20 of 22, 91%; Fig. 2 and Table 2; Ref. 2). One of the two non-V599 mutations is in exon 15 and is in the adjacent residue (K600E). The other non-V599 mutation is in exon 11 (K438Q), similar to the novel K438T mutation in exon 15 and is in the adjacent residue (K600E). This mutation results in substitution of Lys438, likely required for AKT phosphorylation of the adjacent Thr439, thus likely to be an activating mutation (7, 8, 10).

No KRAS mutations and one NRAS mutation of unknown significance (S65C) were identified in the 35 melanomas. Specifically, no NRAS codon 61 mutations, reported in 15% of melanoma cell lines (16), were identified. The codon 65 NRAS mutation was further investigated in three additional melanoma cell lines from the same individual, all derived from axillary lymph node metastases. This mutation (S65C) is not present in the primary tumor nor in a metastatic deposit sampled in June 1983 and is present in only one of two cell lines established from lymph node biopsies performed 2 months later. These data provide evidence that this mutation is not a germ-line polymorphism, nor did it contribute to malignant transformation in this tumor; whether it is important in disease progression is unknown.

In summary, we have confirmed the high prevalence of BRAF mutations in melanoma, shown that BRAF exon 11 and 15 mutations are not a common cause of the MAP kinase pathway activation in NSCLC, and identified four novel BRAF mutations. These mutations provide the first in vivo evidence that activation of BRAF through loss of AKT-induced inhibitory phosphorylation is associated with tumorigenesis, and studies to understand this relationship may uncover additional therapeutic targets. We provide strong statistical evidence that BRAF mutations in NSCLCs are qualitatively different that those in melanoma, with possible therapeutic implications when considering BRAF inhibitors. These results define the frequency of BRAF mutations in NSCLC (2–3%) and in melanomas (>60%). In both cases, future studies will determine whether these BRAF mutations represent promising new therapeutic drug targets for these chemoresistant tumors. Even if the BRAF mutations are rare, as in lung cancer, they may identify a tumor sensitive to targeted therapy, resulting in significantly improved outcomes for the patients that harbor them.

REFERENCES

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