Kinase inhibitors are accepted treatment for metastatic melanomas that harbor specific driver mutations in BRAF or KIT, but only 40% to 50% of cases are positive. To uncover other potential targetable mutations, we conducted whole-genome sequencing of a highly aggressive BRAF (V600) and KIT (W557, V559, L576, K642, and D816) wild-type melanoma. Surprisingly, we found a somatic BRAF L597R mutation in exon 15. Analysis of BRAF exon 15 in 49 tumors negative for BRAF V600 mutations as well as driver mutations in KIT, NRAS, GNAQ, and GNA11, showed that two (4%) harbored L597 mutations and another two involved BRAF D594 and K601 mutations. In vitro signaling induced by L597R/S/Q mutants was suppressed by mitogen-activated protein (MAP)/extracellular signal–regulated kinase (ERK) kinase (MEK) inhibition. A patient with BRAF L597S mutant metastatic melanoma responded significantly to treatment with the MEK inhibitor, TAK-733. Collectively, these data show clinical significance to BRAF L597 mutations in melanoma.

**SIGNIFICANCE:** This study shows that cells harboring BRAF L597 mutants are sensitive to MEK inhibitor treatment, providing a rationale for routine screening and therapy of BRAF L597-mutant melanoma.

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**Note:** Supplementary data for this article are available at Cancer Discovery Online (http://www.cancerdiscovery.aacrjournals.org/).

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INTRODUCTION

Melanoma is a malignant tumor of melanocytes that caused nearly 9,000 deaths in the United States in 2011 (1). Recently, the kinase inhibitors vemurafenib and, to a lesser extent, imatinib have become standard treatments for patients whose metastatic malignant melanomas harbor specific driver mutations in BRAF (V600E; ref. 2) or KIT (exons 11 and 13; ref. 3), respectively; however, only approximately 40% to 50% of cases are positive for these mutations. Currently, clinical algorithms recommend assessing BRAF status in melanomas at only the most common actionable mutant site, BRAF\textsuperscript{V600E} (c.1799T>A).

To uncover other potentially targetable mutations, we conducted whole-genome sequencing (WGS) of a tumor-normal pair from a patient with a highly aggressive BRAF (V600E) and KIT (W557, V559, L576, K642, and D816) wild-type melanoma. Among the many mutations identified, we focused on the biological and clinical significance of a confirmed somatic mutation at the BRAF\textsuperscript{L597} codon. Our findings have direct therapeutic implications for patients with metastatic melanoma.

RESULTS

Identification of a BRAF\textsuperscript{L597} Mutation by Whole-Genome Sequencing

A 75-year-old white man presented with an ulcerated right ear melanoma that was widely excised with involved sentinel lymph nodes. Four months later, he developed local recurrence and underwent additional surgery as well as postoperative radiation. This specimen was negative for the BRAF\textsuperscript{V600E} (c.1799T>A) mutation using an allele-specific PCR assay, and negative for KIT exons 9, 11, 13, 17, and 18 mutations by PCR-based methods. Twelve months later, the patient developed widespread metastasis and required a palliative thyroidectomy. He died 13 days later with both cardiac and brain involvement.

To identify potential driver mutations in his tumor using an unbiased genome-wide approach, we conducted WGS of DNA from his metastatic thyroid lesion, along with DNA from matched blood (see Supplementary Methods for case description and variation calling). A subset of the single-nucleotide polymorphisms (SNP), insertions, and deletions were validated (Supplementary Tables S1–S8 and Supplementary Figs. S1–S7). The validated somatic SNP with the combined highest depth and quality scores was BRAF\textsuperscript{L597R} (c.1789T>C; Fig. 1; Supplementary Table S8 and Supplementary Fig. S7). The high depth of coverage for this SNP was in part because of concurrent amplification of the BRAF locus on chromosome 7 (Supplementary Table S5 and Supplementary Fig. S6). Screening of an earlier biopsy confirmed that this mutation was present before radiation therapy (data not shown), suggesting that it occurred early in the pathogenesis of the patient’s disease.

Frequency of BRAF\textsuperscript{L597} and Other Exon 15 Mutations in “BRAF Wild-type” Melanoma

Both BRAF\textsuperscript{L597} and V600 are encoded by exon 15. To determine how many exon 15 mutations might be overlooked by assessing only the V600 position, we analyzed the mutational status of the entire coding exon in 49 additional tumor samples negative for mutations at V600 as well as for recurrent mutations in NRAS (G12/13, Q61), KIT (W557, V559, L576, K642, and D816), GNAQ (Q209), and GNA11 (Q209; ref. 4). Two (4%) additional tumors had BRAF\textsuperscript{L597} mutations (c.1790T>A, p.L597S; c.1789_1790CT>T; Table 1). A third tumor harbored a BRAF\textsuperscript{K601E} mutation (c.1801G>A), whereas a fourth had a D594N mutation (c.1780G>T). Two of the three patients treated with vemurafenib had the BRAF\textsuperscript{L597} mutation.

Table 1. Mutations detected in BRAF exon 15 in 49 SNaPshot screen “pan-negative” melanomas

<table>
<thead>
<tr>
<th>Sample</th>
<th>Nucleotide</th>
<th>Amino acid</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>c.1801G&gt;A</td>
<td>p.K601E</td>
</tr>
<tr>
<td>2</td>
<td>c.1790T&gt;A</td>
<td>p.L597Q</td>
</tr>
<tr>
<td>3</td>
<td>c.1789_1790CT&gt;T</td>
<td>p.L597S</td>
</tr>
<tr>
<td>4</td>
<td>c.1780G&gt;A</td>
<td>p.D594N</td>
</tr>
</tbody>
</table>

*Samples considered melanoma SNaPshot screen “pan-negative” were those that did not have mutations in BRAF (V600), NRAS (G12/13, Q61), KIT (W557, V559, L576, K642, and D816), CTNNB1 (S37/45), GNAQ (Q209), GNA11 (Q209), and NRAS (G12/13, Q61). The mutations in Table 1 are those that significantly altered the V600K60E (1). Two (4%) additional tumors had BRAF\textsuperscript{L597} mutations (c.1790T>A, p.L597S; c.1789_1790CT>T; Table 1). A third tumor harbored a BRAF\textsuperscript{K601E} mutation (c.1801G>A), whereas a fourth had a D594N mutation (c.1780G>T). Two of the three patients treated with vemurafenib had the BRAF\textsuperscript{L597} mutation.

Signaling Induced by BRAF L597 and K601E Mutants Is Suppressed by a MEK Inhibitor

BRAF L597 and K601 are located in the activation segment of the kinase domain and are adjacent to V600. Because V600 mutants are sensitive to specific BRAF and mitogen-activated protein (MAP)/extracellular signal-regulated kinase (ERK) kinase (MEK) inhibitors, we studied whether signaling induced by L597 and K601 mutants in 293H cells was inhibited by the mutant BRAF inhibitor, vemurafenib, and the MEK inhibitor, GSK1120212. We chose to study L597R/Q/S and K601E mutations because they have been reported to occur in melanoma in the Catalogue of Somatic Mutations in Cancer (COSMIC) database (5) and we identified these mutations in our “pan-negative” samples (Table 1). We did not study endogenous melanoma cell lines because to our knowledge, none harbor and are dependent upon an L597 or K601E mutation for survival. We did not further investigate the sensitivity of the D594N mutation because it has been reported that D594 mutations result in an inactive kinase (6). Compared with a vector control, ectopic expression of V600E, L597R/Q/S, and K601E mutants elevated phospho-MEK and ERK levels (Supplementary Fig. S8), although the L597R/Q mutants did so to a lesser extent, consistent with studies on an analogous L597V mutant (7). Vemurafenib treatment of all of the BRAF mutant–expressing cells led to a decrease in phospho-MEK and ERK protein levels, whereas treatment with the MEK inhibitor led to a more dramatic decrease in phospho-ERK signaling (Fig. 2; Supplementary Figs. S8 and S9). These data suggest that patients whose tumors harbor BRAF L597 and K601 mutations could benefit from treatment with MEK inhibitors.
Figure 1. Detection and validation of the BRAF<sup>L597R</sup> mutation. A, alignment of next-generation sequence reads displaying the BRAF<sup>L597R</sup> mutation compared with the reference human genome. The region shown represents base pairs 140,453,089-140,453,201 on chromosome 7. Seventy-two reads overlap the mutant position (chr:140,453,145), including 47 reverse (in red) and 25 forward (in blue) strands, respectively. B, sequencing chromatograms show the presence of a heterozygous BRAF<sup>L597</sup> mutation in the tumor but not in the matched blood. Arrows indicate the position of the mutant or wild-type peaks.
Objective Radiographic Response to MEK Inhibitor Therapy in a Patient with a Metastatic Melanoma with a BRAF L597 Mutation

A 69-year-old patient with a metastatic melanoma who had previously received therapy with dacarbazine chemotherapy was enrolled in a phase I trial testing of the allosteric MEK inhibitor TAK-733 (8). After 2 cycles of therapy, the patient was noted to have a partial radiographic response with a decrease of 31% in the sum of maximum diameters of target metastatic lesions in the liver and spleen and as of this submission remains progression free at more than 24 weeks (Fig. 3 and Supplementary Table S9). Follow-up sequencing analysis of DNA from the patient’s tumor revealed a somatic BRAF L597S (c.1789_1790CT > TC) mutation (Supplementary Fig. S10). These data validate the notion that BRAF L597S-mutated melanomas are sensitive to MEK inhibitors in patients.

DISCUSSION

Inhibitors of mutant BRAF and the mitogen-activated protein kinase (MAPK) pathway have been shown to improve the overall survival of patients with melanomas that harbor recurrent genetic alterations involving BRAF\textsuperscript{V600E} (c.1799T > A; refs. 2, 9). Here, WGS of a tumor–normal pair revealed that a BRAF wild-type tumor harbored an unexpected BRAF\textsuperscript{L597} mutation occurring in exon 15. Through analysis of additional tumors negative for recurrent mutations in BRAF (V600E/K/M/R/D) as well as NRAS (G12/13, Q61), KIT (W557, V559, L576, K642, and D816), GNAQ (Q209), and GNA11 (Q209; ref. 4), we show that BRAF exon 15 mutations not involving the V600 codon are relatively common [4 of 49 samples (8%), including 2 L597 mutations], consistent with other studies in melanoma (10). We further show in vitro that signaling induced by ectopic expression of BRAF\textsuperscript{L597} and \textsuperscript{K601} mutants is suppressed by MEK and BRAF inhibition.

Figure 2. Signaling induced by BRAF\textsuperscript{L597R} and L597S is sensitive to BRAF and MEK inhibitors. Immunoblotting of lysates from 293H cells transfected with plasmids encoding FLAG-BRAF\textsuperscript{V600E}, FLAG-BRAF\textsuperscript{L597R}, or FLAG-BRAF\textsuperscript{L597S} show that RAF/MEK/ERK pathway signaling can be inhibited by increasing doses (0, 0.1, 0.5, 1, and 5 \(\mu\)mol/L) of the BRAF inhibitor vemurafenib (A) or the MEK inhibitor GSK1120212 (B), 2 hours post inhibitor treatment. BRAF\textsuperscript{L597R} and L597S signaling compared to the vector control is shown in Supplementary Fig. S8.

Figure 3. Computed tomographic images from a patient with BRAF\textsuperscript{L597S}-mutant metastatic melanoma responding to therapy with the MEK inhibitor TAK-733. Arrows indicate the tumor in the liver (left) and spleen (right) at baseline (A) and after 4 cycles of treatment (B).
Finally, we report a case of a patient whose BRAFV600E-mutant metastatic melanoma responded radiographically to the MEK inhibitor TAK-733. Collectively, these data show that tumor cells harboring BRAF L597 and possibly K601E mutants can be dependent upon ERK signaling and therefore susceptible to treatment with MEK inhibitors. Prior studies have shown that BRAF L597 mutations are activating (7), to our knowledge, this is the first report on the sensitivity of such mutations to MEK inhibitors in vitro and in patients.

Whether MEK inhibitors will be clinically better than mutant BRAF inhibitors for BRAF L597 and K601E mutants cannot be determined by the in vitro experiments conducted in this study. Cells expressing BRAFV600E have been shown to be moderately inhibited by vemurafenib; however, the few patients whose melanomas harbored this mutation did not display responses to another BRAF inhibitor, GSK2118436 (dabrafenib; refs. 11–13). There is 1 patient with a K601E mutation in BRAF that did respond to GSK1120212 (trametinib; ref. 14). Additional in vitro and human studies will need to be conducted to address which class of agents is the most appropriate.

The choice of tumor mutations to be interrogated in the clinic requires a balance among feasibility, cost, and comprehensiveness. Single-mutation testing [i.e., BRAFV600E (c.1799T>A)] is relatively cost effective but will clearly overlook other actionable mutations, as shown here. Whole-genome sequencing is comprehensive, but currently prohibitively expensive for routine clinical use. Presently, an intermediate solution involves use of multiplex tests that can interrogate a limited number of known mutations in selected genes that may act as targets for drug therapy. For example, tumors from patients with malignant melanomas at Vanderbilt are routinely screened for recurrent mutations that occur with at least greater than or equal to 1% frequency in the disease [i.e., BRAF (V600E/K/M/R/D), NRAS (G12/13, Q61), KIT (W557, V559, L576, K642, and D816), GNAQ (Q209), and GNA11 (Q209)], using a SNaPshot-based assay (4). Such screening results in 33% of cases having a “pan-negative” status (Supplementary Fig. S1). Non-V600 mutations in BRAF were not originally chosen for examination, as these were observed to occur in the COSMIC database at a frequency of less than 1% (5). The observations that L597 and K601 mutations may occur at a frequency of 4% and 2%, respectively, in “pan-negative” cases and that patients harboring tumors with these mutations may be sensitive to MAPK pathway inhibitors suggest that such tumors should subsequently undergo BRAF exon 15 mutational analyses to exclude the possibility of rare but potentially actionable BRAF mutations.

WGS of the tumor/normal pair also revealed a number of other somatic mutations potentially relevant to melanoma biology (Supplementary Table S8). For example, we validated 3 mutations in the glutamate receptor encoded by GRIN2A (c.3395C>T, p.P1132L; c.3103G>A, p.A1035N; and c.C154T, p.R52X). GRIN2A mutations were recently reported to occur in up to 33% of melanomas (15). The role of this mutation in melanoma is currently unknown. We also identified a tumor-specific noncanonical KRAS mutation (c.466T>C, p.F156L) that has not been previously reported in cancer but has been described as a germline mutation in patients with Noonan or cardio-facio-cutaneous syndromes (16, 17). Interestingly, this mutant protein accumulates in the active conforma-

**METHODS**

**DNA Extraction from Patient Samples**

Genomic DNA was extracted from a flash-frozen melanoma thyroid metastasis (90% tumor content) using standard proteinase K digestion and phenol extraction. Genomic DNA from matched patient blood was extracted using the Gentra Puregene Blood Kit (QIAGEN). Identity testing was conducted to confirm that tumor and blood genomic DNA originated from the same individual (Applied Biosystems). See Supplementary Methods for patient details. For examining BRAF exon 15 from the 49 patient samples, DNA from formalin-fixed paraffin-embedded (FFPE) tissue was extracted using the QIAGEN DNA FFPE Tissue Kit. All patient samples were analyzed with informed consent on an Institutional Review Board (IRB)–approved protocol (IRB 030220 and IRB 100178).

**Whole-Genome Sequencing**

Paired-end sequencing of tumor and matched blood genomic DNA was conducted on an Illumina Genome Analyzer Iix platform. Average coverage was ≥55.7 and ≥47.8 for the tumor and matched blood samples, respectively. The 100-bp reads were aligned to the Human Genome (UCSC hg19) using ELAND (Version 2; ref. 21). FastQC (Version 0.9.1; ref. 22) was used to conduct a quality control check of the raw data. See Supplementary Methods for SNP, insertion/deletion, structural variant, and copy number variation detection and validation details.

**Direct Dideoxynucleotide-Based Sequencing**

Somatic SNPs and structural variants were validated by direct sequencing of genomic DNA extracted from 49 FFPE samples that were pan negative for 43 driver mutations in BRAF, NRAS, KIT, CTNNB1, GNAQ, and GNA11 (ref. 4; see Supplementary Table S10 for BRAF PCR primers). Sequences were analyzed using Mutation Surveyor DNA Variant Analysis Software (SoftGenetics) and manual inspection of the sequence traces.

**Cloning BRAF Exon 15**

Exon 15 of BRAF was PCR amplified using HotStarTaq Master Mix (QIAGEN; Supplementary Table S10). If 2 mutations were detected in exon 15, the PCR products were cloned using the TOPO TA Cloning Kit (Invitrogen) to determine if the mutations were in cis or trans. Sequences were analyzed using BioEdit v.7.0.5.3.

**Transfections and Drug Treatment**

Wild-type BRAF and BRAFV600E plasmids were described previously (23). The BRAF L597R, L597Q, L597S, and K601E mutations were introduced into the wild-type BRAF plasmid using the QuickChange II XL Site-Directed Mutagenesis Kit (Agilent Technologies). Direct sequencing of entire cDNAs was conducted to confirm introduction of
the mutation and no other mutations. 293H cells (Invitrogen) were transfected using Lipofectamine 2000 (Invitrogen) and 80 ng DNA; cells that were serum starved for 6 hours were treated with vehicle (dimethyl sulfoxide), PLX4032/ vemurafenib (Chromixtek), or GSK1210212 (Chromixtek) at 0, 0.1, 0.5, 1, and 5 μmol/L for 2 hours. The 293H cells were passaged in the laboratory for more than 6 months after receipt. Cells were tested for identity using isozyme and karyotype analysis by Invitrogen.

**Western Blotting**

Cells were lysed using standard radioimmunoprecipitation assay buffer supplemented with protease and phosphatase inhibitors. Lysates were quantified and subjected to SDS-PAGE and Western blot analysis using the following antibodies: phospho-MEK1/2 (Ser217/221), total-MEK1/2, phospho-ERK1/2 (Thr202/Tyr204), total-ERK1/2, FLAG, and BRAF. All antibodies were purchased from Cell Signaling except for FLAG (Sigma-Aldrich) and BRAF (Santa Cruz Biotechnology).

**Patient Treatment**

Subject 88005-514 was treated with oral daily dosing with TAK-733 (Millennium Pharmaceuticals) at 16 mg on days 1 to 21 of 28-day cycles within an ongoing phase I clinical trial (24). Objective response was assessed by CT scans conducted every 2 months according to the Response Evaluation Criteria in Solid Tumors (RECIST) guideline (version 1.1; ref. 25). This study is registered with ClinicalTrials.gov (NCT00948467) and full information about this clinical trial will be provided elsewhere when completed.

**Disclosure of Potential Conflicts of Interest**

K. Dahlman has received an honorarium from Illumina. V. Bozon is an employee of Millennium Pharmaceuticals. N. Rosen has participated on Astra Zeneca, Novartis, and GlaxoSmithKline advisory boards. J. Somas has participated on advisory boards for GlaxoSmithKline, Roche, and Millennium Pharmaceuticals. A. Ribas has participated on advisory boards for Amgen, Celgene, GlaxoSmithKline, Prometheus, Roche-Genentech, and Millennium Pharmaceuticals. W. Pao was a consultant for MolecularMD, Bristol-Myers Squibb, Clovis, Symphogen, and AstraZeneca. No potential conflicts of interest were disclosed by the other authors.

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Acquisition of data (provided animals, acquired and managed patients, provided facilities, etc.): K.B. Dahlman, K. Hutchinson, C. Ng, D. Hucks, Z. Su, D.J. Hicks, J.L. Netterville, J.A. Somas, A. Ribas, W. Pao

Analysis and interpretation of data (e.g., statistical analysis, biostatistics, computational analysis): K.B. Dahlman, J. Xia, K. Hutchinson, D. Hucks, P. Jia, Z. Su, N. Rosen, C.L. Vencack-Jones, J.A. Somas, A. Ribas, Z. Zhao, W. Pao

Writing, review, and/or revision of the manuscript: K.B. Dahlman, J. Xia, K. Hutchinson, D. Hucks, V. Bozon, J.A. Glaspie, N. Rosen, C.L. Vencack-Jones, J.A. Somas, A. Ribas, Z. Zhao, W. Pao

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**Study supervision:** K.B. Dahlman, V. Bozon, A. Ribas, W. Pao

**Performing experiments and providing some of the data:** M. Atsfi

**Research study coordinator:** S. Branch

**Pathologist, reviewed cases:** P. Lyle

**Medical director at Millennium managing the clinical study:** C20001: V. Bozon

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**BRAF<sup>L597</sup> Mutations in Melanoma Are Associated with Sensitivity to MEK Inhibitors**

Kimberly Brown Dahlman, Junfeng Xia, Katherine Hutchinson, et al.


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