MINI REVIEW

TRKING DOWN AN OLD ONCOGENE IN A NEW ERA OF TARGETED THERAPY

Aria Vaishnavi, Anh T. Le, and Robert C. Doebele

ABSTRACT

The use of high-throughput next-generation sequencing techniques in multiple tumor types during the last few years has identified NTRK1, 2, and 3 gene rearrangements encoding novel oncogenic fusions in 19 different tumor types to date. These recent developments have led us to revisit an old oncogene, Trk (originally identified as OncD), which encodes the TPM3–NTRK1 gene fusion and was one of the first transforming chromosomal rearrangements identified 32 years ago. However, no drug has yet been approved by the FDA for cancers harboring this oncogene. This review will discuss the biology of the TRK family of receptors, their role in human cancer, the types of oncogenic alterations, and drugs that are currently in development for this family of oncogene targets.

Significance: Precision oncology approaches have accelerated recently due to advancements in our ability to detect oncogenic mutations in tumor samples. Oncogenic alterations, most commonly gene fusions, have now been detected for the genes encoding the TRKA, TRKB, and TRKC receptor tyrosine kinases across multiple tumor types. The scientific rationale for the targeting of the TRK oncogene family will be discussed here. Cancer Discov; 5(1); 1–10. © 2014 AACR.

INTRODUCTION

The identification of dominant oncogenic mutations and our ability to specifically inhibit these genetic abnormalities with targeted inhibitors have altered the therapeutic approach for many patients with cancer, particularly those with non–small cell lung cancer (NSCLC). Activating point mutations, in-frame insertions/deletions, gene amplification, and gene rearrangements can serve as predictive biomarkers for oncogene-targeted therapies and thus help select patients that have a high likelihood of benefiting from a particular therapy. There are currently two well-established paradigms of this targeted therapy approach in NSCLC, both of which highlight the potential success of this strategy for other oncogene targets. Epidermal growth factor receptor (EGFR) mutation–positive NSCLC patients (comprising ~18% of lung adenocarcinomas) and anaplastic lymphoma kinase (ALK) gene rearrangement–positive NSCLC patients (encompassing ~5% of lung adenocarcinomas) respond significantly better to the targeted therapies erlotinib and crizotinib, respectively, compared with the standard-of-care chemotherapy (1). EGFR mutation–positive patients who are treated with an EGFR tyrosine kinase inhibitor (TKI) have an objective response rate (ORR) of about 70% and a progression-free survival (PFS) time of approximately 11 months, both of which are superior to chemotherapy (2). ALK gene rearrangement–positive patients showed a response rate of approximately 65% and a PFS of approximately 8 months when treated with crizotinib, also superior to chemotherapy (3).

The paradigm of cancer treatment is shifting toward precision oncology. In this model, patients are selected for therapy using predictive biomarkers, such as oncogenic mutations, rather than using empiric chemotherapy. Many of the actionable or potentially actionable oncogenes that represent molecular subtypes in NSCLC involve genomic rearrangements with genes encoding receptor tyrosine kinases (RTK), such as ALK, ROS1, RET, and most recently NTRK1 (4–7). The unprecedented improvement in patient outcomes with oncogene-targeted therapies suggests that even rare oncogenes, such as ROS1 gene rearrangements (which occur at a frequency of ~1%–2%), should be investigated as therapeutic targets, as this molecular subset represents approximately 2,500 patients in the United States each year (8, 9). Indeed, a recent study of crizotinib in patients with ROS1-positive NSCLC highlights the ability to successfully accrue rare oncogene subtypes (10). The study of these low-frequency oncogenes not only applies to NSCLC, but also is directly relevant to the treatment of numerous other cancer types: ALK, ROS1, RET, and NTRK1 gene rearrangements have also been observed in other malignancies.
expanding the relevance of this work to colorectal cancer, thyroid cancer, cholangiocarcinoma, glioblastoma, inflammatory myofibroblastic tumors (IMT), ovarian cancer, bladder cancer, sarcomas, and others (11–17). Indeed, isolated reports show the success of targeting oncogenes across multiple tumor types (15, 18). It was estimated in 2007 that gene fusions were reported in approximately 20% of all cancers, accounting for a significant proportion of cancer morbidity and mortality (19). The emergence of high-throughput genomic technologies and programmatic sequencing efforts, such as the NCI/National Human Genome Research Institute Cancer Genome Atlas Network and the Sanger Cancer Genome Project, have generated the molecular profiles of numerous cancers, and this emergent technology has enabled the identification of many additional gene fusions that are putative oncogenes generated from such studies (19). The success of targeting oncogenes across multiple tumor types (15, 18). It was estimated in 2007 that gene fusions were reported in approximately 20% of all cancers, accounting for a significant proportion of cancer morbidity and mortality (19). The emergence of high-throughput genomic technologies and programmatic sequencing efforts, such as the NCI/National Human Genome Research Institute Cancer Genome Atlas Network and the Sanger Cancer Genome Project, have generated the molecular profiles of numerous cancers, and this emergent technology has enabled the identification of many additional gene fusions that are putative oncogenes generated from such studies (19). The success of targeting oncogenes across multiple tumor types (15, 18). It was estimated in 2007 that gene fusions were reported in approximately 20% of all cancers, accounting for a significant proportion of cancer morbidity and mortality (19). The emergence of high-throughput genomic technologies and programmatic sequencing efforts, such as the NCI/National Human Genome Research Institute Cancer Genome Atlas Network and the Sanger Cancer Genome Project, have generated the molecular profiles of numerous cancers, and this emergent technology has enabled the identification of many additional gene fusions that are putative oncogenes generated from such studies (19). The success of targeting oncogenes across multiple tumor types (15, 18). It was estimated in 2007 that gene fusions were reported in approximately 20% of all cancers, accounting for a significant proportion of cancer morbidity and mortality (19). The emergence of high-throughput genomic technologies and programmatic sequencing efforts, such as the NCI/National Human Genome Research Institute Cancer Genome Atlas Network and the Sanger Cancer Genome Project, have generated the molecular profiles of numerous cancers, and this emergent technology has enabled the identification of many additional gene fusions that are putative oncogenes generated from such studies (19).
a cDNA of the fusion expressed in various cell lines, such as fibroblasts, resulting predominantly in activation of the RAS–MAPK signaling pathway, but also PI3K–AKT, often simultaneously (Fig. 1; ref. 38). The potential for simultaneous dual activation of multiple downstream pathways may result in a potent oncogene, as this enables the activation of both proproliferative and antiapoptotic pathways (46). Studies by the same group have also demonstrated a critical role for upstream RTK signaling, through the insulin-like growth factor receptor (IGF1R) in autocrine signaling, which can be considered as a protumorigenic role in several malignancies (38). Indeed, autocrine and paracrine signaling by TRK receptors has also been shown to promote anoikis resistance and induce metastatic programs in numerous cancers (41, 59, 60). TRKB has also been shown to play a protumorigenic role in several malignancies, including both breast and prostate cancers (59, 60). TRKB signaling has also been shown to promote anoikis resistance and induce metastatic programs in numerous cancers (61). Expression of TRKA and TRKC wild-type receptors is associated with a positive prognosis in patients with neuroblastoma (excluding expression of the splice variant TRKAIII), whereas TRKB expression is correlated with a poorer prognosis (62, 63).

**TRK Family Oncogenic Fusions**

The typical gene structure for an oncogenic fusion is that the 3’ region of a proto-oncogene (encoding the kinase domain) and the 5’ region of the gene partner (encoding the kinase domain) result in a potent oncogene, as this enables the activation of both proproliferative and antiapoptotic pathways (46). Studies by the same group have also demonstrated a critical role for upstream RTK signaling, through the insulin-like growth factor receptor (IGF1R) in autocrine signaling, which can be considered as a protumorigenic role in several malignancies (38). Indeed, autocrine and paracrine signaling by TRK receptors has also been shown to promote anoikis resistance and induce metastatic programs in numerous cancers (41, 59, 60). TRKB signaling has also been shown to promote anoikis resistance and induce metastatic programs in numerous cancers (61). Expression of TRKA and TRKC wild-type receptors is associated with a positive prognosis in patients with neuroblastoma (excluding expression of the splice variant TRKAIII), whereas TRKB expression is correlated with a poorer prognosis (62, 63).

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Figure 2. TRKA oncogenic variants and TRK gene fusion partners. A, schematic of TRKA isoforms, deletions, and mutations are shown. Mutations are shown in the TRKAI isoform. Amino acid position numbers are shown in black. Schematic showing the known domains: BTB, bric-a-brac, tramtrack, and broad complex domain; ETS, E26 transformation-specific domain; TD, trimerization domain; IG-C2, Immunoglobulin-like C2-type domain; IG-V, Immunoglobulin-like V domain; OD, oligomerization domain; ZF QUA1, Quaking 1 domain; P203A, Low grade glioma; P283A, Low grade glioma; R342C, Glioblastoma; C345S, Glioblastoma; 5’ partner protein domain. Red, (green) domains shown in blue (NTRK3). No protein domains are shown for fusions that lack a domain; BTB, bric-a-brac, tramtrack, and broad complex domain; ETS, E26 transformation-specific domain.

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Targeting TRK Oncogenes in Cancer

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Targeting NTRK1 and Chromosomal rearrangements have been observed between fusions can vary slightly with regard to the breakpoint in of the salivary gland, congenital fibrosarcoma, congenital oncogene in several malignancies, including secretory breast ETV6–NTRK1 TCAs in colorectal cancer was recently revisited after 32 years by Ardini and colleagues (22), reaffirming that this TRKB have also been shown to form oncogenic gene in this particular tissue, similar to NTRK1 32 years by Ardini and colleagues (22), reaffirming that this

NGS Identification of NTRK1, 2, and 3 Fusions

In the last year, many next-generation sequencing (NGS) efforts, including programmatic, disease-oriented whole-genome, and/or transcriptome projects and also targeted clinical NGS platforms have resulted in the identification of NTRK family fusions in numerous tumor types. NTRK1 fusions were recently identified in lung adenocarcinoma, intrahepatic cholangiocarcinoma, spitzoid neoplasms, glioblastoma, and pontine glioma (4, 75–79). These findings were further validated in lung adenocarcinoma, as well as the discovery of novel fusions in PTC, and glioblastoma using a novel, targeted technique known as anchored multiplex PCR (80). It is also important to note that although TRK fusions were not detected initially by The Cancer Genome Atlas (TCGA), revisiting these data in 20 different cancers with a more efficient computational pipeline for the detection of gene fusions identified TRK fusions in eight additional tumor types (Table 1; refs. 9, 17). The first evidence of gene fusions involving the NTRK2 gene came in pilocytic astrocytoma and very soon afterward in pontine glioma (66, 74, 75). New tumor types with NTRK3 fusions were also identified, including PTC, pontine glioma, and Philadelphia chromosome–like acute lymphoblastic leukemia (Ph-ALL; refs. 68, 75, 81). Each of the three NTRK family genes can rearrange with multiple S’ gene partners (Fig. 2).

A unique biologic aspect of the ETV6–NTRK3 fusion is that it was the first oncogenic gene fusion to be identified in numerous different cancer tumor tissues. In each of those different tumor types, all of which are relatively rare malignancies, ETV6–NTRK3 is the dominant oncogene. For example, 100% of MASC of salivary glands and 93% of secrete breast cancers harbor ETV6–NTRK3 fusions (45, 70). This observation is similar to CML, where BCR–ABL is found in the vast majority of cases. However, in most tumors in which TRK fusions are identified, they represent only a small proportion of patients (Table 1). Collectively, the TRK family represents a sizeable number of cases distributed across multiple tumor types.

TRK INHIBITORS

Given the long history of oncogenic TRK alterations, one might ask why it has taken so long to develop drugs for this target in cancer. Several reasons likely contribute to the slow development of this target, including the lack of selective inhibitors and the relative difficulty in screening large tumor cohorts when this oncogene was first identified in the early 1980s. Similar to TRK family alterations, oncogenic ALK gene rearrangements were found to be important in cancer long before the first ALK inhibitor was FDA approved. The first ALK gene rearrangement was identified in anaplastic large cell lymphoma in 1994, but no ALK-targeted therapies were developed in this disease until many years later. The critical moment for ALK inhibitor development came in 2007 with the discovery of ALK gene rearrangements in NSCLC (5). The corresponding FDA approval of crizotinib for ALK-positive metastatic NSCLC was exceedingly fast, taking only 4 years from the time of first identification of ALK rearrangements in this patient population (5). This rapid approval highlights the successful strategy of precision oncology by matching targeted therapies with biomarker-selected patients. Neurotrophins and TRK receptors, particularly TRKA, have been pursued in the past as drug targets for the treatment of chronic pain (35), and a few studies have pursued the
TRK family as a therapeutic target in cancer (60, 82, 83). High levels of homology between TRKA, TRKB, and TRKC within the intracellular kinase domains have resulted in the synthesis of small-molecule inhibitors that target all three TRK family members (pan–TRK inhibitors; Table 2).

Clinical trials of TRK inhibitors will need to investigate potential side effects that may arise from inhibition of the full-length TRK receptors in normal tissues. Loss of normal regulation of TRKA, TRKB, or TRKC receptor activity can result in numerous human diseases. TRK receptors are known for mediating pain sensation and can play a role in chronic pain (35, 84). TRKA loss-of-function mutations are seen in class IV hereditary sensory and autonomic neuropathies (HSAN), such as the genetic disorder congenital insensitivity to pain with anhidrosis (CIPA; refs. 36, 84). Loss-of-function mutations in TRKB result in energy imbalances, the loss of appetite control and obesity, and neuronal defects such as memory impairment (37). Similarly, loss of BDNF expression in the cerebellum of the mutant stargazer mouse is associated with a severe ataxia phenotype (85), and Ntrk2 homozygous mutant mice have severe neurologic deficits (37), suggesting a critical role for the BDNF–TRKB signaling axis in normal neurologic development. However, it remains unclear whether inhibition of the full-length TRK receptors will produce symptoms that mimic developmental loss of signaling in this receptor family. A more detailed evaluation

<table>
<thead>
<tr>
<th>Gene fusion</th>
<th>Cancer</th>
<th>Frequency</th>
<th>Detection method(s)</th>
</tr>
</thead>
<tbody>
<tr>
<td>NTRK1</td>
<td>Lung adenocarcinoma</td>
<td>3/91 (3.3%)</td>
<td>Targeted NGS (FMI), FISH</td>
</tr>
<tr>
<td>NTRK1</td>
<td>Intrahepatic cholangiocarcinoma</td>
<td>1/28 (3.6%)</td>
<td>Targeted NGS (FMI)</td>
</tr>
<tr>
<td>NTRK1</td>
<td>Colorectal cancer</td>
<td>3 Isolated reports</td>
<td>cDNA library, FISH, PCR</td>
</tr>
<tr>
<td>NTRK1</td>
<td>Papillary thyroid cancer</td>
<td>28/228 (12.3%)</td>
<td>PCR</td>
</tr>
<tr>
<td>NTRK1</td>
<td>Spitzoid neoplasms</td>
<td>23/140 (16.4%)</td>
<td>Targeted NGS (FMI), FISH, IHC</td>
</tr>
<tr>
<td>NTRK1</td>
<td>Glioblastoma</td>
<td>2/185 (1.1%)</td>
<td>NGS</td>
</tr>
<tr>
<td>NTRK1</td>
<td>Sarcoma (TCGA)</td>
<td>1/103 (1%)</td>
<td>RNA-Seq</td>
</tr>
<tr>
<td>NTRK2</td>
<td>Astrocytoma</td>
<td>3/96 (3.1%)</td>
<td>NGS</td>
</tr>
<tr>
<td>NTRK2</td>
<td>Lung adenocarcinoma (TCGA)</td>
<td>1/513 (0.2%)</td>
<td>RNA-Seq</td>
</tr>
<tr>
<td>NTRK2</td>
<td>Head and neck squamous cell carcinoma (TCGA)</td>
<td>1/411 (0.2%)</td>
<td>RNA-Seq</td>
</tr>
<tr>
<td>NTRK2</td>
<td>Brain lower grade glioma (TCGA)</td>
<td>2/461 (0.4%)</td>
<td>RNA-Seq</td>
</tr>
<tr>
<td>NTRK3</td>
<td>Secretory breast carcinoma</td>
<td>12/13 (92%)</td>
<td>FISH, PCR</td>
</tr>
<tr>
<td>NTRK3</td>
<td>Mammary analogue secretory carcinoma</td>
<td>15/15 (100%)</td>
<td>FISH</td>
</tr>
<tr>
<td>NTRK3</td>
<td>Papillary thyroid cancer</td>
<td>9/62 (14.5%)</td>
<td>RNA-Seq</td>
</tr>
<tr>
<td>NTRK3</td>
<td>Acute myeloid leukemia</td>
<td>2 Case reports</td>
<td>PCR, FISH</td>
</tr>
<tr>
<td>NTRK3</td>
<td>Congenital mesoblastic nephroma</td>
<td>5/6 (83%)</td>
<td>PCR and FISH</td>
</tr>
<tr>
<td>NTRK3</td>
<td>Congenital fibrosarcomas</td>
<td>10/11 (91%)</td>
<td>PCR</td>
</tr>
<tr>
<td>NTRK3</td>
<td>Ph-like acute lymphoblastic leukemia</td>
<td>1/154 (0.7%)</td>
<td>NGS</td>
</tr>
<tr>
<td>NTRK3</td>
<td>Colon adenocarcinoma (TCGA)</td>
<td>2/286 (0.7%)</td>
<td>RNA-Seq</td>
</tr>
<tr>
<td>NTRK3</td>
<td>Thyroid carcinoma (TCGA)</td>
<td>7/498 (1.5%)</td>
<td>RNA-Seq</td>
</tr>
<tr>
<td>NTRK3</td>
<td>Skin cutaneous melanoma (TCGA)</td>
<td>1/374 (0.3%)</td>
<td>RNA-Seq</td>
</tr>
<tr>
<td>NTRK3</td>
<td>Head and neck squamous cell carcinoma (TCGA)</td>
<td>1/411 (0.2%)</td>
<td>RNA-Seq</td>
</tr>
<tr>
<td>NTRK1/NTRK2/NTRK3</td>
<td>Pediatric gliomas</td>
<td>8/112 (7.1%)</td>
<td>NGS</td>
</tr>
</tbody>
</table>

NOTE: The frequency of NTRK1 (blue), NTRK2 (red), and NTRK3 (green) gene fusions indicating the tumor type and the detection method that was used in each study. Only positive studies are listed, and thus the actual prevalence may be lower than reported.

*Post-Chernobyl.
*Sporadic.

Abbreviations: FMI, Foundation Medicine, Incorporated; TCGA, The Cancer Genome Atlas.
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### Table 2. TRK inhibitors under development

<table>
<thead>
<tr>
<th>Drug</th>
<th>Stage of development</th>
<th>Targets</th>
<th>Clinical trial identifier</th>
</tr>
</thead>
<tbody>
<tr>
<td>DCC-2701</td>
<td>Phase la/Ib in advanced solid tumors</td>
<td>TRKA/B/C, MET, TIE2, and VEGFR</td>
<td>NCT02228811</td>
</tr>
<tr>
<td>LOXO-101</td>
<td>Phase la/Ib in patients with genetic alterations in TRKA, TRKB, or TRKC</td>
<td>TRKA/B/C</td>
<td>NCT02122913</td>
</tr>
<tr>
<td>MGCD516</td>
<td>Phase I/ib in patients with advanced NSCLC with genetic alterations in MET, AXL, RET, TRK, DDR2, KDR, PDGFRα or KIT, or HNSCC with alterations in MET</td>
<td>TRK, MET, AXL, RET, DDR2, KDR, PDGFRα, and KIT</td>
<td>NCT02219711</td>
</tr>
<tr>
<td>PLX7486</td>
<td>Phase I as single agent and in combination with gemcitabine and nab-paclitaxel in solid tumors (pancreatic cancer expansion cohort)</td>
<td>TRKA/B/C and FMS</td>
<td>NCT01804530</td>
</tr>
<tr>
<td>RXDX-101</td>
<td>Phase Ia/Ila in patients with genetic alterations in TRKA, TRKB, TRKC, ROS1, and ALK</td>
<td>TRKA/B/C, ALK, and ROS1</td>
<td>NCT02097810</td>
</tr>
<tr>
<td>TSR-011</td>
<td>Phase I/II in solid tumors and hematologic malignancies (ALK or TRKA positive)</td>
<td>TRKA and ALK</td>
<td>NCT02048488</td>
</tr>
<tr>
<td>XL-184</td>
<td>Phase II in advanced NSCLC with NTRK, RET, or ROS1-positive fusions, or increased MET or AXL activity</td>
<td>TRKA, RET, ROS1, MET, and AXL</td>
<td>NCT01639508</td>
</tr>
</tbody>
</table>

**NOTE:** A chart listing the TRK inhibitors that are currently in clinical trials, additional non–TRK targets, the current stage of clinical development, and the identifier for the relevant clinical trial at clinicaltrials.gov. Items in bold are the primary drug targets.

Abbreviations: HNSCC, head and neck squamous cell carcinoma; FMS, McDonough Feline Sarcoma Viral.

of TRK receptors in non–cancer-related diseases is beyond the scope of this review, but can be found elsewhere (86, 87). Interestingly, one of the potential beneficial side effects of targeting TRK receptors in cancer might be a decrease in pain sensation, a frequent symptom among patients with cancer. Conversely, it will be important to monitor for potential neurologic side effects in clinical trials, given the expression pattern of the TRK family of receptors. Currently, little data exist on the toxicities of the more selective TRK inhibitors. A phase I study of PHA-848125AC with significant blood–brain penetration produced dose-limiting (grade 3) ataxia and tremors, but as this drug inhibits cyclin-dependent kinases in addition to TRKA, it is unclear which drug target was responsible for these side effects (88). One of the largest reported studies of a drug with TRKA inhibition was a randomized study of lestaurtinib in FLT3-mutant AML (89). Only one neurologic adverse event was noted, a death due to cerebellar toxicity; however, given the multiple kinase targets of this drug, no conclusions can be drawn about the relationship of this toxicity to TRKA inhibition. Monoclonal antibodies against TRKA or NGF have been developed for the treatment of pain (35); however, antibodies to TRKA or other TRK family members would not be effective against TRK fusions, as the extracellular domains for these fusions are routinely lost in the gene rearrangement.

Currently, several TKIs with activity against the TRK family are being explored in clinical trials (Table 2). Two patients with identified NTRK1 fusions were recently treated with inhibitors that demonstrated the potential clinical benefit of targeting this family of oncoproteins. The first was a patient with lung cancer harboring the MPRIP–NTRK1 fusion, which was treated off-label with the multikinase inhibitor crizotinib (4). Crizotinib has only modest activity against TRKA and produced only a proportionally transient, minor radiographic response, emphasizing the need for more potent TRK inhibitors in the clinic. More recently, a patient with colorectal cancer with a TPM3–NTRK1 gene fusion was treated in the phase I portion of a clinical trial investigating an interrupted dosing schedule of RXDX-101 (Ignyta; ref. 90). RXDX-101 is a pan–TRK inhibitor that also has activity against two other gene fusion targets, ALK and ROS1. The TRKA-positive (TPM3–NTRK1) patient experienced a partial response, providing the first evidence of clinical activity of a TRK inhibitor in a patient with an oncogenic TRK alteration (90). A phase I/II study of RXDX-101 called STAR-TRK-1 is currently accruing patients with TRK alterations (NCT02097810). LOXO-101 (Loxo Oncology) is a selective pan–TRK inhibitor that has no significant activity outside of the TRK family and is currently being investigated in a phase Ia/Ib trial across multiple tumor types (NCT02122913). TSR-011 (Tesaro) is a TRKA and ALK inhibitor that is currently in a phase I study (NCT02048488). PLX-7486 (Plexxikon) is a pan–TRK inhibitor that also targets FMS (McDonough Feline Sarcoma Viral; CSF1R). It is currently being investigated as monotherapy or in combination with nab-paclitaxel in pancreatic cancer, but there are plans to explore activity in patients with oncogenic TRK alterations in the future (NCT01804530). DCC-701 (Deciphera), XL-184 (Exelixis), and MGCD516 (Mirati) are all multikinase inhibitors that are currently in clinical trials that allow multiple different molecular subtypes, including the TRK family. Lestaurtinib (CEP-701; Cephalon) showed promising preclinical activity in NTRK1 fusion models, but its clinical development remains unclear (4).

### CONCLUSIONS

TRK was one of the first oncoproteins identified, more than three decades ago. The TRK oncogenes occur across a broad array of
tumor types. Oncogenic fusions involving NTRK1, NTRK2, and NTRK3 and in-frame deletions or splice variants of NTRK1 are likely to be actionable oncogenes based on preclinical data. The first clinical evidence of tumor response to TRK-targeted therapy in a patient with an NTRK1 fusion suggests that this family of oncogenes will represent a new valid drug target in cancer.

**Disclosure of Potential Conflicts of Interest**

A.T. Le has received licensing fees from Abbott Molecular. R.C. Doebele reports receiving a commercial research grant from Mirati Therapeutics; has received honoraria from the speakers’ bureau of OxOnc; and is a consultant/advisory board member for Loxo Oncology and OxOnc; and has received licensing fees from Abbott Molecular. No potential conflicts of interest were disclosed by the other author.

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