mRNA Splicing Variants: Exploiting Modularity to Outwit Cancer Therapy

Scott M. Dehm

Abstract
Systemic cancer therapy has traditionally exploited vulnerabilities in cancer cells, a strategy which has become more precise with the identification and targeting of driver oncogenes. However, persistent tumor growth due to primary (de novo) or secondary (acquired) resistance limits therapeutic efficacy for many patients. Alternative splicing is important for increasing the diversity of the cellular proteome, and is a process frequently deregulated during cancer development and progression. In cancer cells, diverse splicing alterations have been identified that eliminate protein domains or enzymatic activities required for efficacy of cancer therapies, promote gain of novel signaling functions that circumvent cancer therapies, and uncouple signaling pathways from upstream regulatory points that are blocked by cancer therapies. The mechanisms underlying these splicing changes range from stable alterations in gene sequence/structure to deregulation of splicing regulatory factors. In this review, the role of splice variants in cancer therapy resistance will be discussed, with examples of how mechanistic understanding of these processes has led to the development of novel strategies for therapy resensitization. Cancer Res; 73(17); 5309-14. ©2013 AACR.
Primary Resistance Supported by Germline Splicing Variants

**BIM-γ and tyrosine kinase inhibitor resistance**

The tyrosine kinase inhibitor (TKI) imatinib is the first targeted cancer therapy developed for inhibition of the BCR-ABL fusion in chronic myelogenous leukemia (CML). Upregulation of BCL2-like 11 (BIM) is required for induction of apoptosis by TKIs, and BIM suppression is sufficient for TKI resistance (6). Multiple BIM splice variants have been described, one of which is BIM-γ, lacking the exon 4-encoded BH3 domain required for BIM proapoptotic function. Whole-genome sequencing of imatinib-resistant CML samples led to the identification of a recurrent 2,903 bp deletion in intron 2 of the BIM gene (7). This deletion, which favors BIM exon 3 splicing over exon 4, is a germline polymorphism occurring in 12.3% of the East Asian population that was found to be associated with an increased likelihood of CML resistance to imatinib and second-line TKIs (7). BIM deletion polymorphism was also found to be associated with decreased progression-free survival in lung cancer, a disease that can be treated with the EGF receptor (EGFR) TKI gefitinib (7). On the basis of its germline origin, this deletion polymorphism would be expected to drive primary resistance to TKIs. Indeed, cell line models of CML and non–small cell lung cancer with an engineered BIM deletion displayed resistance to imatinib and gefitinib, respectively. However, imatinib or gefitinib sensitivity could be restored therapeutically in deletion polymorphism-positive CML or lung cancer cells by treatment with a BH3 mimetic drug (7).
Primary Resistance Supported by Oncogenic Driver Splicing Variants

**EGFRvIII and radiation/chemotherapy resistance**

Various EGFR splice variants have been described, the most frequent of which is EGFRvIII, an NH2-terminally truncated EGFR variant similar to the v-erb-B oncogene (8). EGFRvIII does not bind any known ligand and displays constitutive, ligand-independent tyrosine kinase activity (8). EGFRvIII is expressed in 20%–30% of glioblastoma multiforme, a disease highly resistant to radio- and chemotherapy. Radiation resistance of glioblastoma multiforme is mediated by EGFRvIII activation of the catalytic subunit of DNA-dependent protein kinase (DNA-PKcs), which supports enhanced repair of DNA double-strand breaks (9). This led to the discovery that EGFRvIII-expressing cells could be resensitized to radiotherapy via inhibition of DNA-PKcs kinase activity, which delayed DNA-repair kinetics (9). Chemoresistance of glioblastoma multiforme has also been linked to EGFRvIII through sustained activation of mTOR complex 2 (mTORC2; ref. 10). mTORC2 is activated frequently in glioblastoma multiforme, leading to activation of NF-xB, and this EGFRvIII-mTORC2-NF-xB pathway was shown to drive resistance to cisplatin, temozolomide, and etoposide. This led to the discovery that blockade of the mTORC2 or NF-xB pathways with pharmacologic inhibitors resensitized glioblastoma multiforme cells to these DNA-damaging agents (10).

In glioblastoma multiforme, expression of EGFRvIII is linked to complex rearranged and amplified EGFR gene structures (8). For example, there is a strong statistical correlation between EGFR intragenic losses encompassing EGFR exons 2–7 and expression of EGFRvIII in glioblastoma multiforme (11). Similarly, EGFRvIII is expressed in approximately 10% of lung squamous cell carcinoma due to underlying intragenic deletions in the *EGFR* gene, and this is associated with TKI resistance (12). These studies show that oncogenic EGFRvIII expression in cancer is a stable phenomenon caused by somatic architectural changes in the *EGFR* gene, which drives primary radio- and chemoresistance in various human cancers.

**Ik6 and imatinib resistance**

In BCR–ABL-positive acute lymphoblastic leukemia (ALL), primary imatinib resistance has been linked to a loss-of-function Ikaros splicing variant, Ik6. Ikaros is important for development of lymphocytes and other hematopoietic lineages. The Ik6 splice variant resulting from skipping of exons 3–6 of the Ikaros gene (IKZF1) lacks all NH2-terminal zinc finger DNA-binding motifs and displays localization to the cytoplasm as opposed to the nucleus (13). Mechanically, Ik6 synthesis is due to intragenic deletions of IKZF1 exons 3–6, which appears to be a driver event during lymphoid blast crisis when CML progresses to ALL (14). In a cohort of 47 BCR–ABL-positive ALL patients, Ik6 expression was detected in 43 patients, and in 23 of these cases Ik6 was the predominant isoform (13). The level of Ik6 expression in these clinical specimens was proportional to the percentage of blast cells, indicating that Ik6 expression is restricted to the blast cell population. Importantly, ectopic expression of Ik6 in a BCR–ABL-positive ALL cell line was sufficient to drive resistance to imatinib (13).

**AIMP2-DX2 and doxorubicin resistance**

Aminoacyl-tRNA synthetase-interacting multifunctional protein 2 (AIMP2) is a haploinsufficient tumor suppressor gene important for controlling cell fate. A splice variant of AIMP2 lacking exon 2, termed AIMP2-DX2, occurs in lung, and perhaps other cancers (15). Following treatment with etoposide or doxorubicin, wild-type AIMP2 mediates the apoptotic DNA damage response by binding p53 and preventing Mdm2-mediated degradation. The AIMP2-DX2 splice variant also binds p53 but does not inhibit Mdm2-mediated degradation. AIMP2-DX2 expression in lung cancer specimens is associated with lung cancer stage and shorter overall survival (15). In a carcinogen-induced mutation model, normal lung cells surviving carcinogen treatment showed increased expression of AIMP2-DX2, concomitant with several mutations in the *AIMP2* gene. In a minigene reporter assay, modeling one of the mutations in AIMP2 exon 2 showed that this mutation disrupted binding of the spliceosome assembly factor serine/arginine rich splicing factor (SRSF1) to an exon 2 ESE, leading to exon 2 skipping (15). These findings implicate a role for AIMP2 exon 2 ESE mutations and AIMP2-DX2 expression in oncogenesis as well as primary resistance to chemotherapy in lung cancer, which is consistent with p53 suppressive function.

Secondary Resistance Supported by Stable Changes in Splice Variant Expression

**FPGS splicing alterations and antifolate resistance**

Upon cellular uptake, folates and antifolates such as methotrexate undergo FPGS-mediated polyglutamylation, which prevents cellular efflux. In methotrexate-resistant ALL cell lines and clinical ALL specimens, diverse FPGS splicing aberrations occur, including intron retention and exon exclusion (16). FPGS splicing defects did not occur in methotrexate-sensitive parental lines, indicating that these events support secondary resistance. Indeed, an FPGS splice variant resulting from exon 10 skipping was unable to support FPGS activity in stably transfected cells (16). Interestingly, altered FPGS splicing in methotrexate-resistant ALL cell lines was associated with altered splicing patterns for various additional genes, indicating a stable, global defect in splicing regulation. It will be important for future studies to identify component(s) of the spliceosome that may be responsible for these global splicing alterations in methotrexate-resistant ALL, as this may reveal opportunities for restoring therapeutic sensitivity.

**Truncated androgen receptor variants and castration resistance**

The androgen receptor (AR) is a steroid receptor transcription factor and lineage-survival gene in cells of prostatic origin. Because of its lineage-survival role, AR is a central therapeutic target in advanced prostate cancer. Multiple AR splice variants have been identified in castration-resistant prostate cancer cell lines, xenografts, and transgenic mouse models (17). These splice variants arise through cryptic exon inclusion or exon
skipping, ultimately leading to the synthesis of truncated AR variant proteins lacking the ligand-binding domain (LBD), which is the protein domain through which AR activity is targeted in prostate cancer (17). In various functional experiments, truncated AR variants have been shown to translocate to the nucleus and drive constitutive, ligand-independent activation of the AR transcriptional program in a manner insensitive to antiandrogens (18, 19). In castration-resistant prostate cancer cell lines and tissues, intragenic rearrangements in the AR gene have been shown to underlie high-level expression of truncated AR variants (19–21). Moreover, in a cell-based model of prostate cancer progression, emergence of castration-resistant cells under conditions of AR-targeted therapy is associated with enrichment of cells harboring AR gene rearrangements and high-level expression of truncated AR variants (20). These studies indicate that AR gene rearrangements can drive secondary resistance to AR-targeted therapy by supporting expression of constitutively active truncated AR variants lacking the AR LBD.

Truncated V600E BRAF splice variants and vemurafenib resistance

Oncogenic V600E BRAF mutations are frequent in melanoma and serve as the molecular target for the V600E BRAF kinase inhibitor, vemurafenib. Vemurafenib inhibits constitutively active V600E BRAF monomers but paradoxically activates wild-type BRAF dimers, which require active Ras signaling for dimerization and activation. In many vemurafenib-resistant melanoma cell lines as well as tissue from patients displaying vemurafenib resistance, a V600E BRAF splice variant is expressed, which results from skipping of BRAF exons 4–8 (22). BRAF exons 4–8 encode the Ras-binding domain, and deletion of this domain allows the shorter splice variant of V600E BRAF to undergo constitutive dimerization in a Ras-independent manner. Despite vemurafenib binding to this truncated BRAF V600E splice variant, downstream activation of ERK persists (22), showing that this is an important driver of BRAF V600E reactivation and secondary resistance to vemurafenib in melanoma. The mechanism for synthesis of this truncated BRAF variant is not clear, but skipping of exons 4–8 is restricted to mRNAs harboring the V600E mutation (22). This implies a mechanism of allele-specific alternative splicing or underlying genomic alterations involving the BRAF allele harboring the V600E mutation.

Survivin 2B and taxane resistance

Increased survivin expression has been observed in taxane-resistant ovarian cancer. The survivin (BIRC-5) gene encodes five alternatively spliced isoforms. The development of isoform-specific reverse transcription PCR (RT-PCR) primer sets led to the finding that the survivin 2B isoform is responsible for most of the increase in total survivin expression in isogenic sets of taxane-resistant versus taxane-sensitive ovarian cancer cell lines (23), indicating that survivin 2B mediates secondary resistance to taxanes. Consistent with this finding, isoform-specific siRNA-mediated knockdown of survivin 2B increased apoptosis, inhibited cell-cycle progression, and sensitized-resistant ovarian cancer cell lines to docetaxel (23). This mechanistic finding was translated to a preclinical subcutaneous model of ovarian cancer, wherein liposome nanoparticles were used for systemic delivery of survivin 2B-targeted siRNA, resulting in reduced tumor growth and enhanced docetaxel sensitivity in vivo (23).

Resistance Supported by Plasticity in Splice Variant Expression

MKN2b and gemcitabine resistance

The mitogen-activated protein kinase interacting kinase-2 (MKN2) gene gives rise to two splice variants differing only in composition of their COOH-termini due to alternative splicing of exon 13a (MKN2a isoform) or exon 13b (MKN2b). Exon 13a, but not Exon 13b, encodes a mitogen-activated protein kinase (MAPK)-interacting domain. Therefore, the MKN2b splice isoform does not harbor a MAPK-interacting domain and displays constitutive, MAPK-independent kinase activity (24). Gemcitabine is one of the main treatment modalities for advanced pancreatic cancer, but primary resistance occurs frequently. Pancreatic cancer tissues display high levels of S209 phosphorylation of eIF4E, the core component of the translation initiation complex, and levels of eIF4E S209 phosphorylation are associated with worse overall survival (25). In pancreatic cancer cell lines, eIF4E S209 phosphorylation increases acutely in response to gemcitabine, cisplatin, and rapamycin, and these effects persist during treatment. In addition to increased eIF4E S209 phosphorylation, gemcitabine treatment also results in acute changes in MKN2 splice favoring production of MKN2b (25). This plasticity in splicing favoring MKN2b was shown to be due to gemcitabine-mediated induction of SRSF1. Interestingly, although both MKN2a and MKN2b can mediate S209 phosphorylation of eIF4E, only MKN2a requires activation by upstream MAPK signaling. Indeed, ectopic expression of MKN2b but not MKN2a could drive gemcitabine resistance in pancreatic cancer cell lines. Importantly, an MNK chemical inhibitor or siRNA directed to MKN2 re sensitized pancreatic cancer cells to gemcitabine. This effect was likely mediated through the MKN2b splice variant, as knockdown of SRSF1 led to an increased MNK2a:2b ratio, reduced eIF4E phosphorylation, and gemcitabine resen sitization (25).

Expression plasticity of BIM-γ in breast cancer

SRSF1 has also been implicated in plasticity in BIM splicing in breast cancer, which highlights an additional mechanism for increased expression of the BIM-γ splice variant. In a model of breast cancer induced by overexpression of SRSF1, synthesis of the BIM-γ was observed (26). Overexpression of BIM-γ was able to drive increased acinar size and decreased apoptosis in mammary epithelial cells, indicating it may play an active oncogenic role (26). This contrasts with functional analysis of BIM-γ in CML harboring an underlying BIM deletion polymorphism, which indicated that this was a loss-of-function splice variant (7). More broadly, SRSF1 overexpression has been observed in various human cancers, and SRSF1 overexpression by itself is transforming in various cell types (26, 27). This indicates that SRSF1 may play a more global role in supporting...
splicing plasticity and therapeutic resistance in cancer cells, which can be manifest in part through expression of BIM-γ and MNK2b splice variants.

**Expression plasticity of truncated AR variants in prostate cancer**

Plasticity in AR splicing has also been observed in prostate cancer, with expression of truncated AR variants lacking the AR LBD displaying acute expression increases in response to castration or treatment with enzalutamide, a next-generation AR antagonist (18). This indicates that another mechanism exists in addition to AR gene rearrangements as a basis for truncated AR variant expression. Interestingly, these acute increases in truncated AR variant expression were accompanied by increased expression of several genes involved in mitotic progression, indicating that truncated AR variants support a novel transcriptome that maintains prostate cancer cell mitosis during AR-targeted therapy (18).

**Opportunities for Development of New Therapies**

Several of the above examples have illustrated that mechanistic understanding of splice variants and their role in therapeutic resistance can lead to novel treatment ideas (e.g., BH3 mimetics to enhance TKI sensitivity in BIM-γ driven cancers, TKIs to increase radiation sensitivity in EGFVRVIII-driven glioblastoma multiforme, nanoparticle delivery of siRNAs to selectively target the survivin 2B splice variant in ovarian cancer). However, all of these strategies are based on inhibiting expression of splice variants or targeting pathways downstream of splice variant expression. More recently, strategies have been developed to target the splicesome in cancer cells directly. For example, knockdown of SRSF1 can restore therapeutic sensitivity in cancers in which resistance is driven by MNK2b or BIM-γ (25, 26). Similarly, short hairpin RNA-mediated knockdown of serine–arginine protein kinase (SRPK)-1, a kinase that phosphorylates SR domains in SRSF1 and other SR splicing factor proteins, leads to increased sensitivity of pancreas, breast, and colon cancer cell lines to gemcitabine and cisplatin (28). There are also several antitumor drugs, such as spliceostatin A and pladienolides, that target the splicing factor 3B (SF3B) component of the spliceosome U2 snRNP, and these are being tested in clinical trials (29). These SF3B inhibitors may be particularly useful in hematologic neoplasms, where recurrent mutations in SF3B1 have been reported (29). In addition, oligonucleotide-directed splice-switching strategies have been developed to correct RNA missplicing or to prevent mutated exons from being incorporated into mature mRNAs (30). This splice-modulating technology may be another approach to restoring or enhancing therapeutic responses in cancer cells in which splice variants are drivers of resistance.

**Conclusions and Future Directions**

The vignettes discussed in this review have shown that the mechanisms leading to functional expression of alternatively spliced protein variants are diverse, ranging from germline or somatic alterations in gene sequence/structure to deregulation of splicing regulatory factors. To obtain a more complete view of the contribution of these various mechanisms to splicing alterations, it will be important to design integrative analyses of genome sequence/structure and splicing patterns in therapy-resistant tissues. This knowledge is expected to reveal instances where there is plasticity in splicing-associated resistance mechanisms, or instances where these splicing alterations are stable. This may be important for designing optimal therapeutic resensitization strategies, which could include modulating the expression and/or activity of the splicing machinery, direct targeting of splice variant expression, or targeting downstream signaling pathways that are required for splice variants to drive therapeutic resistance.

**Disclosure of Potential Conflicts of Interest**

No potential conflicts of interest were disclosed.

**Grant Support**

This study was supported by American Cancer Society Research Scholar Grant (RSG-12-031-01), NIH (R01CA174777) and Department of Defense Prostate Cancer Research Program New Investigator Award (W81XWH-10-1-0353).

References

mRNA Splicing Variants: Exploiting Modularity to Outwit Cancer Therapy

Scott M. Dehm


<table>
<thead>
<tr>
<th>Updated version</th>
<th>Access the most recent version of this article at: doi:10.1158/0008-5472.CAN-13-0444</th>
</tr>
</thead>
</table>

<table>
<thead>
<tr>
<th>Cited articles</th>
<th>This article cites 30 articles, 14 of which you can access for free at: <a href="http://cancerres.aacrjournals.org/content/73/17/5309.full#ref-list-1">http://cancerres.aacrjournals.org/content/73/17/5309.full#ref-list-1</a></th>
</tr>
</thead>
</table>

<table>
<thead>
<tr>
<th>E-mail alerts</th>
<th>Sign up to receive free email-alerts related to this article or journal.</th>
</tr>
</thead>
<tbody>
<tr>
<td>Reprints and Subscriptions</td>
<td>To order reprints of this article or to subscribe to the journal, contact the AACR Publications Department at <a href="mailto:pubs@aacr.org">pubs@aacr.org</a>.</td>
</tr>
<tr>
<td>Permissions</td>
<td>To request permission to re-use all or part of this article, contact the AACR Publications Department at <a href="mailto:permissions@aacr.org">permissions@aacr.org</a>.</td>
</tr>
</tbody>
</table>