

RNA Editing in Pathogenesis of Cancer

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Abstract

Several adenosine or cytidine deaminase enzymes deaminate transcript sequences in a cell type or environment-dependent manner by a programmed process called RNA editing. RNA editing enzymes catalyze A>I or C>U transcript alterations and have the potential to change protein coding sequences. In this brief review, we highlight some recent work that shows aberrant patterns of RNA editing in cancer. Transcriptome sequencing studies reveal increased or decreased global RNA editing levels depending on the tumor type. Altered RNA editing in cancer cells may provide a selective advantage for tumor growth and resistance to apoptosis. RNA editing may promote cancer by dynamically recoding oncogenic

genes, regulating oncogenic gene expression by noncoding RNA and miRNA editing, or by transcriptome scale changes in RNA editing levels that may affect innate immune signaling. Although RNA editing markedly increases complexity of the cancer cell transcriptomes, cancer-specific recoding RNA editing events have yet to be discovered. Epitranscriptomic changes by RNA editing in cancer represent a novel mechanism contributing to sequence diversity independently of DNA mutations. Therefore, RNA editing studies should complement genome sequence data to understand the full impact of nucleic acid sequence alterations in cancer. *Cancer Res*; 77(14); 3733–9. ©2017 AACR.

Introduction

The central dogma of biology refers to the faithful transmission of genetic information from DNA to RNA and from RNA to protein. This dogma underlies the rationale to examine the genome to understand pathogenesis of human diseases especially cancer. Abundant data now show that DNA mutations are fundamental to cancer initiation and progression (1). Although genetic linkage-based approaches in rare cancer-prone families have identified many classical tumor suppressor genes, recent high-throughput sequence analyses of cancer genomes showed somatic mutations driving the neoplastic process (2). Recent studies also show that enzymatic alterations in RNA sequences, without any corresponding mutation at the DNA level, can also contribute to pathogenesis of cancer (3–7).

RNA editing refers to programmed alterations in transcripts catalyzed by adenosine or cytidine deaminating enzymes, and benefits the organism by allowing cell-type specific, developmentally regulated or environmentally-induced expression of protein isoforms (8, 9). RNA editing alters adenine to inosine

(A>I) and cytosine to uracil (C>U) by adenosine and cytidine deaminases, respectively. These base transitions at the transcript level can lead to missense (by A>I and C>U editing) or nonsense (by C>U editing) protein alterations. Recent sequencing studies highlight that cancer cell transcriptomes are more complex than their genomes in part due to widespread RNA editing (4–7). Because levels of RNA editing may dynamically change by microenvironmental factors or during tumor progression, and that edited transcripts have a limited life span, the functional impact of RNA editing on cancer cells will be different than those of permanent DNA mutations. Here, we provide a brief overview of the known RNA editing enzymes and highlight some recent studies on the role of RNA editing in cancer.

RNA Editing by ADARs

A>I RNA editing is catalyzed by the ubiquitously expressed ADAR (ADAR1) and ADARB1 (ADAR2) adenosine deaminase enzymes (Table 1; ref. 8). ADARB2 (ADAR3) enzyme is considered catalytically inactive. Full-length ADAR1p150 and amino terminal truncated ADAR1p110 isoforms of ADAR are transcribed by alternative promoter usage. Except for ADARp150, an interferon-inducible isoform that can accumulate in the cytoplasm, all other ADARs are localized to the nucleus. ADARs catalyze site-specific RNA editing in short imperfect RNA duplexes, whereas hyperediting that involves many adenosines occurs in long perfect RNA duplexes. Majority of ADAR-mediated RNA editing events in long duplex RNAs occurs in the 3'-UTR and 5'-UTR of mRNAs and in introns, especially in the context of Alu sequences. Noncoding edited sites may play roles in the regulation of splicing, gene expression, and miRNA binding (10). In addition, RNA editing by ADAR recodes mRNAs of several genes including *NEIL1* (11), *BLCAP*, *FLNA* (12), and *NARF* (13).

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Table 1. RNA editing enzymes in humans

Enzyme (editing activity)	Function of RNA editing	Cell type where RNA editing occurs	Subcellular localization	Recoding RNA editing targets
ADAR (A>I)	Suppression of innate immunity and protein diversification	Many	Nuclear ^a	Several (e.g., <i>NEIL1</i>)
ADARB1 (A>I)	Protein diversification for normal neuronal signaling	Many, but mostly CNS cells	Nuclear	Several dozen (e.g., <i>GluR-B</i>)
ADARB2 (A>I)	Inactive (expressed in brain)	None	Nuclear	Unknown
APOBEC1 (C>U)	Apo B isoform (Apo B-48) production for absorption of dietary fat	Intestine, liver	Nuclear	<i>APOB</i>
APOBEC3A (C>U)	Protein diversification for unknown function	Monocytes and macrophages	Nuclear/cytoplasm	Hundreds to thousands
APOBEC3G (C>U)	Protein diversification for unknown function	Unknown	Cytoplasm	Hundreds

^aADARp150 isoform is localized to cytoplasm.

Site-specific A>I RNA editing events that alter the amino acid code by missense substitutions occurs only in a handful of genes, which are often involved in neurotransmission in brain. For example, ADARB1 edits *GluR-B* mRNA, leading to near 100% change from the germ line encoded glutamine at amino acid 607 to arginine at the mRNA level. This change significantly alters the AMPA receptor neurotransmitter function. Loss of this editing in *Adarb1*^{-/-} mice leads to lethal seizures shortly after birth (14). In contrast, loss of *Adar* gene leads to early embryonic lethality via defective hematopoietic stem cells, increased activation of interferon signaling and apoptosis (15), although the identity of the edited RNAs involved is unknown.

Recently germ line mutations in *ADAR* were identified in the autoimmune disorder Aicardi-Goutières syndrome (AGS; ref. 16). *ADAR* mutations in AGS and *Adar*^{-/-} mice upregulate IFN type I (IFN1) regulated genes. AGS is a genetically heterogeneous Mendelian disease caused by mutations in several genes involved in nucleic acid metabolism and is characterized by early onset progressive brain disease, certain skin lesions, glaucoma and, in some cases, features resembling systemic lupus erythematosus (17). Upregulation of IFN1 signaling pathway by *ADAR* mutations suggests that the editing activity of *ADAR* is required to block activation of innate immune signaling. It is thought that the lack of *ADAR*-mediated RNA editing in double stranded RNAs stimulates cytosolic RNA sensing by MDA5-MAVS pathways, which are normally blocked by mismatched I-U base pairs (18, 19).

RNA Editing by APOBECs

C>U RNA editing catalyzed by the APOBEC cytidine deaminases is significantly less common than A>I editing in baseline transcriptome sequencing studies. The prototype of cytidine deaminases that edit RNA is the APOBEC1 enzyme. APOBEC1 site-specifically edits mRNA of the *APOB* gene to introduce a premature stop codon enabling intestinal cells to produce a short protein isoform of Apo B (20). Recent transcriptome sequencing studies identified additional RNA editing sites of APOBEC1, mostly in the 3'-UTRs (21, 22). APOBEC1 was the only C>U RNA editing enzyme known until the discovery of APOBEC3A (A3A; ref. 23). A3A differs from other RNA editing enzymes in that its editing function is observed only after induction by certain stimulations in monocytes and macrophages or by exogenous overexpression in 293T cells (24). Hypoxia (1% O₂) or IFN1 in

primary peripheral blood monocytes or IFN1 in monocyte-derived macrophages induce widespread site-specific RNA editing by A3A. In monocytes, hypoxia and IFN1 additively increases RNA editing levels, which leads to recoding of over 80% of transcripts of certain genes. In contrast to ADARs, most RNA editing by A3A is highly site-specific and targets the coding regions of genes, often resulting in missense/nonsense alterations.

Whether other APOBECs, including APOBEC2, A3B, A3C, A3DE, A3F, A3G, A3H, and APOBEC4, also edit cellular RNAs under certain physiological circumstances is unknown. Although deamination of viral genetic materials or cancer genome by some APOBEC3s was observed (25), cytidine deaminase activity of these enzymes under noninfectious, nonneoplastic physiologic conditions has not yet been demonstrated. We recently described that transient overexpression of A3G in HEK293T cells also induces C>U RNA editing of distinct cellular transcripts (26). Although physiological function of RNA editing by A3A and A3G is unknown, the targeting of hundreds of cellular RNAs raises the possibility that aberrant activation of APOBECs, by overexpression, hypoxia or inhibition of mitochondrial respiration (27), may contribute to transcriptome-level mutations in cancer cells. Because certain hypermutations in cancer genome have been attributed to A3A (28, 29), it is conceivable that A3A may also mediate RNA editing of cancer-related genes. We have shown that overexpression of A3A in 293T cells causes missense mRNA alterations in tumor associated genes *ATM*, *BARD1*, *BRCA1*, *BRCA2*, *BRIPI1*, *MDM2*, *KMT2A*, *MSH2*, *PTEN*, *SF3B1*, and *TSC2* (24). The mechanism by which A3A is expressed in cancer cells to cause genome mutations is uncertain, because A3A expression is largely confined to myeloid cells. Perhaps, epigenetic alterations in cancer lead to aberrant expression of A3A. Alternatively, A3A RNA or protein may be physically transferred from myeloid cells to cancer cells through exosomes or by cell fusion (30). A3A-mediated RNA editing may also be induced in myeloid cells of tumor microenvironment (e.g., macrophages, myeloid-derived suppressor cells) in hypoxic or inflammatory conditions, and affect tumor progression by altering the immunologic milieu (31).

Altered RNA Editing in Cancer

Recoding RNA editing in cancer

RNA editing has been linked to tumorigenesis by either site-specific editing of tumor-promoting genes or by transcriptome-scale changes in RNA editing levels.

A>I RNA editing of *AZIN1*, which encodes an antizyme inhibitor, causes S367G amino acid substitution. RNA editing level of *AZIN1* increases by at least 10% in hepatocellular carcinoma compared to normal unaffected liver (3). This editing generates an isoform with increased affinity to antizyme, promoting cell proliferation by reducing antizyme-mediated degradation of ornithine decarboxylase and cyclin D1. Site-specific A>I RNA editing of transcription factor PROX1 causes several missense alterations including E328G, R334G, and H536R in a small number of esophageal, pancreatic, and colon cancer samples, but no such editing is seen in a number of cDNA libraries of many normal tissues (32). By comparing the genome/transcriptome sequences, recoding A>I RNA editing, causing N136S amino acid change in *RHOQ* is found in colorectal cancer (33). This editing increases RhoQ GTPase enzyme activity, cancer invasion potential and recurrence of colorectal cancer when present in the tumor. Increased recoding (M2269V) RNA editing of filamin B gene (*FLNB*) is noted in hepatocellular (34) and esophageal squamous cell carcinomas (35). Increased recoding RNA editing of DNA repair enzyme NEIL1 (K242R) is identified in non-small cell lung cancer samples as a result of *ADAR* gene amplification (36). A rare example of C>U RNA editing in cancer involves the neurofibromatosis type I gene (*NF1*) mRNA editing that introduces a nonsense mutation in subset of peripheral nerve sheath tumors (37–39).

Reduced recoding RNA editing has also been observed in several tumors. For instance, RNA editing of *GluR-B* also causes R701G substitution in normal cerebellum and skin but it is markedly reduced in medulloblastoma cell lines and basal cell carcinoma samples (40). *GluR-B* Q607R editing is substantially lower in malignant gliomas, which have reduced expression of the *ADARB1* enzyme (41). In gastric cancer, oncogenic activity is promoted by the loss of *ADARB1*, which normally mediates recoding RNA editing H241R in *PODXL* to eliminate tumor promoting function of the wild-type gene (42). Chen and colleagues (43) suggested that RNA editing enables proapoptotic function of IGFBP7, the loss of which may promote tumorigenesis in esophageal squamous cell carcinoma. The chloride receptor *Gabra3* transcripts undergo recoding editing in the brain (44). Reduced RNA editing of *GABRA3* in breast cancer is suggested to promote tumor progression, invasion and metastatic potential (45).

Noncoding RNA editing in cancer

Noncoding RNA editing is also suggested to promote tumorigenesis. In CD34⁺/CD117⁺ myeloblasts of acute myeloid leukemia, transcripts of *PTPN6*, which encodes SH2 domain-containing tyrosine phosphatase, were found to retain an intron as a result of multiple A>I RNA editing events mainly at the intronic putative branch site (46). Such editing occurred at lower levels in remission blasts, suggesting a link between editing and leukomogenesis. miRNAs are small noncoding RNAs that play an important role in posttranscriptional gene regulation by silencing gene expression. RNA editing of miRNAs can alter these regulatory functions of miRNAs. Several studies have suggested that altered RNA editing of miRNAs or miRNA-binding sites promote tumorigenesis. Increased *ADAR*-mediated RNA editing of stem cell regulatory let-7 miRNAs may enhance leukemic self-renewal and contribute to blast crisis in CML (47). In contrast, decreased RNA editing of miR455-5p in melanoma enables downregulation of tumor

suppressor CPEB1 and promotes tumor progression (48). Increased RNA editing of miR381, which is involved in stemness and chemoresistance is observed in non-small cell lung cancer (36). Zhang and colleagues (7) suggested that RNA editing at miRNA-binding sites at 3'-UTR of gene transcripts may play an important role in suppressing the expression of tumor suppressor genes or increasing the expression of oncogenes. This study showed that increased RNA editing at miRNA-binding sites at 3'-UTR of *MDM2* increases the protein levels of *MDM2*, which is a negative regulator of p53 protein and is known to be elevated in many cancer types.

Transcriptome scale analysis of RNA editing events in cancer

Development of high-throughput sequencing and analysis techniques has enabled researchers to analyze transcriptome-scale RNA editing events in cancer. These studies reveal unanticipated heterogeneity of the cancer transcriptome, conferred largely due to A>I RNA editing. The first genome scale analysis of RNA editing in cancer examined sequences of expressed sequence tags in normal and neoplastic tissues, and found hypoeediting of Alu repetitive elements in brain, prostate, lung, kidney, and testis tumors (49). More recently, several groups examined the high-throughput cancer RNA sequencing data, mostly from The Cancer Genome Atlas (TCGA) database, to determine the frequency of RNA editing in various neoplasms. Han and colleagues (4) analyzed 17 cancer types and found abundant A>I editing, mostly in intronic, intergenic regions, and in 3'-UTR. They found increased global editing levels in breast tumors, as well as in head/neck squamous cell, thyroid, lung adenocarcinoma, bladder, kidney renal cell carcinomas. Decreased global editing levels were seen in kidney chromophobe and renal papillary carcinoma. No difference in editing levels was seen in prostate, lung squamous, liver, stomach adenocarcinoma compared to the normal tissues. Interestingly, they found a positive correlation between global RNA editing levels with *ADAR*, but not with *ADARB1/ADARB2* expression. In all tumors, editing levels in most sites were similar between normal control tissues and their cancer counterpart. For example, only 16.7% of all edited sites showed increased editing levels in BRCA and 19.3% of all edited sites showed decreased levels in kidney chromophobe cell cancer. Only several dozen nonsynonymous editing sites were identified. Correlations with one or more clinical outcomes (tumor subtype, stage, and survival) were detected for S367G in *AZIN1*, I164V in *COPA*, I635V in *COG3*, R764G in *GRIA2*, T262A in *ACBD4*, S59G in *PPIL3*, Q5R in *BLCAP*, and H241R in *PODXL*. Edited gene variants in *AZIN1*, *GRIA2*, and *COG3* increased cell viability in MCF10A (normal human breast epithelium cell line) and Ba/F3 (a murine leukemia cell line) cells.

Paz-Yaacov (5) showed increased A>I RNA editing levels (>5%) in most cancer types, largely at Alu sites, but also at 60 recoding sites. Lower editing levels correlated with a better survival in hepatocellular and head/neck carcinoma cases. Authors suggested that mutation load contributed by RNA editing may be more than those contributed by DNA mutations. Fumagalli and colleagues (6) showed that the same sites are edited in primary breast cancer, normal breast tissue, and breast cancer cell lines. However, higher frequency of editing is observed in tumor tissues as compared to normal and correlates positively with higher *ADAR* expression. Editing was mostly confined to Alu sites.

Zhang and colleagues (7) showed widespread A>I RNA editing events in cancer but they were not specific to a certain cancer type and were present in all tissues including normal controls. They identified 166 differentially edited genes between normal and tumor tissues. Smallest number ($n = 11$) of differentially edited genes occurred in esophageal carcinoma, largest ($n = 62$) in breast adenocarcinoma. They confirmed increased editing levels of *AZIN1* and decreased levels in *IGFBP7* in most tumor types. The authors did not find a strong correlation between editing levels and ADAR expression levels, and suggested that RNA editing of 3'-UTR miRNA-binding sites may strongly influence expression levels of tumor promoting or suppressor genes.

Transcriptome sequencing studies in different cancer types are summarized in Supplementary Table S1. Although ADAR is the primary mediator of the A-to-I RNA editing events, there is no strong consensus on how to explain the editing efficacy of the events by correlation analysis against ADAR expression profiles. RNA editing efficacy is generally defined by the frequency of editing events or the extent of editing. Several studies reported that frequency of editing events is correlated with ADAR expression levels (4), however, others also show that editing levels might not be directly associated with the ADAR expression profiles (7). This might suggest an alternative editing mediator (e.g., ADARB1) is activated to regulate the editing

mechanism. In general, majority of the events have low editing levels and consequently it is often difficult to make a confident estimation when the sequencing depth is low. Increasing the sequencing depth might contribute to identifying the true positive hits and could improve the correlation of editing levels and ADAR expression profiles or better able to address the inconsistencies reported in the literature. We obtained reported gene expression profiles based on RNA-sequencing for the cancer types with at least five normal samples, from TCGA project (<https://portal.gdc.cancer.gov/>). Comparing the distribution of expression levels for ADAR and ADARB1 between the tumor and normal samples for the selected cancers, fold change in their median expression levels and corresponding significance was calculated using Mann-Whitney *U* test (see Supplementary Table S1; Fig. 1). Figure 1 organizes the cancer types based on reported editing levels in the literature (4-7, 42, 49, 50) for an easy comparison with the observed expression alterations for ADAR genes. Our analysis suggests that the increase in ADAR expression levels is correlated with the reported increases in editing levels in majority of the TCGA cancers. Extent of editing and ADAR expression levels are consistently increased in majority of the tumor types compared to the tissue matched normal samples, however, kidney cancers [i.e., kidney renal clear cell carcinoma (KIRC), kidney renal

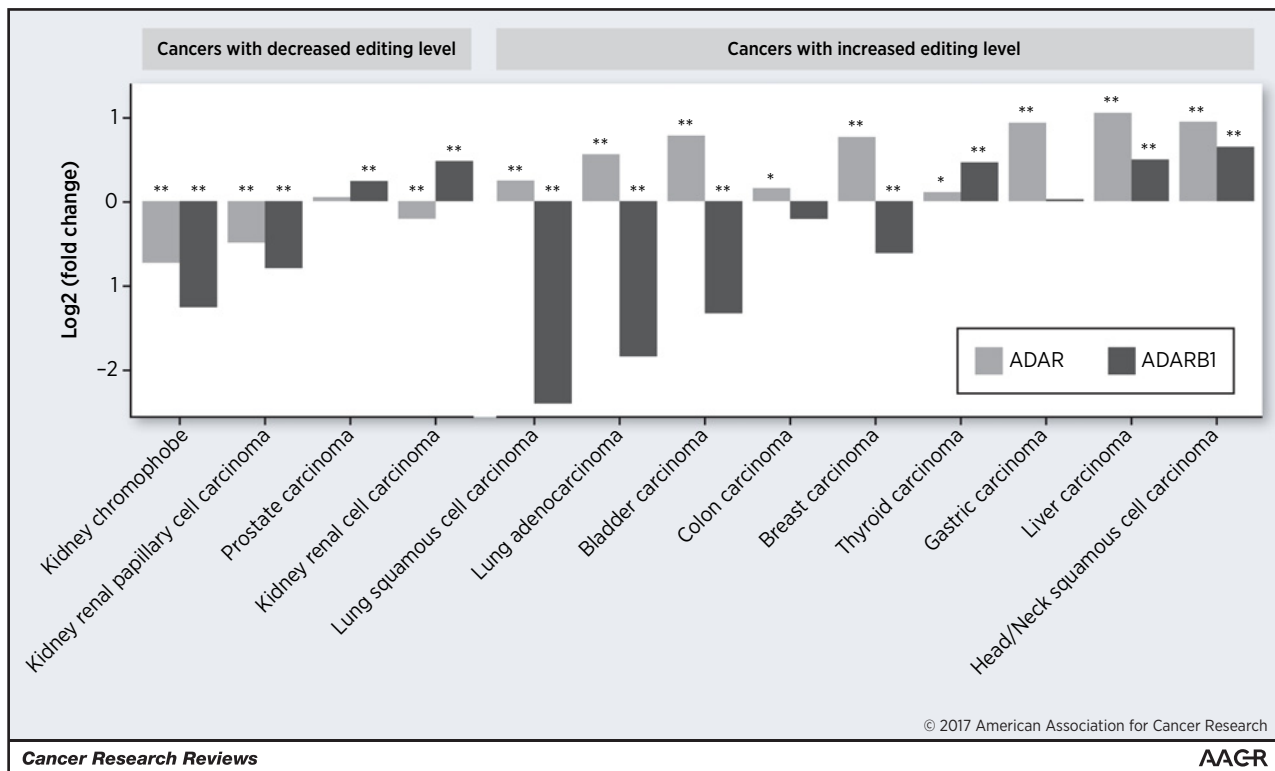
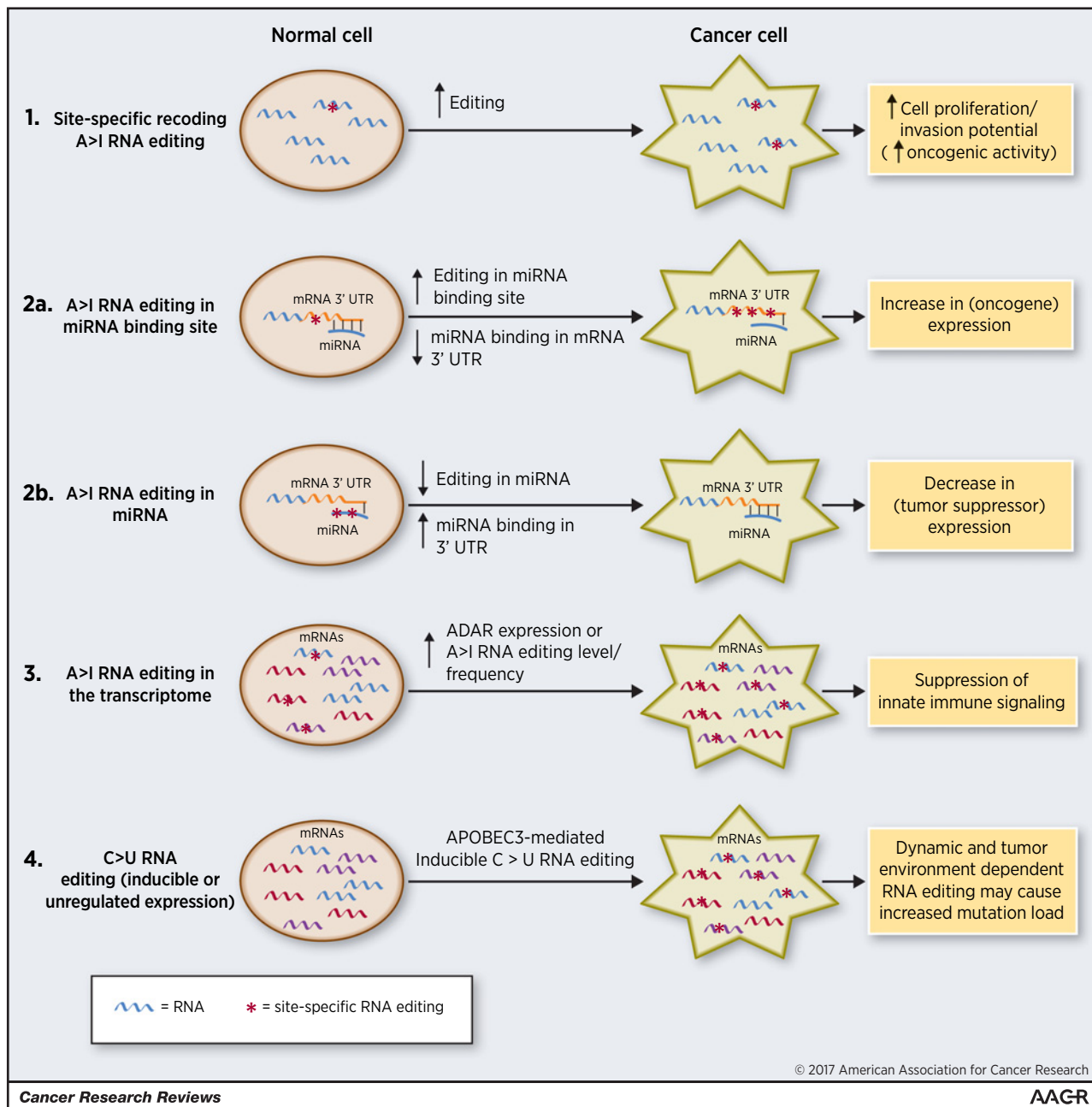


Figure 1.

Histograms showing the fold change in median expression of ADAR and ADARB1 in a cancer type compared with normal samples. RNA-sequencing based gene expression profiles for ADARs were obtained for cancer types, with at least five normal samples from the same tissue, from the TCGA project (<https://portal.gdc.cancer.gov/>). Statistical significance was calculated using Mann-Whitney *U* test comparing ADAR expression in normal and tumor samples (*, $P < 0.05$; **, $P < 0.01$). Cancer types are organized on the basis of reported editing levels in literature. Majority of the cancer types with increased extent of editing exhibited elevated ADAR1 expression in cancer compared with normal samples. Overedited sites outnumber underedited sites in kidney renal cell carcinoma (4, 7), although global RNA editing levels are decreased (5).

**Figure 2.**

Summary of various mechanisms through which RNA editing plays a role in the pathogenesis of cancer. **1**, Increased or decreased recoding RNA editing can occur site-specifically in oncogenes or tumor suppressor genes (3, 32, 39). **2**, Increased or decreased RNA editing occurs in miRNA binding sites or miRNAs, resulting in increased or decreased expression of oncogenes or tumor suppressor genes, respectively (7, 36, 46–48). **3**, Increased global RNA editing occurs in the transcriptome, resulting in suppression of the innate immune signaling (4–6). **4**, APOBEC3-mediated RNA editing occurs dynamically (23), which might result in increased mutational load in cancer cells.

papillary cell carcinoma (KIRP), and kidney chromophobe (KICH)] exhibited low ADAR expression in agreement with the reported reduced editing levels (4, 5, 7). However, the change in ADAR1 expression did not appear to be associated with the corresponding reported changes in editing levels across cancers (Fig. 1).

Summary and Outlook

Initial studies of RNA editing in cancer suggests that both genome and transcriptome sequencing studies are required to capture all sources of protein mutations in cancer.

Several patterns emerge from these initial studies. (i) Although RNA editing levels are altered in cancer, RNA editing does not appear to create new cancer-specific alterations since all sites edited in cancer are also edited in normal control tissues to some degree. Thus, cancer-related changes in RNA editing appear to be in quantity rather than quality. (ii) Most editing events detected to date occur in introns and 3'-UTRs. RNA editing in coding regions of genes are rare. (iii) Tumor types show consistent patterns of increased or decreased RNA editing levels at the transcriptome scale. Despite these global patterns, editing levels change in the opposite direction at some edited sites in a given tumor type. For example, editing levels decrease in less than 10% of the edited sites in breast cancer, which overall show increased RNA editing levels. (iv) Increase in editing levels in cancer often correlates with increased expression of the ADAR enzyme.

In summary, recent studies have revealed abundant A>I RNA editing events in cancer, which have been linked to tumor development through altered protein function caused by mis-sense mutations, disrupted regulation by intronic or noncoding RNAs such as miRNAs and global or dynamic changes in RNA editing levels (Fig. 2). Despite these promising data, how critical protein recoding RNA editing events are for the initiation and progression of cancer as well as the significance of vast number of noncoding RNA editing events in cancer remains uncertain. Recent studies linking ADAR-mediated RNA editing to suppression of IFN1 signaling raise the possibility that increased global A>I RNA editing observed in several cancers may serve to antagonize activation of IFN1 responses, which is known to be proapoptotic, antiproliferative, and antitumori-

genic (51). The lack of cancer specific RNA editing events starkly contrasts with numerous somatic DNA mutations in hundreds of genes identified in cancer, and raises the question as to why recoding RNA editing variants implicated in cancer (e.g., *AZIN1*) do not occur at the DNA level. Perhaps, mutations advantageous for cancer cell in most microenvironments are hardwired in the DNA, whereas those advantageous only in certain stage or changing environments may be regulated by RNA editing. Therefore the advantage of RNA editing for cancer cell may be in its dynamic nature. Consequently, RNA sequencing of cancer cells in different stages, histologic grades, or microenvironments may be required to identify the full compendium of fluctuating targets of RNA editing. Such dynamic alterations may especially apply for C>U RNA editing by APOBEC3 enzymes because A3A-mediated RNA editing occurs only after hypoxia and/or IFN exposure. RNA editing represents an exciting new frontier in cancer research with the potential to discover a rich source of epitranscriptomic mutations elusive to DNA sequencing.

Disclosure of Potential Conflicts of Interest

No potential conflicts of interest were disclosed.

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