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Authors

George, Cyril X John, Lijo Samuel, Charles E

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An RNA Editor, Adenosine Deaminase Acting on Double-Stranded RNA (ADAR1)

Cyril X. George,* Lijo John,* and Charles E. Samuel

Adenosine deaminase acting on RNA1 (ADAR1) catalyzes the C6 deamination of adenosine (A) to produce inosine (I) in regions of RNA with double-stranded (ds) character. This process is known as A-to-I RNA editing. Alternative promoters drive the expression of the *Adar1* gene and alternative splicing gives rise to transcripts that encode 2 ADAR1 protein size isoforms. ADAR1 p150 is an interferon (IFN)-inducible dsRNA adenosine deaminase found in the cytoplasm and nucleus, whereas ADAR1 p110 is constitutively expressed and nuclear in localization. Dependent on the duplex structure of the dsRNA substrate, deamination of adenosine by ADAR can be either highly site-selective or nonspecific. A-to-I editing can alter the stability of RNA structures and the coding of RNA as I is read as G instead of A by ribosomes during mRNA translation and by polymerases during RNA replication. A-to-I editing is of broad physiologic significance. Both the production and the action of IFNs, and hence the subsequent interaction of viruses with their hosts, are among the processes affected by A-to-I editing.

Introduction

OUBLE-STRANDED RNA (dsRNA) is a potent inducer of interferon (IFN) production. Both synthetic dsRNAs and naturally occurring dsRNAs generated during pathogen infection are effective IFN inducers (Stewart 1979). Among the natural inducers, Philip Marcus and Margaret Sekellick demonstrated nearly 40 years ago that a copyback defective interfering viral RNA, vesicular stomatitis virus (VSV) DI-011, was an efficient trigger of the innate immune response and that just a single DI particle was sufficient to induce a quantum yield of IFN (Marcus and Sekellick 1977). We now have considerable insight into the dsRNA signaling mechanisms that lead to the transcriptional activation of IFN genes. IFN system sensors of dsRNA include the RIG-like receptors RIG-I and MDA5 (Yoneyama and Fujita 2010; Ramos and Gale 2011) and the Toll-like receptor TLR3 (Kawai and Akira 2010; Yu and Levine 2011). The IFNinducible protein kinase regulated by RNA (PKR) also is a sensor of dsRNA (Toth and others 2006; Pindel and Sadler 2011). Likewise, the IFN-inducible RNA adenosine deaminase that utilizes dsRNA as a substrate, adenosine deaminase acting on RNA1 (ADAR1), is a sensor of dsRNA (Toth and others 2006; Hundley and Bass 2010; Nishikura 2010; George and others 2011). ADAR1 catalyzes the deamination of adenosine in dsRNA structures to yield inosine, thereby potentially altering the coding capacity and structure of the substrate RNA. However, in contrast to the activity of PKR,

ADAR1 responses often are proviral and antiapoptotic (Pfaller and others 2011; Samuel 2011). ADAR1, although IFN inducible, has emerged as a suppressor of the type I IFN response. What, then, is ADAR1? What are the biochemical mechanisms by which ADAR1 acts, and what is the evidence that ADAR1 impairs the type I IFN response?

Adar1 Gene and Proteins

There are 3 characterized Adar genes in the mouse and human, Adar1, Adar2, and Adar3 (Bass and others 1997; Toth and others 2006; Nishikura 2010; George and others 2011). Among these, Adar1 is IFN inducible (Patterson and Samuel 1995; Patterson and others 1995). The Adar1 gene maps to human chromosome 1q21.1 and mouse chromosome 3F2 (Wang and others 1995; Weier and others 1995, 2000). Transcription of the mammalian Adar1 gene is driven by multiple promoters; one is IFN inducible and the others are constitutively active, both in human and mouse (George and Samuel 1999a, 1999b; Kawakubo and Samuel 2000; George and others 2005). The IFN inducible promoter of Adar1 possesses a consensus IFN-stimulated response element. The human Adar1 gene includes 17 exons and spans \sim 40-kbp (Liu and others 1997). The exon-intron organizations of the human and mouse Adar1 genes are highly conserved (Liu and others 1997; Hartner and others 2004; Wang and others 2004; George and others 2008).

Department of Molecular, Cellular and Developmental Biology, University of California, Santa Barbara, California. *These authors equally contributed to this work.

Adar1 transcripts undergo alternative splicing, including exon 1 that occurs in at least 3 alternative forms, to generate the mature transcripts that encode 2 differently sized ADAR1 proteins: an IFN-inducible p150 ADAR1; and, a constitutively expressed p110 ADAR1 (Patterson and Samuel 1995). The predominant IFN-inducible transcript possesses the alternative exon 1A that includes an AUG translation initiation codon and also an alternative form of exon 7; this transcript encodes the p150 protein of 1,200 amino acids in human cells and 1,152 amino acids in mouse cells (Toth and others 2006; George and others 2011). By contrast, the alternative exons 1B and 1C of constitutively expressed Adar1 transcripts lack a functional AUG codon; translation of the ORF of these mRNAs, therefore, begins at AUG296 present in exon 2 to generate the p110 protein that is 931 amino acids in human cells (Toth and others 2006; George and others 2011). The constitutively expressed mouse protein is 903 amino acids.

ADAR1 proteins possess 2 kinds of nucleic acid binding domains (Fig. 1A). Three copies of a double-stranded RNA binding motif are present in the central region of the p110 and p150 proteins (Patterson and Samuel 1995; Liu and Samuel 1996; Fierro-Monti and Mathews 2000). The dsRNA binding motifs found in ADAR1 proteins are similar to the prototypical dsRNA binding motif discovered initially in PKR (Toth and others 2006). Either 1 (p110) or 2 (p150) copies of a Z-DNA binding motif ($Z\alpha$, $Z\beta$) are present in the N-terminal region of ADAR1 (Herbert and others 1997). The Z-DNA binding motifs found in ADAR1 share homology with the N-terminal region of the poxvirus E3L protein (Patterson and Samuel 1995), also a Z-DNA binding protein (Schwartz and others 1999; Kim and others 2003). Because the A-form of dsRNA with purine-pyrimidine repeats can be transformed to generate a left-handed Z-RNA helix and because the Za domain of p150 can bind Z-RNA (Placido and others 2007), the precise nature of nucleic acid (Z-DNA or Z-RNA) bound by the Z-domain of ADAR1 p150 under physiologic conditions remains unclear. The Cterminal region of ADAR1 p110 and p150 proteins includes the deaminase catalytic domain (Kim and others 1994; O'Connell and others 1995; Patterson and Samuel 1995; Liu and Samuel 1996). The biochemical activities assigned to the nucleic acid binding and catalytic domains have been verified by mutational analyses (Toth and others 2006; George and others 2011). Both p150 and p110 are active enzymes that catalyze the C6 deamination of adenosine in duplex RNA structures; the product is inosine (Fig. 1B). The p150 protein possesses a nuclear export signal and p150 is present in both the cytoplasm and nucleus, whereas the p110 form of ADAR1 is predominantly if not exclusively a nuclear protein (Patterson and Samuel 1995; Poulsen and others 2001). Genetic disruption of the mouse Adar1 gene in a manner that either knocks out expression of both p150 and p110 ADAR1 proteins (Hartner and others 2004; Wang and others 2004) or only the p150 protein (Ward and others 2011) results in embryonic lethality.

RNA Substrates of ADAR1

Both cellular and viral RNAs are edited by ADAR1 and, dependent upon the duplex structure and sequence of the substrate RNA, the editing can be either highly siteselective with one or very few adenosine residues edited or nonselective with multiple sites edited (Samuel 2011). Ato-I editing is effectively an RNA nucleotide substitution process. Hence, A-to-I editing of RNA has the capacity to alter RNA coding and RNA structure (Hundley and Bass 2010; Nishikura 2010; George and others 2011; Maas 2012). The purine I is decoded as G instead of A by ribosomes during mRNA translation and also by viral polymerases during RNA-dependent RNA replication, thereby potentially altering the coding of genetic information. A-to-I editing can also alter the stability of RNA structures, either by decreasing stability as I:U mismatches are less stable than A:U base pairs or by increasing stability as I:C base pairs are more stable than A:C mismatch pairs (Bass and Weintraub 1988; Wagner and others 1989; Levanon and others 2004).

FIG. 1. Domain organization and reaction catalyzed by adenosine deaminase acting on RNA1 (ADAR1). (A) Domain organization of human ADAR1. Alternative promoters and alternative splicing generate 2 sizeisoforms of ADAR1, an interferon (IFN)-inducible p150 protein and a constitutively expressed p110 protein. The 2 Z-DNA binding domains (Z α , $Z\beta$), the 3 double-stranded RNA (dsRNA) binding domains (R_I, R_{II}, and R_{III}), and the deaminase catalytic domain are shown. Alternative exon 1 and exon 7 structures give rise to the 1,200 amino acid p150 protein and 931 aa p110 protein in human cells. (B) Both p150 and p110 ADAR1 catalyze the hydrolytic C6 deamination of adenosine (A) to yield inosine (I) in dsRNA. Adapted from George and others (2011).



A-to-I editing was discovered during antisense RNA studies because of destablization of dsRNA within cells. An activity described initially as a dsRNA unwinding activity present in Xenopus and mammalian cells was later shown instead to covalently modify dsRNA substrates by adenosine deamination, thereby changing A:U base pairs to less stable I:U mismatches (Bass and Weintraub 1988; Wagner and others 1989). Two Adar genes are now known that specify catalytically active dsRNA adenosine deaminases, Adar1 and Adar2 (Bass and others 1997; Samuel 2011). The ADAR1 and 2 enzymes act with overlapping specificity on duplex RNA, without sequence specificity for binding dsRNA, but showing a 3'-neighbor preference of a purine for adenosine deamination and with selectivity of the deamination conferred by bulges and mismatches and presumably a higher order structure within the dsRNA substrates (Lehmann and Bass 1999; Dawson and others 2004; Riedmann and others 2008).

Among the first biologically relevant and still best characterized substrates of ADAR1 that result in amino acid coding changes following editing are transcripts for the GluR-B and 5-HT2c-R neurotransmitter receptors for glutamate and serotonin, respectively (Sommer and others 1991; Higuchi and others 1993; Burns and others 1997; Liu and Samuel 1999; Liu and others 1999). In the cases of these RNA substrates, the high selectivity of the editing reaction is conferred by imperfect duplex structures that form between exonic and adjacent intronic sequences. This results in site-specific deamination by ADAR1 and ADAR2 of specific adenosine residues present in ORFs of GluR-B and 5-HT2c-R transcripts that subsequently lead to amino acid substitutions to produce receptor proteins with altered functional activity (Seeburg and Hartner 2003; Hood and Emeson 2012). A-to-I editing of hepatitis delta virus (HDV) agent antigenome RNA also provides another early and well-characterized example of a highly selective adenosine deamination reaction (Casey and others 1992; Casey and Gerin 1995). In the case of HDV, the editing involves the selective conversion by ADAR1 of an amber UAG stop codon within a dsRNA duplex rod-like structure to a UIG codon that then is decoded as tryptophan (UGG), thereby allowing for synthesis of large delta antigen (Casey 2012). By contrast, the hyperediting of measles virus RNA during persistent infection is nonspecific (Oldstone 2009; Samuel 2011).

Deep sequencing and bioinformatic approaches have identified additional candidate A-to-I editing sites in the human transcriptome, some present in nonrepetitive coding sequences, but most occurring in repetitive elements present in noncoding regions of the RNA, including *Alu* elements (Athanasiadis and others 2004; Kim and others 2004; Levanon and others 2004; Paz-Yaacov and others 2013). Garncarz and others 2013; Ramaswami and others 2013). However, the functional significance of editing of *Alu* elements is not well established. Among the newly validated A-to-I editing targets in coding regions identified by transcriptome sequencing is that for the cellular protein AZIN1 that encodes antizyme inhibitor 1. Selective editing of



FIG. 2. A-to-I RNA editing affects multiple biochemical processes, thereby altering gene expression and function. Because I base pairs as G instead of A, nucleotide substitution of an A with an I may affect mRNA translation by altering a codon potentially leading to an amino acid substitution; RNA structure-dependent activities that trigger IFN responses may be suppressed if dsRNA structures are destabilized; the pre-mRNA splicing pattern of an RNA may be altered by editing a conserved A involved in splice site selection; RNA silencing may be altered by affecting dsRNA structures involved in either micro RNA processing or targeting; RNA virus genome stability may be altered by changing template and therefore complementary product sequences during viral RNA synthesis leading to A-to-G (U-to-C) transitions; and, A-to-I editing of noncoding repetitive (*Alu*) or nonrepetitive RNA elements may potentially affect RNA stability by altering cellular localization or nuclease recognition. Adapted from Samuel (2011).

AZIN1 RNA by ADAR1, resulting in a Ser to Gly amino acid substitution, confers phenotypes manifested by augmented tumor-initiating potential and a more aggressive behavior that predisposes to hepatocellular carcinoma (Chen and others 2013).

Biological Activities Mediated by Alterations in ADAR1 and A-to-I Editing

Studies with cell culture and intact animal systems have revealed a range of physiological changes caused by altered expression of ADAR1 and subsequent perturbation of A-to-I editing homeostasis. ADAR1-mediated RNA editing has been shown to affect a number of biologic responses including virus growth and persistence, cell proliferation, neurotransmitter function, and innate immune responses. Changing the sequence of an RNA by deamination can affect multiple biochemical processes (Fig. 2), thereby impacting gene expression and function.

Virus growth and persistence

Sequence changes consistent with A-to-I editing have been described for viral RNAs of a number of viruses including measles virus, influenza virus, parainfluenza virus, VSV, hepatitis C virus (HCV), hepatitis D virus, lymphocytic choriomeningitis virus, and polyoma virus (Toth and others 2006; Gelinas and others 2011; Samuel 2011). How the observed sequence changes attributed to A-to-I RNA editing affect virus replication appears to differ for different virus-host combinations. For example, with HDV, the selective editing of viral RNA has a proviral effect by permitting synthesis of large delta antigen required for RNA replication (Casey 2012). A long history also exists for the involvement of A-to-I editing in measles virus-host interactions. In subacute sclerosing panencephalitis, a rare but often fatal disease in which persistent measles virus infection occurs in the brain, clustered A-to-G mutations are described mostly in the M gene and less so in other genes (Cattaneo and others 1988; Oldstone 2009). The mutations found in the M gene RNA would prevent synthesis of the matrix protein that is required for virion assembly and release, and therefore are believed to contribute to the viral persistence phenotype. A combination of approaches including overexpression, genetic knockout, and stable knockdown established ADAR1 as a proviral host factor in the context of measles virus acute infection (Toth and others 2009; Okonski and Samuel 2013), VSV (Nie and others 2007; Li and others 2010), and human immunodeficiency virus (HIV) (Phuphuakrat and others 2008; Clerzius and others 2009; Doria and others 2009; Schoggins and others 2011). However, under some conditions, ADAR1 also displays an antiviral role with measles virus (Ward and others 2011) and HIV (Biswas and others 2012). The emerging picture is one of a finely balanced interplay between ADAR1 and other IFN-stimulated gene products including PKR that together contribute to determining the outcome of an infection (Pfaller and others 2011).

IFN is a therapeutic presently used for treatment of HCV infection, which can lead to chronic liver disease including hepatocellular carcinoma. In addition to HCV virus genotype, among the cellular genes identified that affect HCV responsiveness to IFN therapy is ADAR1 (Welzel and others 2009). Interestingly, overexpression of ADAR1 in cell culture was found to be proviral for a number of medically important RNA viruses (Gelinas and others 2011; Samuel 2011; Schoggins and others 2011), and an increased A-to-I editing of the cellular AZIN1 transcript recently has been reported to predispose to hepatocellular carcinoma (Chen and others 2013). ADAR1 and PKR differentially affect the formation of stress granules, cytosolic aggregates of stalled translation preinitiation complexes (Okonski and Samuel 2013). In combination with IFN, HCV infection induces dynamic oscillation of stress granules that HCV may exploit to establish persistence (Ruggieri and others 2012).

Among the biochemical mechanisms suggested to account for the apparent pan-viral enhancement of virus growth by ADAR1 seen with some virus-cell combinations but not others is the antagonism of PKR activation by ADAR1 (Gelinas and others 2011; Samuel 2011). This mechanism is exemplified by measles virus. Studies with human cells stably knocked down for ADAR1 show increased activation of PKR, increased apoptosis, increased stress granule formation, and reduced viral growth following infection with measles virus (Toth and others 2009; Li and others 2012; Okonski and Samuel 2013). Complementation of ADAR1-deficient cells with ADAR1 p150 wild type but not the p150 catalytic mutant enhances virus growth and suppresses both PKR activation and stress granule formation (Okonski and Samuel 2013). Likewise, with mouse cells genetically knocked out for ADAR1 p150 expression, increased virus-induced cytotoxicity is observed compared with ADAR1-sufficient wild type cells following infection with negative-strand RNA viruses including measles virus, Newcastle disease virus, Sendai virus, canine distemper virus, and influenza virus (Ward and others 2011). These results are consistent with a protective function of the ADAR1 p150 cytoplasmic protein against RNA virus-induced cellular stress.

Neurotransmitter function

A-to-I RNA editing represents an important mechanism by which neuronal activity is modulated (Seeburg and Hartner 2003; George and others 2011; Hood and Emeson 2012). Some of the best characterized substrates of ADAR enzymes are neurotransmitter receptor and channel mRNAs. Among the most extensively studied are transcripts coding for AMPA and kainate glutamate-gated ion channel receptors, the serotonin 5-HT2c receptor, the α 3 subunit of the GABA_A receptor and the Kv1.1 potassium ion channel. Editing of these RNAs results in the expression of proteins with altered amino acid sequence and altered physiologic function. For example, the ionotrophic glutamate receptors, GluRs, regulate excitatory synaptic neurotransmission (Seeburg and Hartner 2003). A-to-I editing of GluR mRNAs regulate calcium permeability of the channels (Burnashev and others 1992), assembly and stoichiometry of the channel subunits (Greger and others 2003), and the rate of recovery from receptor desensitization (Lomeli and others 1994). Of the 2 editing sites present in GluR-B mRNA, the Q/R and R/G sites, ADAR1 contributes to the editing of the R/G site. ADAR1 also efficiently edits the GluR-B pre-mRNA at the intron 11 hotspot site +60 (Liu and Samuel 1999). The 5-HT2c serotonin receptor is a 7-transmembrane, phospholipase C-linked receptor encoded by mRNA transcripts that undergo editing at 5 sites termed A, B, C, D (Burns and others 1997), and E (Fitzgerald and others 1999; Niswender and others 1999; Wang and others 2000). Editing of the 5-HT2c transcript at all sites results in 3 amino acid substitutions in the rat and human receptor proteins, which cause a reduction in G-protein signaling compared with unedited RNA. Sites A and B are primarily edited by ADAR1 (Liu and Samuel 1999; Hartner and others 2004; Wang and others 2004).

Alterations in editing of RNAs encoding glutamate and serotonin neurotransmitter receptors have been implicated with neurologic and behavioral disorders (Morabito and Emeson 2009; O'Neil and Emeson 2012; Slotkin and Nishikura 2013). Altered editing patterns of 5-HT2c receptor transcripts, including at the A site primarily edited by ADAR1, have been observed in suicide victims with a history of major depression and in response to antidepressant treatment (Niswender and others 2001; Gurevich and others 2002). Increased cortical expression of ADAR1 but not ADAR2 also has been described in depressive suicide victims compared with patients who do not commit suicide (Simmons and others 2010). Increased expression of ADAR1 and ADAR2 and increased editing of 5-HT2c receptor mRNAs also has been implicated with addictive substance abuse behavior in model organisms (Dracheva and others 2009; Watanabe and others 2013). Depression can be a negative effect of IFN α therapy that adversely affects quality of life with potentially serious complications, and while the molecular mechanism has yet to be established, serotonin-mediated effects have been implicated, which could have as their basis altered RNA editing mediated by IFN-inducible ADAR1 p150 (Menkes and Mac-Donald 2000; Hood and Emeson 2012; O'Neil and Emeson 2012). Finally, mutations in ADAR1 resulting in its dysfunction has been shown to cause Aicardi-Goutieres (AG) syndrome, which is a genetically determined inflammatory disorder that affects newborns and infants resulting in severe mental and physical handicaps (Rice and others 2012). AG syndrome disease is associated with an upregulation of type I IFN in the absence of normal ADAR1 function (Rice and others 2012; Livingston and others 2013).

Cell proliferation and cancer

A growing body of evidence has revealed that disruption of the normal balance of ADAR1- and ADAR2-mediated A-to-I RNA editing influences the growth and progression of some human tumors (Galeano and others 2012; Chan and others 2013; Chen and others 2013; Qin and others 2013). Disruption of ADAR1 function also influences apoptotic responses both in virus-infected cells (Toth and others 2009; Ward and others 2011) and during embryonic development (Hartner and others 2004; Wang and others 2004; XuFeng and others 2009).

During embryonic development, ADAR1 is essential for hematopoiesis in mice (Hartner and others 2009; XuFeng and others 2009). ADAR1 is necessary for maintenance of both fetal and adult hematopoietic stem cells; genetic disruption of *Adar1* in hematopoietic stem cells leads to rapid apoptosis (Hartner and others 2009). ADAR1 is required for survival of differentiating hematopoietic progenitor cells in adult mice via an RNA-editing dependent mechanism (XuFeng and others 2009). ADAR1 also suppresses measles virus-induced apoptosis and cytotoxicity in cell culture. HeLa cells stably knocked down for ADAR1 and mouse MEFs genetically deficient in ADAR1 show enhanced measles virus-induced apoptosis measured by PARP cleavage, reduced cell viability measured by colorimetric MTS assay, and enhanced cytotoxicity assessed microscopically (Toth and others 2009; Ward and others 2011).

Dysregulation of A-to-I RNA editing by ADAR1 also has been implicated in the functional alteration of proteins relevant to cancer biology, including AZIN1 and FLNB in hepatocellular carcinoma (Chen and others 2013) and esophageal squamous cell carcinoma (ESCC) (Qin and others 2013), respectively. ADAR1-mediated editing of AZIN1 RNA (antizyme inhibitor 1) has been demonstrated to associate with increased risk of liver cirrhosis and predisposition to liver carcinoma. The AZIN1 protein blocks the effects of an antizyme on ornithine decarboxylase (ODC). ADAR1mediated A-to-I editing causes a Ser367Gly substitution that generates an AZIN1 protein that is more stable and hence binds antizyme in a manner that impairs its interaction with ODC, compared with the wild type AZIN1. Hence, the edited form of AZIN1 inhibits the antizyme tumor suppressor function and promotes cell proliferation (Chen and others 2013). Large-scale genome sequencing of hepatocellular carcinoma samples also identified, in addition to AZIN1, FLNB (filamin B) as a major target of ADAR1. ADAR1, but not ADAR2 or 3, is overexpressed in primary ESCC, a major form of esophageal cancer (Qin and others 2013). Functional analysis revealed hyperediting of FLNB RNA in addition to AZIN1 RNA in primary ESCC. In vitro studies also support the oncogenic potential of AZIN1 and FLNB associated with unbalanced editing by ADAR1 (Qin and others 2013).

In case of chronic myeloid leukemia (CML) patients, whole transcriptome sequencing revealed an enhanced expression of ADAR1 p150 isoform and increased A-to-I editing during CML progression. Overexpression of ADAR1 p150 promotes the expression of myeloid transcription factor pu.1, which induces extension of myeloid progenitors and also generates an alternatively spliced form of glycogen synthase kinase involved in self-renewal of leukemia stem cells (Jiang and others 2013). A-to-I editing by ADAR1 also occurs within the 3'-untranslated region (UTR) of the F11R gene transcript. The editing is increased upon hypoxic conditions, thereby altering nuclear retention of the RNA; F11R is associated with cell adhesion and spreading (Ben-Zvi and others 2013). Finally, the Hedgehog signaling pathway implicated in tumor progression and embryonic development is deregulated by A-to-I editing of the glioma-associated oncogene 1 by ADAR1 and ADAR2 (Shimokawa and others 2013). Glioblastoma, an aggressive, malignant brain tumor involving astrocyte glial cells also is associated with hypoediting of glutamate receptor RNA and decreased ADAR2 activity in astrocytoma tumor tissue (Galeano and others 2012).

The biochemical mechanism whereby editing affects tumor growth in most instances is not yet clear. A-to-I editing by ADARs is known to affect both the processing and targeting of micro RNAs (Nishikura 2010). Editing by ADAR1 in invasive ductal breast cancer and glioblastoma specimens inhibits the binding of miR-30b-3p and miR-573 within the 3'-UTR of Rho GTPase activating protein 26 (ARHGAP26) transcripts. ARHGAP26 is a regulator of the Rho family and a putative tumor suppressor, negatively regulating RhoA and Cdc42 in human cancers. miR-47 and miR-432 down-regulate the expression of ADAR1 in cancer cells (Wang and others 2013). Attenuated A-to-I editing of microRNA miR-376a has been found to promote invasiveness of glioblastoma cells (Choudhury and others 2012).

Type I IFN production

The ADAR1 cDNA was initially identified and characterized as an IFN-stimulated gene (Patterson and Samuel 1995; Patterson and others 1995). ADAR1 then was shown through loss of function and complementation studies to suppress innate immune responses and IFN induction in virus-infected cells in culture in a manner dependent upon ADAR1 catalytic activity (Toth and others 2009; Li and others 2012; Okonski and Samuel 2013). Mutation of ADAR1 was also established to enhance IFN production and to trigger a type I IFN signature in mice (Hartner and others 2009) and humans (Rice and others 2012; Livingston and others 2013). Thus, one emerging role of ADAR1 is the downregulation of dsRNA-triggered innate immune responses through destablization of the activator dsRNA and hence suppression of its IFN inducing capacity.

The IFN system is a cornerstone of antiviral innate immunity (Borden and others 2007). Among the pathogenassociated molecular patterns of viruses that trigger the transcriptional induction of type I IFN is dsRNA, which is recognized as foreign by host cell nucleic acid sensors. In the case of measles virus, RIG-I senses infection and signals an IPS-dependent induction of IFN (Randall and Goodbourn 2008). PKR enhances IFN β induction by measles virus in a manner that depends upon PKR catalytic activity and is prevented by viral C protein expression (McAllister and others 2010, 2012). C protein impairs production of defective copyback viral dsRNA and PKR activation (Pfaller and others 2014). ADAR1 suppresses the activation of PKR (Toth and others 2009), suppresses the activation of IRF3 (Li and others 2012), suppresses the formation of cytoplasmic stress granules (Okonski and Samuel 2013), and suppresses the induction of IFN β (Li and others 2012; Okonski and Samuel 2013). In human cells stably knocked down for both the p110 and p150 ADAR1 proteins, the transcriptional induction of IFN β is enhanced by wild type and V mutant measles viruses, whereas in the presence of ADAR1 these viruses are very poor IFNB inducers (Li and others 2012). The enhanced induction of IFNB seen with ADAR1-deficient cells correlates with enhanced activation of both IRF3 and PKR (Li and others 2012); activation of PKR leads to enhanced activation of NFkB (McAllister and others 2010, 2012). Complementation of ADAR1-deficient cells reveals that the p150 ADAR1 isoform suppresses both PKR activation and IFN induction (Okonski and Samuel 2013).

The elevated production of type I IFN observed in human cells in culture stably knocked down for ADAR1 also has been observed in $Adar1^{-/-}$ mice genetically knocked out for ADAR1 protein expression (Hartner and others 2009) and in human AG syndrome patients with mutations in ADAR1(Rice and others 2012; Livingston and others 2013). Genetic disruption of *Adar1* causes embryonic lethality in mice and results in the upregulation of type I IFN and of IFN-stimulated gene expression in hematopoietic stem cells in the absence of infection (Hartner and others 2009). Mu-

tations that cause AG syndrome mapped to Adar1, which likewise are associated with a type I IFN signature and elevated levels of IFN in the absence of detectable infection (Rice and others 2012; La Piana and others 2013; Livingston and others 2013). These results suggest that ADAR1 is essential for the suppression of type I IFN responses in cultured cells, mice and humans. The biochemical mechanism responsible for the enhanced type I IFN response seen in ADAR1-deficient cells, based on measles virus-cell culture system studies, appears to involve an increased accumulation of dsRNA (Pfaller and others 2014) that subsequently increases the activation of both IRF3 and PKR (Li and others 2012; Okonski and Samuel 2013). Whether a similar mechanism occurs in mice and humans with mutations in the Adar1 gene, which conceivably might permit accumulation of increased levels of cytoplasmic cellular RNA with stable dsRNA structure sufficient to trigger the observed type I IFN signature, remains to be established.

ADAR1 deficiency in cultured cells, mice and humans all lead to enhanced type I IFN production (Hartner and others 2009; Rice and others 2012; Okonski and Samuel 2013). Whether this is due to an anticipated reduction in inosinecontaining RNA present in ADAR1-deficient cells remains to be established. Synthetic inosine-containing dsRNA exemplified by poly rI:poly rC was identified long ago as a potent inducer of IFN in a variety of cultured cells (Field and others 1967). Recently, inosine incorporation into synthetic single-stranded RNA (ssRNA) also has been demonstrated to potentiate production of IFN α and tumor necrosis factor α in human peripheral blood mononuclear cells by TLR7/8 sensing of the ssRNA (Sarvestani and others 2014). A-to-I editing of influenza virus ssRNA also enhanced TLR7 sensing. The biological effect of the presence of inosine within an RNA, presumably generated under physiological conditions by the action of an ADAR, on the IFN-inducing capacity of a given ssRNA or dsRNA is likely determined by the combination of factors including size, overall structure and concentration of the I-containing RNA, the subcellular localization of the RNA, and the kind of cell in which the I-containing RNA is present and hence the innate immune response triggered.

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Address correspondence to: Prof. Charles E. Samuel Department of Molecular, Cellular and Developmental Biology University of California Santa Barbara, CA 93106

E-mail: samuel@lifesci.ucsb.edu

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