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Expression of a noncoding RNA is elevated in Alzheimer's disease and drives rapid feed-forward regulation of β-secretase expression

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Abstract

Recent transcriptomics efforts have revealed that numerous protein-coding messenger RNAs have natural antisense transcript partners, most of which seem to be noncoding RNAs. Here we identify a conserved noncoding antisense transcript for β-secretase-1 (*BACE1*), a crucial enzyme in Alzheimer's disease pathophysiology. The BACE1-antisense transcript (*BACE1*-AS) regulates *BACE1* mRNA and subsequently BACE1 protein expression *in vitro* and *in vivo*. It seems that the argument for concordant regulation can only be made in the experiments with the siRNA against BACE1-AS. This convention has been followed throughout the manuscript. Please check carefully.]. Upon exposure to various cell stressors including amyloid-β 1–42 (Aβ 1–42), expression of *BACE1*-AS becomes elevated, increasing *BACE1* mRNA stability and generating additional Aβ 1–42 through a post-transcriptional feed-forward mechanism. *BACE1*-AS concentrations were elevated in subjects with Alzheimer's disease as well as in amyloid precursor protein transgenic mice. These data show that *BACE1* mRNA expression is under the control of a regulatory noncoding RNA that may drive Alzheimer's disease–associated pathophysiology. In summary, we report that a long noncoding RNA is directly implicated in the increased abundance of Aβ 1–42 in Alzheimer's disease.

Sequential cleavage of amyloid precursor protein (APP) by BACE1, the β-site cleaving enzyme essential for Aβ 1–42 and amyloid-β 1–40 (Aβ 1–40) biosynthesis[1], and γ-secretase

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initiates the 'amyloid cascade' that is central to Alzheimer's disease pathophysiology[2,3]. Oligomers of Aβ 1–42 produced by BACE1 influence key aspects of Alzheimer's disease[4-9]. Studies have revealed elevated brain *BACE1* concentrations in subjects with Alzheimer's disease compared with normal controls[10-15]. However, controversy exists concerning the extent of *BACE1* upregulation and whether this upregulation involves *BACE1* mRNA or protein[16-18].

Loss of BACE1 results in numerous behavioral and physiological deficits, including memory loss[19], emotional deficits[20], myelination defects in peripheral nerves[21,22] and loss of synaptic plasticity[20]. Thus, the subtle but crucial boundaries between BACE1 physiology and pathology indicate that BACE1 expression must be tightly regulated, allowing the enzyme to perform its physiological functions while avoiding the serious consequences of over- or underexpression.

Here we report that *BACE1*-AS, a natural antisense transcript, plays a part in determining *BACE1* expression. *BACE1*-AS rapidly and reversibly upregulates *BACE1* levels in response to a variety of stresses, including Aβ 1–42 exposure. Furthermore, we show elevated *BACE1*-AS in several brain regions of individuals with Alzheimer's disease. These data suggest that this previously unexamined noncoding RNA has a role in regulating BACE1 and in driving Alzheimer's disease pathology.

RESULTS

Identification of *BACE1* natural antisense transcript

BACE1-AS was originally identified through the FANTOM large-scale transcriptomics efforts as one member of some 1,000 sense-antisense pairs conserved between human and mouse[23]. *BACE1*-AS is a conserved ~2-kb RNA transcribed from the positive strand of chromosome 11, on the opposite strand of the *BACE1* locus (11q 23.3), including 104 nucleotides of full complementarity to exon 6 of human *BACE1* mRNA (Fig. 1a). We performed rapid amplification of cDNA ends (RACE) for directional sequencing of 5′ and 3′ ends and identified two splice variants for human and mouse *BACE1*-AS that overlap the *BACE1* sense transcript (Fig. 1b,c). We found a poly-A tail and cap structure in both human and mouse sequences, indicating that *BACE1*-AS is a fully processed transcript of RNA polymerase II. However, there is no apparent open reading frame. Sequencing data for human and mouse *BACE1*-AS are illustrated in **Supplementary Data** 1 and 2 online.

Expression analysis of *BACE1* and *BACE1*-AS

BACE1 mRNA expression levels were 25–75% greater than *BACE1*-AS transcript levels across all samples examined from various tissues and cell lines, in contrast to the relative concentrations in Alzheimer's disease brain (described below). We also observed *Bace1* and *Bace1*-AS transcripts in various regions of the mouse brain. (**Supplementary Figs. 1** and **2** online).

In cultures of glia and cortical neurons of human origin, *APP* mRNA was about twice as abundant in neuronal cultures compared to glial cultures, whereas *BACE1* and *BACE1*-AS transcripts were two to three times more abundant in the glial cells (Fig. 1d). Northern blot analysis with *in vitro*–transcribed strand-specific RNA probes confirmed that various human tissues express both *BACE1* and *BACE1*-AS (Fig. 1e). This observation suggests that *BACE1* and *BACE1*-AS expression may be regulated concordantly, as was recently shown for other sense-antisense pairs[24,25].

BACE1-AS regulates *BACE1* RNA and protein *in vitro*

We next investigated whether the *BACE1*-AS transcript regulates expression of *BACE1* mRNA. Unexpectedly, transfection of human SH-SY5Y cells with any one of three distinct small interfering RNA (siRNA) sequences targeting nonoverlapping regions of the *BACE1*-AS transcript resulted in a statistically significant knockdown of not only the targeted *BACE1*-AS transcript, but also *BACE1* mRNA (Fig. 2a). There are broadly two types of regulation between sense and antisense transcripts. In concordant regulation, like in the case of *BACE1-AS,* the antisense transcripts change the level of the sense RNA, or corresponding protein levels, in a positive way. In contrast, in discordant regulation, the antisense transcripts have negative (opposing) effects on sense transcripts. We also observed this concordant pattern of regulation in human HEK293T and HEK-SW cells, in which siRNA-mediated knockdown of *BACE1*-AS resulted in a similar reduction in *BACE1* mRNA (data not shown). In a control experiment in HEK-SW cells, the level of *BACE2* did not change with *BACE1*-AS siRNA treatment, lending further support to the specificity of the observed *BACE1* regulation by *BACE1*-AS (Supplementary Fig. 3 online). Furthermore, because three distinct siRNA molecules that exclusively target the *BACE1*-AS transcript resulted in concomitant reduction of sense *BACE1* transcript, it is highly unlikely that the siRNAs acted to knock down *BACE1* transcript through a nonspecific (or 'off-target') mechanism.

To investigate the effects of long-term siRNAs directed against *BACE1*-AS on *BACE1* expression, we generated stable HEK293T cell lines expressing four distinct short hairpin RNAs (shRNAs) to *BACE1* or *BACE1*-AS transcripts. Three of the *BACE1* shRNAs and two of the *BACE1*-AS shRNAs were functional and induced sustained reduction of *BACE1* and *BACE1*-AS, respectively (Fig. 2b). Cells expressing *BACE1*-AS shRNA showed reduced *BACE1* levels, and vice versa (Fig. 2b).

To examine the dose-response relationship of *BACE1* mRNA and *BACE1-AS* siRNA, we measured the reduction in *BACE1* mRNA expression across a range of concentrations of *BACE1*-AS siRNA (100 pM–20 nM) in HEK-SW cells. The resulting data confirmed that siRNA targeting *BACE1*-AS reduces the expression of *BACE1* mRNA in a concentration-dependent manner (Fig. 2c).

Next, we assessed BACE1 protein abundance after transfection of HEK293T cells with *BACE1*-AS siRNA or shRNA. Western blotting showed that siRNA against *BACE1*-AS as well as siRNA against *BACE1,* (but not control siRNAs), reduced the expression of BACE1 protein (Fig. 2d,e). Thus, *BACE1*-AS seems to control the expression of BACE1 at both the mRNA and the protein levels. Additionally, for accurate quantification of the effects of siRNA treatments on BACE1 protein expression, we established a method for protein quantification by enzyme complementation assay (ECA, **Methods** and Supplementary Fig. 4 online). We then measured the changes in BACE1 protein concentration after treatment with siRNAs and shRNAs and observed that siRNAs against either *BACE1* or *BACE1*-AS reduce BACE1 protein abundance by 40–60% (Supplementary Fig. 5 online).

Moreover, overexpression of *BACE1*-AS led to a fourfold increase in *BACE1* mRNA (Fig. 2f). When measured by western blotting, the overexpression of *BACE1*-AS resulted in increased BACE1 protein abundance (Fig. 2g). These observations further confirm the regulation of BACE1 expression by *BACE1*-AS, not only at the mRNA but also at the protein level.

Knockdown of *BACE1*-AS reduces Aβ 1–40 and Aβ 1–42 production

We measured by ELISA the amount of Aβ 1–40 and Aβ 1–42 after depletion of *BACE1*-AS in the HEK-SW cell line that contains mutated APP, $swAPP_{751,}$ so-called Swedish mutation[26]. We found a reduced concentration of both Aβ 1–40 and Aβ 1–42 in cells treated

with *BACE1*-AS siRNA (Fig. 2h). To rule out possible nonspecific effects of siRNA treatment on APP concentration that may account for the observed decreases in Aβ 1–40 and Aβ 1–42, we assayed the amount of soluble APPα (sAPPα, soluble product of α-secretase in the supernatants of the HEK-SW cells) and total APP abundance by ELISA. Neither sAPPα nor total APP abundance was altered upon *BACE1* siRNA or *BACE1*-AS siRNA treatment (Fig. 2h). These results suggest that *BACE1*-AS siRNA treatment results in reduced BACE1 protein function without affecting APP or α-secretase products.

Knockdown of *BACE1*-AS reduces *BACE1* levels *in vivo*

The above data support a role for *BACE1*-AS in regulating BACE1 function *in vitro* in human cells. Next, we assessed whether orthologous *Bace1*-AS also regulates *Bace1* mRNA and protein *in vivo* in mouse brain. After 14 d of continuous siRNA infusion, *Bace1* mRNA levels were reduced across forebrain regions located adjacent to the third ventricle in mice treated with either *Bace1* siRNA or *Bace1*-AS siRNA, compared to levels unaltered by control siRNA (Fig. 3a–d). *Bace1* and *Bace1*-AS transcripts were unaltered in the cerebellum, a structure that is spatially restricted from the third ventricle, of siRNA-treated mice, consistent with previous work that indicates limited penetration of pump-mediated infusion of siRNA into the brain[27] (Fig. 3e). We also measured the amount of Bace1 protein in the ventral hippocampus and the cerebellum by western blotting after siRNA treatment. We found that both *Bace1* siRNA and *Bace1*-AS siRNA treatment resulted in reduced Bace1 protein abundance (Fig. 3f). Our *in vivo* findings agree with the *in vitro* data described above and indicate that reduced *Bace1*-AS expression results in reduction of *Bace1* mRNA and protein expression *in vivo*.

Cell stressors increase *BACE1*-AS and BACE1 protein

Different cell stressors have long been implicated in the pathogenesis of Alzheimer's disease[12,28]. We exposed HEK-SW cells to hyperthermia, serum starvation, staurosporine, Aβ 1–42, Aβ 1–40, hydrogen peroxide (H_2O_2) or high glucose for 12 h. We found that exposure of the cells to high temperature, serum starvation, Aβ 1–42, H_2O_2 or high glucose resulted in a ~30–130% increase in *BACE1*-AS levels and a ~20–60% increase in *BACE1* mRNA levels (Fig. 4a). Serum starvation generated the strongest response, whereas Aβ 1–40 and staurosporine exposure did not significantly alter *BACE1*-AS expression levels(Fig. 4a). These results suggest that many, but not all, cell stressors can contribute to the pathogenesis of Alzheimer's disease by altering *BACE1*-AS expression and subsequently BACE1 enzyme activity.

Accumulating evidence describes Aβ 1–42 itself as a potent cell stressor[10,29-32]. To test the hypothesis that Aβ 1–42 increases *BACE1* expression by a *BACE1*-AS dependent mechanism, we exposed SH-SY5Y cells for 2 h to conditioned media from CHO-7PA2 cells, which overexpress APP and generate Aβ 1–42 dimers and oligomers[33]. Exposure of the SH-SY5Y cells to conditioned media from CHO-7PA2 cells, but not conditioned media from control parental CHO cells resulted in an increase in cytoplasmic concentrations of *BACE1*-AS transcript (Fig. 4b). We obtained similar results when incubating SH-SY5Y cells with synthetic Aβ 1–42 (1 μM for 2 h; Fig. 4c). Removal of the cell stressors normalized *BACE1*-AS expression patterns. Using an ECA, we found that synthetic Aβ 1–42 (1 μM for 12 h) elicited an increase in BACE1 protein abundance as well (Fig. 4d). Taken together, the above data indicate that cell stress increases *BACE1*-AS levels, which in turn increases *BACE1* levels; this may result in an increase in APP processing and Aβ 1–42 production. Subsequently, increased Aβ 1–42 levels can further increase *BACE1*-AS expression, driving the APP processing cascade in a feed-forward manner.

BACE1-AS forms RNA duplex and increases stability of *BACE1*

We used an RNase protection assay (RPA) on RNA from SH-SY5Y cells to test the possibility of RNA duplex formation (Supplementary Methods). RT-PCR data showed that the overlapping part of both transcripts was protected from degradation, indicating that *BACE1* and *BACE1*-AS indeed form a RNA duplex (Fig. 5a). We also validated the RPA data on a 10% Tris-borate-EDTA–urea gel using radiolabeled *BACE1*-AS probes (data not shown).

RNA duplex formation may act to alter the secondary or tertiary structure of BACE1 and thereby increase its stability. We assessed the stability of *BACE1* and *BACE1*-AS transcripts by blocking new RNA synthesis with α-amanitin and measuring the loss of *BACE1, BACE1*-AS, β-actin (*ACTB*) and *18s* RNA over a 24-h period. We found that *BACE1*-AS had a shorter half-life than *BACE1* mRNA (8.5 h versus 17.5 h Fig. 5b). *18s* ribosomal RNA, which is a product of RNA polymerase I, was not affected by α-amanitin treatment (Fig. 5b). In a cell line that constitutively expresses *BACE1*-AS shRNA and thereby has depleted *BACE1*-AS levels, we found decreased stability of *BACE1* mRNA compared with cells transfected with a control shRNA (Fig. 5c). Conversely, cells that overexpress *BACE1*-AS showed increased stability of *BACE1* (Fig. 5d). Collectively, our data demonstrate that *BACE1*-AS increases the stability of *BACE1* mRNA.

BACE1-AS is elevated in subjects with Alzheimer's disease

Elevated *BACE1*-AS concentrations may facilitate increased BACE1 activity and disease progression in the brains of human subjects with Alzheimer's disease. To examine this question, we assessed *BACE1*-AS and *BACE1* mRNA abundance in RNA samples prepared from parietal lobes and cerebellum from five postmortem brains of human subjects with Alzheimer's disease and from five age- and sex-matched control brains. In the Alzheimer's disease samples, the relative quantity of *BACE1*-AS transcript was increased by two to three times, along with a smaller increase in *BACE1* transcript (Fig. 6a and Supplementary Fig. 6a online). In a separate group of 35 subjects with Alzheimer's disease and 35 age- and sex-matched controls[34], we examined RNA samples derived from cerebellum (25 Alzheimer's disease samples and 21 control samples), hippocampus (13 Alzheimer's disease samples and 11 control samples), entorhinal cortex (13 Alzheimer's disease samples and 11 control samples) and superior frontal gyrus (16 Alzheimer's disease samples and 17 control samples). The *BACE1*-AS transcript concentrations were elevated in subjects with Alzheimer's disease by up to sixfold, with an average elevation of about twofold across all brain regions (Fig. 6b–d and Supplementary Fig. 6b,c). We detected a smaller (~30%) increase in *BACE1* mRNA concentrations in these subjects compared to their matched controls (Fig. 6a,b) **[AU: Figure callout or 'data not shown'?]**. Taken together, these results support our hypothesis that increases in *BACE1*-AS expression, probably related to cell stressors, drives upregulation of *BACE1* mRNA and protein level, thereby facilitating Aβ 1–42 biosynthesis in human Alzheimer's disease brain.

BACE1-AS may have utility as a new biomarker of Alzheimer's disease[35]. To this end, we calculated the ratio of *BACE1*-AS relative *to BACE1* and *ACTB* mRNA in different brain regions of control subjects and subjects with Alzheimer's disease. We found that the *BACE1*-AS to *ACTB* ratio was increased in various brain regions in subjects with Alzheimer's disease as compared to control individuals (Fig. 6e). A smaller increase in the *BACE1*-AS to *BACE1* ratio was also observed in the brains of individuals with Alzheimer's disease (Fig. 6f). These data demonstrate that the ratio between *BACE1*-AS and other RNA transcripts, including *BACE1*, could potentially be used as a biomarker of Alzheimer's disease.

APP transgenic mice have increased levels of *Bace1*-AS

Tg19959 mice, considered a mouse model of Alzheimer's disease, overexpress a doubly mutated human APP (APP-tg19959)36 and consequently have increased levels of Aβ 1–42 (ref. 37). Samples from whole brains excised from four six-week-old male mice had increased (~300-fold) levels of Aβ 1–42 compared with samples from matched wild-type controls, as measured by homogeneous time resolved fluorescence (HTRF) assay (Fig. 6g and Supplementary Methods). Expression of the *Bace1*-AS transcript was increased by about 45%, and *Bace1* mRNA expression was increased by about 25% in the brains of the APP-tg19959 mice compared with wild-type control mice (Fig. 6h), similar to the measurements in the human samples.

DISCUSSION

The contrast between BACE1's essential role in cognitive, emotional and synaptic functions[19,20] and its pathophysiological dysregulation in Alzheimer's disease[38,39] highlights the regulatory complexity of this protein. Owing to the consequences of its dysregulation, *BACE1* gene expression must normally maintain tight robust regulatory control.

In this study, we have characterized a conserved noncoding antisense transcript for *BACE1,* called *BACE1*-AS, which functions as a regulator of BACE1 gene expression. We present data showing that *BACE1*-AS is widely co-expressed with *BACE1* in cell lines, tissues and Alzheimer's disease–sensitive brain regions and that it regulates *BACE1* expression *in vitro* and *in vivo*. We found that selective siRNA targeting of the nonoverlapping regions of the *BACE1*-AS resulted in reduction of *BACE1* mRNA and protein abundance *in vitro*. Administration of siRNA that selectively targeted either *Bace1* or *Bace1*-AS into mouse brains reduced the levels of both transcripts, indicating that this concordant regulation also occurs *in vivo*.

In addition, we have shown that alterations in *BACE1*-AS RNA concentrations can alter Aβ 1–40 and Aβ 1–42 production. Considering the narrow window between essential levels and excessive levels (as in Alzheimer's disease) of BACE1 protein, we believe that neuronal cells must maintain precise physiological regulation of BACE1 expression by using both pre- and post-transcriptional regulatory mechanisms. The RNA transcript, *BACE1*-AS, seems to function as a regulatory component of this machinery.

Because *BACE1*-AS regulates BACE1 expression *in vivo*, we propose that the elevation of *BACE1*-AS, resulting from the actions of Alzheimer's disease–related cell stressors, forms a basis for a deleterious feed-forward cycle of Alzheimer's disease progression. Even small changes in BACE1 activity may lead to a long-lasting and chronic process of Aβ 1–42 accumulation in the Alzheimer's disease brain[38,40]. Our current findings provide further evidence for a feed-forward mechanism of stress-dependent and activity-dependent[41] Aβ 1–42 production. Recent studies have shown that amyloid plaques induce elevation of BACE1 protein expression in adjacent neurons by a post-transcriptional mechanism[10]. This finding is consistent with the present data in which Aβ 1–42 was shown to induce increased levels of *BACE1*-AS, thereby driving BACE1-mediated APP processing and further accumulation of Aβ 1–42. In support of the above interpretation, we found that two independent sets of human Alzheimer's disease brain samples as well as an animal model of Alzheimer's disease express elevated levels of both *BACE1*-AS transcript and, to a lesser degree, *BACE1* sense transcript. In contrast to the downregulation of most transcripts reported to date in Alzheimer's disease brains[42,43], *BACE1*-AS upregulation may be the driving force behind Alzheimer's disease–related BACE1 dysregulation[15,44,45]. Thus, our results implicate a

noncoding RNA in the control of gene expression central to the delicate balance between healthy stress response and the pathophysiological β-amyloid cascade.

Aβ 1–42 induces synaptic depression by triggering endocytosis of glutamatergic *N*-methyl D-aspartate receptors from the post-synaptic membrane[6]. Synaptic activity–dependent production of Aβ 1–42 achieves this depressive effect of *N*-methyl D-aspartate receptor endocytosis by a series of common mechanisms that implicate Aβ 1–42 in the establishment of some forms of long-term depression[46]. Although they contribute to the depth and richness of mammalian memory, if not precisely controlled, these mechanisms may lead to chronic neuronal stress and the onset of Alzheimer's disease. We have previously speculated that noncoding RNAs may be required for some forms of long-term depression[47], and *BACE1*-AS could well be involved in such a function.

Treatment with *BACE1*-AS siRNA may achieve a preferential reduction of stress-induced increases in BACE1 expression without disturbing physiologically essential basal expression levels. Thus, we propose that *BACE1*-AS could potentially constitute a drug target candidate well suited to mediate the transition between the essential physiological functions of BACE1 and its pathological dysregulation in the chronically stressed setting of early Alzheimer's disease[48]. Our *in vivo* experiments using infusion of unmodified synthetic siRNA over an extended period of time in experimental mice support the validity of an siRNA approach to decrease *BACE1* expression, perhaps in humans as well. A recent technological breakthrough suggests that systemic administration of modified siRNA may cross the blood-brain barrier and thereby target RNA transcripts in the brain[49]. Alternatively, proteins involved in *BACE1*-AS localization or turnover could serve as potential targets for therapeutic interventions.

METHODS

Enzyme complementation assay

ECA is a technology developed by DiscoveRx that allows for the measurement of changes in protein abundance (Supplementary Fig. 2). We cloned the cDNA of *BACE1* into a pCMV-ProLabel vector upstream of the ProLabel. We transfected vector into HEK293T cells to produce a fusion protein (BACE1 and the enzyme donor fragment of β-galactosidase) and made a stable cell line, which we called C3. In our experiments, we treated HEK293T cells with Aβ 1–42 peptides for 12 h and then added the lysis buffer (DiscoveRx), which includes the enzyme acceptor fragment of β-galactosidase. When the two fragments of the β-galactosidase combine in solution, the enzyme becomes active and hydrolyzes a substrate that produces a chemiluminescent signal. The strength of this signal is proportional to the protein being produced (in this case, BACE1). In a separate experiment, we transfected the stable cell line C3 overexpressing BACE1 with siRNA or shRNA against *BACE1, BACE1*-AS or control siRNA and measured protein expression 72 h later with this methodology. We plotted data as a percentage of control siRNA.

Human samples

The first set of human brain samples was prepared at the USC Alzheimer's Disease Research Center. The USC Alzheimer's Disease Research Center obtained informed consent from all subjects and the USC Institutional Review Board approved the use of the human tissue. RNA was extracted from parietal lobes and cerebellum of postmortem brains of five subjects with Alzheimer's disease and five matched controls. The average age of subjects with Alzheimer's disease was 85 years (range 75–92 years) and 91.8 years (90–95 years) for controls. The postmortem interval ranged from 3.75–10.1 h with a mean of 5.87 h. We treated RNA samples with DNase and purified them with RNeasy mini columns (QIAGEN).

We prepared cDNA from 400 ng of RNA samples and used RT-PCR for relative quantification of different transcripts. The second set of human brain samples was prepared from rapid autopsy brain tissue that had been obtained from J. Rogers (Sun Health Research Institute); all enrolled subjects or legal representatives had signed a Sun Health Research Institutional Review Board–approved informed consent form allowing both clinical assessments during life and several options for brain and bodily organ donation after death. These cases included 35 autopsy-confirmed cases of Alzheimer's disease with an average age of 81.8 years (range 64–92 years) and 35 controls with an average age of 72.3 years (range 53–91 years). The postmortem interval ranged from 1.25–5 h with a mean of 2.5 h. The average duration of disease in the subjects with Alzheimer's disease was 9.2 years. Total RNA was isolated via CsCl purification from tissue dissected from specific regions of brain. Although not all regions were available from all cases, we examined a total of 128 RNA samples from superior frontal gyrus, entorhinal cortex, hippocampus and cerebellum for *BACE1* and *BACE1*-AS expression by RT- PCR.

Mouse studies

We obtained approval for mouse studies from the Institutional Animal Care and Use Committee at The Scripps Research Institute.

We used 18 six-month-old male mice for *in vivo* siRNA infusion experiments. We prepared mice with chronic indwelling cannulae in the dorsal third ventricle implanted subcutaneously with osmotic minipumps that delivered continuous infusions (0.25 μl/h) of synthetic unmodified siRNA directed against *Bace1, Bace1*-AS or control siRNA (previously shown to have no effects on the expression of human and mouse genes) at a dose of 0.4 mg/d for 2 weeks. We connected tubing to the exit port of the osmotic minipump and tunneled it subcutaneously to the indwelling cannula, such that siRNAs were delivered directly into the brain.

Pump-mediated infusion of siRNA was previously shown to significantly and specifically knock down expression of targeted mRNAs in the brain, but with a limited tissue penetration[27]. Indeed, RNA knockdown upon ventricular infusion of siRNAs for 14 consecutive d was usually obtained in brain regions immediately adjacent to the ventricle, with diminishing effects of the siRNA as the distance from the ventricle increased.

We excised five tissues from each mouse for RNA quantitative measurement—the dorsal hippocampus, ventral hippocampus, cortex, dorsal striatum and cerebellum. RNA extraction is described in Supplementary Methods.

Tg19959 mice were produced by pronuclear microinjection of (FVB × 129S6F1) embryos with a cosmid insert containing human APP with two familial Alzheimer's disease mutations (KM670/671NL and V717F) under the control of the hamster PrP promoter. We euthanized four Tg19959 mice and four control male littermates at 6 weeks old. We used brain tissues for RNA measurements and Aβ 1–42 detection by HTRF. In a separate experiment, we euthanized three wild-type male mice and excised their tissues for expression profiling of *Bace1* and *Bace1*-AS by RT-PCR.

Supplementary Material

Refer to Web version on PubMed Central for supplementary material.

Acknowledgments

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References

1. Goedert M, Spillantini MG. A century of Alzheimer's disease. Science 2006;314:777–781. [PubMed: 17082447]
2. Faghihi MA, Mottagui-Tabar S, Wahlestedt C. Genetics of neurological disorders. Expert Rev. Mol. Diagn 2004;4:317–332. [PubMed: 15137899]
3. Monaco S, Zanusso G, Mazzucco S, Rizzuto N. Cerebral amyloidoses: molecular pathways and therapeutic challenges. Curr. Med. Chem 2006;13:1903–1913. [PubMed: 16842201]
4. Zhu D, et al. Phospholipases A2 mediate amyloid-β peptide–induced mitochondrial dysfunction. J. Neurosci 2006;26:11111–11119. [PubMed: 17065451]
5. Esposito G, et al. CB1 receptor selective activation inhibits β-amyloid-induced iNOS protein expression in C6 cells and subsequently blunts tau protein hyperphosphorylation in co-cultured neurons. Neurosci. Lett 2006;404:342–346. [PubMed: 16837132]
6. Snyder EM, et al. Regulation of NMDA receptor trafficking by amyloid-β. Nat. Neurosci 2005;8:1051–1058. [PubMed: 16025111]
7. Matsuyama S, Teraoka R, Mori H, Tomiyama T. Inverse correlation between amyloid precursor protein and synaptic plasticity in transgenic mice. Neuroreport 2007;18:1083–1087. [PubMed: 17558301]
8. Abramov AY, Canevari L, Duchen MR. β-amyloid peptides induce mitochondrial dysfunction and oxidative stress in astrocytes and death of neurons through activation of NADPH oxidase. J. Neurosci 2004;24:565–575. [PubMed: 14724257]
9. Ohyagi Y, et al. Intracellular Aβ42 activates p53 promoter: a pathway to neurodegeneration in Alzheimer's disease. FASEB J 2005;19:255–257. [PubMed: 15548589]
10. Zhao J, et al. β-site amyloid precursor protein cleaving enzyme 1 levels become elevated in neurons around amyloid plaques: implications for Alzheimer's disease pathogenesis. J. Neurosci 2007;27:3639–3649. [PubMed: 17409228]
11. Sun X, et al. Hypoxia facilitates Alzheimer's disease pathogenesis by up-regulating *BACE1* gene expression. Proc. Natl. Acad. Sci. USA 2006;103:18727–18732. [PubMed: 17121991]
12. Tong Y, et al. Oxidative stress potentiates *BACE1* gene expression and Aβ generation. J. Neural Transm 2005;112:455–469. [PubMed: 15614428]
13. Li R, et al. Amyloid β peptide load is correlated with increased β-secretase activity in sporadic Alzheimer's disease patients. Proc. Natl. Acad. Sci. USA 2004;101:3632–3637. [PubMed: 14978286]
14. Holsinger RM, McLean CA, Collins SJ, Masters CL, Evin G. Increased β-secretase activity in cerebrospinal fluid of Alzheimer's disease subjects. Ann. Neurol 2004;55:898–899. [PubMed: 15174031]
15. Fukumoto H, Cheung BS, Hyman BT, Irizarry MC. β-secretase protein and activity are increased in the neocortex in Alzheimer disease. Arch. Neurol 2002;59:1381–1389. [PubMed: 12223024]
16. Johnston JA, et al. Expression and activity of β-site amyloid precursor protein cleaving enzyme in Alzheimer's disease. Biochem. Soc. Trans 2005;33:1096–1100. [PubMed: 16246054]
17. Ohno M, et al. BACE1 deficiency rescues memory deficits and cholinergic dysfunction in a mouse model of Alzheimer's disease. Neuron 2004;41:27–33. [PubMed: 14715132]
18. Tesco G, et al. Depletion of GGA3 stabilizes BACE and enhances β-secretase activity. Neuron 2007;54:721–737. [PubMed: 17553422]

19. Ma H, et al. Involvement of β-site APP cleaving enzyme 1 (BACE1) in amyloid precursor protein–mediated enhancement of memory and activity-dependent synaptic plasticity. Proc. Natl. Acad. Sci. USA 2007;104:8167–8172. [PubMed: 17470798]
20. Laird FM, et al. BACE1, a major determinant of selective vulnerability of the brain to amyloid-β amyloidogenesis, is essential for cognitive, emotional, and synaptic functions. J. Neurosci 2005;25:11693–11709. [PubMed: 16354928]
21. Hu X, et al. Bace1 modulates myelination in the central and peripheral nervous system. Nat. Neurosci 2006;9:1520–1525. [PubMed: 17099708]
22. Willem M, et al. Control of peripheral nerve myelination by the β-secretase BACE1. Science 2006;314:664–666. [PubMed: 16990514]
23. Engstrom PG, et al. Complex loci in human and mouse genomes. PLoS Genet 2006;2:e47. [PubMed: 16683030]
24. Katayama S, et al. Antisense transcription in the mammalian transcriptome. Science 2005;309:1564–1566. [PubMed: 16141073]
25. Wahlestedt C. Natural antisense and noncoding RNA transcripts as potential drug targets. Drug Discov. Today 2006;11:503–508. [PubMed: 16713901]
26. Su Y, Ryder J, Ni B. Inhibition of Aβ production and APP maturation by a specific PKA inhibitor. FEBS Lett 2003;546:407–410. [PubMed: 12832078]
27. Thakker DR, Hoyer D, Cryan JF. Interfering with the brain: use of RNA interference for understanding the pathophysiology of psychiatric and neurological disorders. Pharmacol. Ther 2006;109:413–438. [PubMed: 16183135]
28. Borghi R, et al. The increased activity of BACE1 correlates with oxidative stress in Alzheimer's disease. Neurobiol. Aging 2006;28:1009–1014. [PubMed: 16769154]
29. Tamagno E, Bardini P, Guglielmotto M, Danni O, Tabaton M. The various aggregation states of β-amyloid 1–42 mediate different effects on oxidative stress, neurodegeneration, and BACE-1 expression. Free Radic. Biol. Med 2006;41:202–212. [PubMed: 16814100]
30. Harkany T, et al. Mechanisms of β-amyloid neurotoxicity: perspectives of pharmacotherapy. Rev. Neurosci 2000;11:329–382. [PubMed: 11065280]
31. Yatin SM, et al. Temporal relations among amyloid β-peptide–induced free-radical oxidative stress, neuronal toxicity, and neuronal defensive responses. J. Mol. Neurosci 1998;11:183–197. [PubMed: 10344789]
32. Meyer-Luehmann M, et al. Rapid appearance and local toxicity of amyloid-β plaques in a mouse model of Alzheimer's disease. Nature 2008;451:720–724. [PubMed: 18256671]
33. Walsh DM, et al. The role of cell-derived oligomers of Aβ in Alzheimer's disease and avenues for therapeutic intervention. Biochem. Soc. Trans 2005;33:1087–1090. [PubMed: 16246051]
34. Link CD, et al. Gene expression analysis in a transgenic *Caenorhabditis elegans* Alzheimer's disease model. Neurobiol. Aging 2003;24:397–413. [PubMed: 12600716]
35. Ray S, et al. Classification and prediction of clinical Alzheimer's diagnosis based on plasma signaling proteins. Nat. Med 2007;13:1359–1362. [PubMed: 17934472]
36. Chishti MA, et al. Early-onset amyloid deposition and cognitive deficits in transgenic mice expressing a double mutant form of amyloid precursor protein 695. J. Biol. Chem 2001;276:21562–21570. [PubMed: 11279122]
37. Li F, et al. Increased plaque burden in brains of APP mutant MnSOD heterozygous knockout mice. J. Neurochem 2004;89:1308–1312. [PubMed: 15147524]
38. McConlogue L, et al. Partial reduction of BACE1 has dramatic effects on Alzheimer plaque and synaptic pathology in APP transgenic mice. J. Biol. Chem 2007;282:26326–26334. [PubMed: 17616527]
39. Zhong Z, et al. Levels of β-secretase (BACE1) in cerebrospinal fluid as a predictor of risk in mild cognitive impairment. Arch. Gen. Psychiatry 2007;64:718–726. [PubMed: 17548753]
40. Li Y, Zhou W, Tong Y, He G, Song W. Control of APP processing and Aβ generation level by BACE1 enzymatic activity and transcription. FASEB J 2006;20:285–292. [PubMed: 16449801]
41. Cirrito JR, et al. Synaptic activity regulates interstitial fluid amyloid-β levels in vivo. Neuron 2005;48:913–922. [PubMed: 16364896]

42. Emilsson L, Saetre P, Jazin E. Alzheimer's disease: mRNA expression profiles of multiple patients show alterations of genes involved with calcium signaling. Neurobiol. Dis 2006;21:618–625. [PubMed: 16257224]
43. Brooks WM, et al. Gene expression profiles of metabolic enzyme transcripts in Alzheimer's disease. Brain Res 2007;1127:127–135. [PubMed: 17109828]
44. Rossner S, Sastre M, Bourne K, Lichtenthaler SF. Transcriptional and translational regulation of BACE1 expression–implications for Alzheimer's disease. Prog. Neurobiol 2006;79:95–111. [PubMed: 16904810]
45. Holsinger RM, McLean CA, Beyreuther K, Masters CL, Evin G. Increased expression of the amyloid precursor β-secretase in Alzheimer's disease. Ann. Neurol 2002;51:783–786. [PubMed: 12112088]
46. Hsieh H, et al. AMPAR removal underlies Aβ-induced synaptic depression and dendritic spine loss. Neuron 2006;52:831–843. [PubMed: 17145504]
47. St Laurent G III, Wahlestedt C. Noncoding RNAs: couplers of analog and digital information in nervous system function? Trends Neurosci 2007;30:612–621. [PubMed: 17996312]
48. Vassar R. The β-secretase, BACE: a prime drug target for Alzheimer's disease. J. Mol. Neurosci 2001;17:157–170. [PubMed: 11816789]
49. Kumar P, et al. Transvascular delivery of small interfering RNA to the central nervous system. Nature 2007;448:39–43. [PubMed: 17572664]

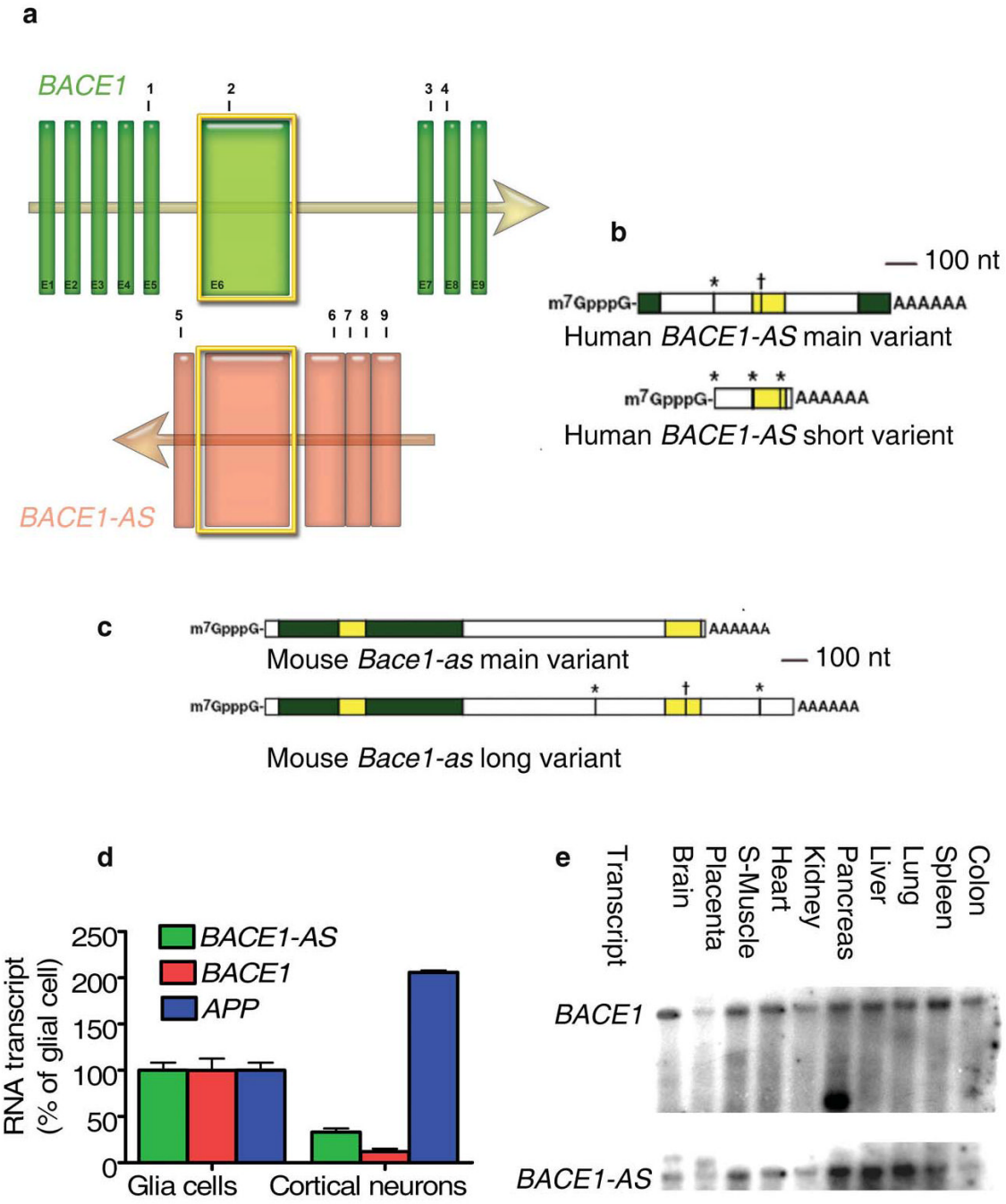

Figure 1.

Genomic organization and expression analysis of *BACE1* and *BACE1*-AS. (**a**) Genomic sequences of *BACE1* and *BACE1*-AS; arrows show the direction of transcription. *BACE1* exons are depicted as vertical bars and marked E1–E9. Human *BACE1*-AS is transcribed from the same region in chromosome 11, but on the opposite strand. Yellow highlighted exons are the overlapping region (104 base pairs) of *BACE1* and *BACE1*-AS, which are conserved across species. Sites numbered 1, 3 and 4 are *BACE1* siRNAs target sites, and site 2 is the northern blot probe site. Sites 5, 6 and 7 are the target sites of the *BACE1*-AS siRNAs and site 8 is the RT-PCR probe target region, which are all in the non-overlapping part of the *BACE1*-AS transcript. Sites 5 and 9 represent the primers for 3′ and 5′ RACE,

respectively. (**b**,**c**) RACE sequencing data revealed that *BACE1*-AS contains cap structure and a poly-A tail and that this transcript undergoes differential splicing in both human and mouse. The yellow highlighted segments are the overlap region to the *BACE1* sense transcript and the green highlighted segments are additional nucleotides observed from our sequencing data. Point mismatches to the genomic sequence are indicated by stars (*) for A to G and crosses (†) for C to T changes. Nt, nucleotides. (**d**) Expression of *BACE1*-AS, *BACE1* and *APP* mRNA in human cortical neurons (HCN1A) compared to glial cells (M059K). (**e**) Northern blot expression analysis of *BACE1* (top) and *BACE1*-AS (bottom) in ten human tissues. S-muscle, skeletal muscle

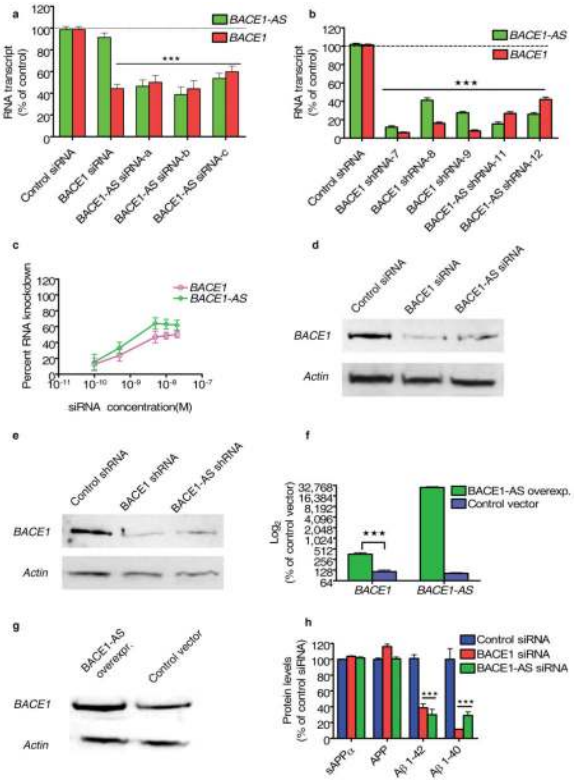

Figure 2.

BACE1-AS regulates *BACE1* mRNA and protein expression *in vitro*. (**a**) Targeting *BACE1*-AS transcript with three different siRNAs caused decreases ($P < 0.0001$) in both *BACE1* and *BACE1*-AS transcripts in neuroblastoma cells (SH-SY5Y). (**b**) Stable transfection of HEK293T cells with shRNA for *BACE1, BACE1*-AS and a control shRNA shows that knockdown of *BACE1* for an extended period of time leads to reduction of *BACE1*-AS and knockdown of *BACE1*-AS also leads to reduction of *BACE1* mRNA levels ($P < 0.001$). (**c**) HEK-SW cells were transfected with 100 pM, 500 pM, 5 nM, 10 nM or 20 nM *BACE1*-AS siRNA. *BACE1*-AS knockdown ranged from 10–60%, and *BACE1* downregulation ranged between 10–50% with increasing concentrations of siRNA. (**d**,**e**) Western blot showing that knockdown of either *BACE1* or *BACE1*-AS with siRNA or shRNA leads to reduction of the BACE1 protein. (**f**,**g**) Overexpression of *BACE1*-AS but not an empty control vector leads to increased *BACE1* mRNA ($P < 0.001$) and protein concentrations. (**h**) HEK-SW cells were transfected with siRNA for *BACE1, BACE1*-AS or a control siRNA and analyzed for Aβ 1–40, Aβ 1–42, sAPPα and total APP concentrations by ELISA. Aβ 1–40 and Aβ 1–42 abundance was reduced ($P < 0.0001$) after transfection of siRNA targeting of either *BACE1* or *BACE1*-AS. Total APP or sAPPα, an enzymatic product of α-secretase, were not changed.

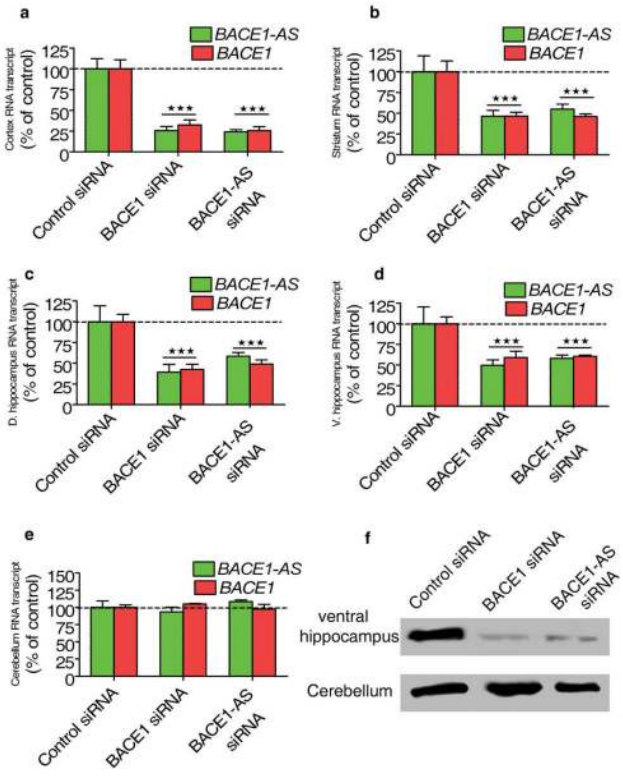

Figure 3.

Bace1-AS regulates *Bace1 in vivo*. (**a**–**e**) Synthetic unmodified siRNAs designed to target the nonoverlapping region of either *Bace1* or *Bace1*-AS and a control siRNA were constantly infused into three groups of mice over a period of two weeks. The siRNAs directed against either *Bace1* or *Bace1*-AS but not the control siRNA resulted in decrease in both *Bace1* and *Bace1*-AS levels ($P < 0.0001$) in cortex (**a**), striatum (**b**), dorsal hippocampus (**c**) and ventral hippocampus (**d**). In the cerebellum (**e**) both transcripts were unchanged, as expected for a tissue that is not directly connected to the third ventricle of the brain. (**f**) Western blot showing decreases of Bace1 protein abundance in the ventral hippocampus but not in the cerebellum after *in vivo* treatment with siRNA against either *Bace1* or *Bace1*-AS.

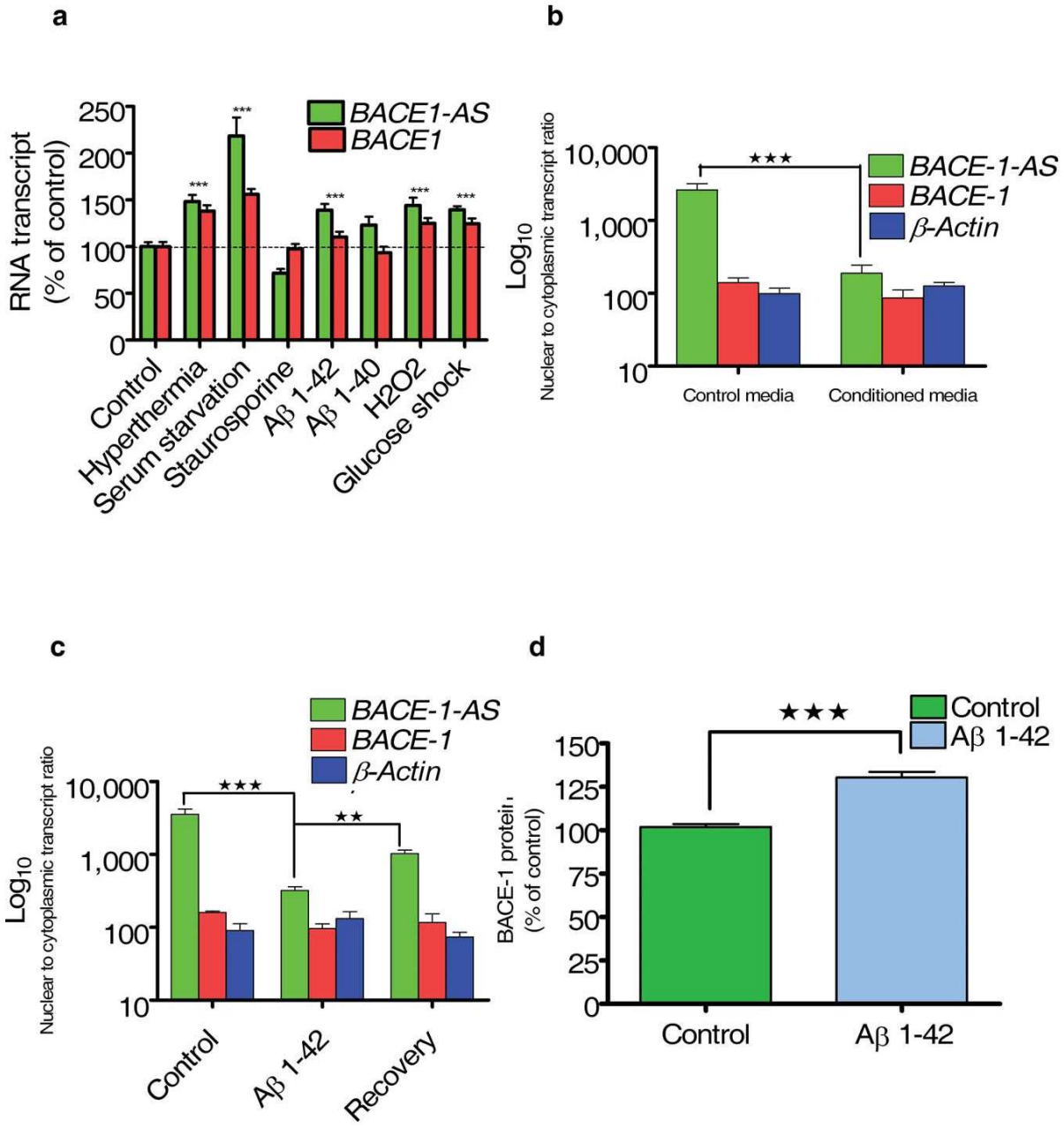

Figure 4.

Effect of cell stressors on *BACE1* and *BACE1*-AS. (**a**) HEK-SW cells were exposed to cell stressors. *BACE1*-AS and *BACE1* transcripts were measured by RT-PCR and normalized to *ACTB* as an endogenous control. Hyperthermia, serum starvation, Aβ 1–42, hydrogen peroxide or glucose shock caused elevation of *BACE1*-AS and, to a lesser degree, elevation of *BACE1* transcripts. Staurosporine or Aβ 1–40 did not increase either transcript level. (**b**) The 7PA2-CHO cells were previously shown to overproduce Aβ 1–42 dimers and oligomers. Conditioned media from these cells or control parental CHO cells were collected and added to SH-SY5Y cells for 2 h after removal of the regular media. Conditioned media from 7PA2-CHO cells, but not control media, caused the *BACE1*-AS transcript to relocate to the cytoplasm ($P < 0.0001$). (**c**) Exposure of SH-SY5Y cells to 1 μM Aβ 1–42 for 2 h caused an increase in cytoplasmic *BACE1*-AS ($P < 0.001$). The nuclear-cytoplasmic ratio was

recovered upon removal of the peptides and maintenance of the cells in regular media for 1 h. (**d**) Exposure to 1 μM Aβ 1–42 peptide caused an elevation in BACE1 protein abundance ($P < 0.001$). Protein amounts were measured with a β-galactosidase ECA.

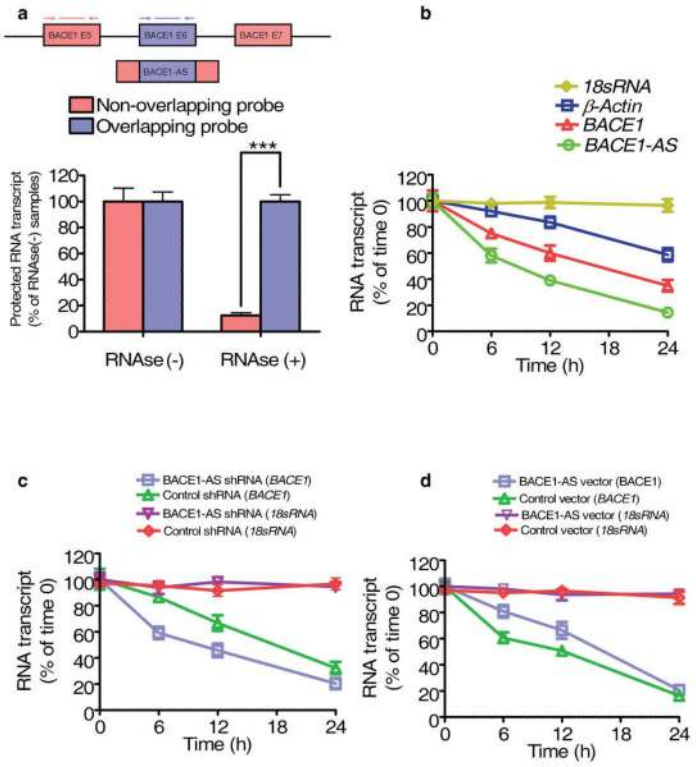

Figure 5.

BACE1-AS increases the stability of *BACE1* mRNA. (**a**) RPA performed on RNA samples from SH-SY5Y cells. Depicted here are RT-PCR results from two sets of primers and probes covering overlapping and nonoverlapping regions of *BACE1* mRNA. The overlapping region of *BACE1* transcript is protected from degradation by RNase A+T, suggesting RNA duplex formation. (**b**) Stability of *BACE1* and *BACE1*-AS transcripts over time was measured by RT-PCR relative to time 0 after blocking new RNA synthesis with α-amanitin (50 μM) in HEK293T cells. *BACE1*-AS showed a shorter half-life than *BACE1* and *ACTB*. *18s* RNA, which is a product of RNA polymerase I, was unchanged. (**c**) The stability of *BACE1* mRNA was measured in stably transfected HEK293T cells expressing a *BACE1*-AS shRNA and a second cell line expressing a negative control shRNA. The stability of *BACE1* mRNA was decreased in cells expressing *BACE1*-AS shRNA relative to the control cell line ($P < 0.01$). (**d**) The stability of *BACE1* mRNA increased in HEK293T cells overexpressing *BACE1*-AS in comparison to a cell line transfected with an empty vector.

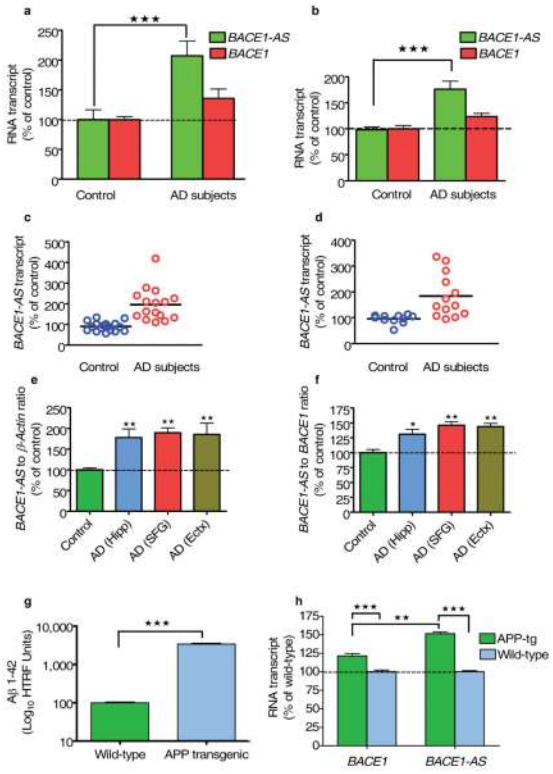

Figure 6.

BACE1-AS and *BACE1* expression is elevated in the brain of individuals with Alzheimer's disease. (**a**) The relative quantity of *BACE1*-AS transcript was elevated by two to three times in parietal cortex and cerebellum of five human subjects with Alzheimer's disease (AD subjects) ($P < 0.0001$) as compared to matched control individuals (20 RNA samples). To a lesser degree, *BACE1* mRNA was also increased, by approximately 30%. (**b**) The relative quantity of *BACE1*-AS transcript was elevated by almost twofold ($P < 0.0001$) and *BACE1* mRNA elevated about 30% in four brain regions (cerebellum, superior frontal gyrus, entorhinal cortex and hippocampus) of 35 individuals with Alzheimer's disease compared to the average of 35 control individuals (128 RNA samples in total). (**c**) Scatter plot of *BACE1*-AS transcript expression in superior frontal gyrus of 17 control subjects and 16 subjects with Alzheimer's disease. Upregulation ($P < 0.0001$) of *BACE1*-AS was observed in subjects with Alzheimer's disease. (**d**) Scatter plot of *BACE1*-AS transcript expression in hippocampus of 11 controls and 13 individuals with Alzheimer's disease. Upregulation ($P < 0.001$) of *BACE1*-AS was observed in the subjects with Alzheimer's disease. (**e**,**f**) *BACE1*-AS to *ACTB* ratio (**e**) and *BACE1*-AS to *BACE1* ratio (**f**) in hippocampus (Hipp), superior frontal gyrus (SFG), entorhinal cortex (Ectx) of subjects with Alzheimer's disease compared to control individuals. Both ratios are higher ($P < 0.001$) in subjects with Alzheimer's disease. (**g**) The concentrations of human Aβ 1–42 peptide are elevated in the brains of APP-tg19599 mice ($P < 0.0001$). (**h**) *Bace1*-AS is elevated by 50% ($P < 0.0001$) in whole brains of APP-tg19599 (APP-tg) mice.