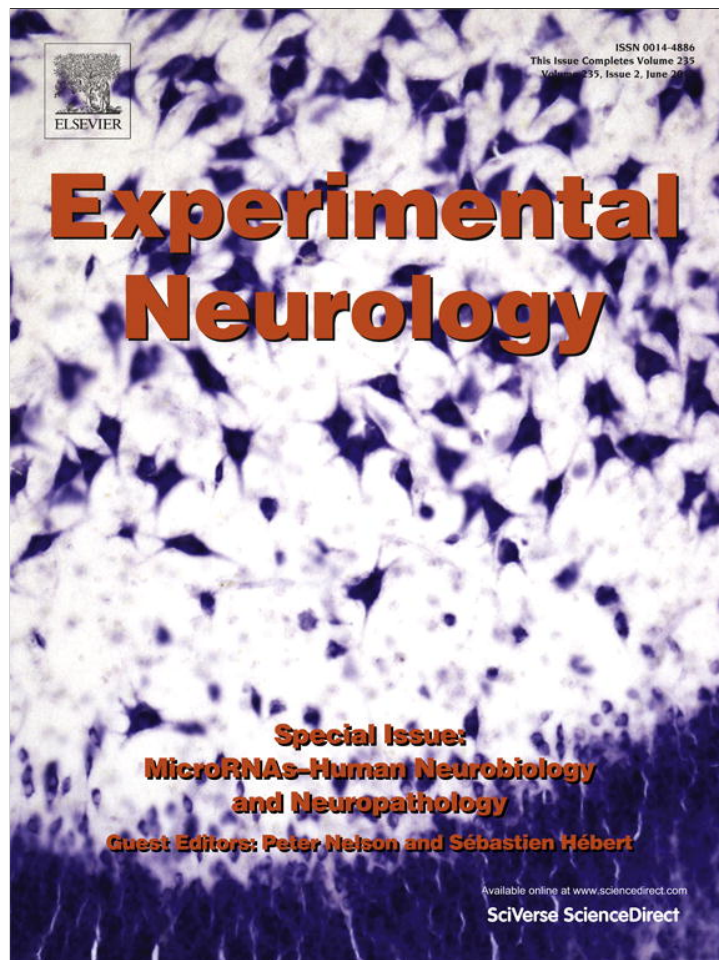




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Review

The search for endogenous siRNAs in the mammalian brain

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ABSTRACT

A decade ago, RNA interference was proposed to serve as a physiologic means of regulating long-term gene expression in the mammalian brain. However, during the intervening years, this hypothesis appeared to be contradicted by both experimental data and theoretical considerations. More recently, the advent of deep sequencing technology has permitted a re-assessment of this issue. As reviewed here, a large population of small RNAs having features characteristic of endogenous siRNAs are detected within adult mouse hippocampus, which derive from genes involved in synaptic structure and signaling, and which show a significant, though modest (16–22%) up-regulation during olfactory discrimination training. Small RNAs derived from abundant cellular noncoding RNAs are also detected; in particular, a subpopulation of RNAs 25–30 nt. in length shows very large (> 100 fold) up-regulation during olfactory discrimination training. Preliminary data suggest that the 25–30 nt. RNAs may associate with MIWI rather than Argonaute 1–4 homologues. I conclude that, despite their apparent low abundance, endogenous siRNAs and noncoding RNA-derived small RNAs are likely to play an important role in regulating synaptic plasticity.

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Introduction

The phenomenon of RNA interference (RNAi) was first noticed and analyzed in lower model organisms including plants, fungi and *Caenorhabditis elegans* (Baulcombe, 2003; Fire, 2006). Briefly,

double-stranded RNA (dsRNA, which can arise from diverse sources including transgenes, viruses, transposons, and cellular genes) is processed by the RNase III enzyme dicer to form ~22 nt. dsRNAs. One strand (called a small inhibitory RNA, or siRNA) is incorporated into RISC (a complex containing an Argonaute homolog and other proteins) which cleaves homologous RNAs in a sequence–sequence manner. This type of post-transcriptional gene silencing is extremely potent. In plants and *C. elegans*, at least, an individual siRNA can bind to RNAs and undergo primer extension using the enzyme RNA-dependent RNA polymerase (RdRP) to form additional long dsRNA molecules that are cleaved by dicer, thus creating a self-amplifying process. Moreover (again, at least in plants and *C. elegans*), gene silencing can be propagated from cell to cell, involving all of the cells

Abbreviations: Ago, Argonaute homologue protein; DGCR8, DiGeorge syndrome critical region gene 8; dsRNA, double-stranded RNA; ES cells, embryonic stem cells; miRNA, microRNA; MIWI, piwi1 (piwi-like homolog 1) in mouse; ncRNA, noncoding RNA; piRNA, piwi-interacting RNA; RdRP, RNA-dependent RNA polymerase; RISC, RNA induced silencing complex; RNAi, RNA interference; siRNA, small inhibitory RNA.

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of the body, including the germline (Fire et al., 1998). Finally, siRNAs can also silence genes via transcriptional interference (e.g. Grishok et al., 2005).

In 2001, we suggested that the features of RNA interference would be ideal as an endogenous mechanism for regulating long-term gene expression in the nervous system (Smalheiser et al., 2001). A scheme was proposed in which specific antisense transcripts are induced at the onset of learning, forming sense–antisense transcript hybrids that are processed to form siRNAs. In turn, the siRNAs would cause long-term silencing of the sense mRNAs encoding genes that regulate synaptic structure, function, and plasticity (e.g., NMDA and other glutamate receptors; PSD95 and other post-synaptic scaffold proteins; SynGAP1 and other signaling adaptor proteins; FMRP, HuD and other RNA-binding proteins; synapsin I, GAP43 and other presynaptic proteins; spinophilin and other actin-binding proteins; etc.). Although one might expect that learning would be associated with long-term gene activation (rather than silencing), many genes are known to be down-regulated during learning, and one can envision that genes involved in synaptic stability may need to be turned off in order for remodeling and growth to occur. At the time, it was not clear whether all of the features of RNAi seen in invertebrates should also be found in vertebrates – especially self-amplification and cell-to-cell silencing (see below). However, the RNAi machinery is clearly present within mammalian neurons, since when used as an experimental technique, both long exogenous dsRNAs and short siRNAs are effective for gene silencing (Yu et al., 2002; Krichevsky and Kosik, 2002).

So what happened to the idea that endogenous siRNAs regulate neuronal gene expression?

Our hypothesis paper appeared in April 2001. In October of the same year, a trio of papers were published in *Science* announcing the discovery of a large family of small RNAs, called microRNAs (miRNAs) (Lagos-Quintana et al., 2001; Lau et al., 2001; Lee and Ambros, 2001). MicroRNAs arise when primary miRNA gene transcripts (pri-miRs) are processed by a complex including drosha and DGCR8 proteins to form 70–100 nt. small miRNA hairpin precursors (pre-miRs); the pre-miRs are exported from the nucleus, processed further by dicer and its co-factors (TRBP and PACT), and incorporated into RISC. It became clear that hundreds of microRNAs are expressed in brain, and that some are brain-specific (or at least highly enriched) and developmentally regulated (Lagos-Quintana et al., 2002; Krichevsky et al., 2003). Subsequent studies have established microRNAs as major regulators of protein translation and mRNA stability with roles in cell fate, differentiation, and synaptic plasticity (Gao, 2010; Siegel et al., 2011). In contrast, numerous cloning studies that revealed abundant microRNAs failed to detect the expression of endogenous siRNAs in *C. elegans* or other animals.

More detailed sequencing analyses (Ambros et al., 2003; Ruby et al., 2006) suggested that endogenous siRNAs are indeed expressed in *C. elegans*, but had been under-detected because the usual cloning strategy added adaptors selectively to RNAs having 5′-monophosphate and 3′-hydroxyl groups (characteristic of RNase III products), whereas many of the endogenous siRNAs had modified 5′-ends (e.g., 5′-triphosphate groups are found on secondary siRNAs, characteristic of RdRP products) and/or had modified 3′-ends (e.g., 2-O-methyl groups). The putative targets of the siRNAs (i.e., the mRNAs of the host genes giving rise to the siRNAs) comprised specific functional categories (Lee et al., 2006; Asikainen et al., 2008) and appeared to modulate expression of the target mRNAs (Lee et al., 2006). The endogenous siRNA pathway impacts development, stress resistance and lifespan (Lucchetta et al., 2009; Lim et al., 2011).

Nevertheless, there were numerous objections raised to the idea that endogenous siRNAs should regulate gene expression in a physiologic manner, especially in mammals: first, the prevailing concept was (and still is) that endogenous siRNAs have the primal function

of fighting transposons and viruses (Fire, 2006). Second, the canonical RNA-dependent RNA polymerase enzyme, which is crucial for the self-amplifying nature of RNAi, has no gene homologue in mammals. Third, long double-stranded RNAs are potent stimulators of the interferon response, so apart from early embryonic cell types that lack this response (e.g., ES cells and oocytes), one would not expect long dsRNAs to be tolerated within cells. As Fire (2006) states, “We presume that once the RNAi mechanism is in place, cells would evolve very diligently to avoid producing dsRNA in amounts that would shut off important endogenous genes.”

These objections slowly evaporated, one by one, in the late 2000s: First, further cloning analyses of small RNAs, particularly using deep sequencing technology, revealed the widespread expression of endogenous siRNAs (as well as piRNAs and a variety of other small RNAs, see below) in *Drosophila* (Czech et al., 2008; Okamura et al., 2008; Kawamura et al., 2008; Lau et al., 2009). Endogenous siRNAs are dicer dependent, modified at their 3′-ends and associated with Argonaute proteins. They were detected as well in mouse cell types that lack an interferon response, namely, oocytes (Tam et al., 2008; Watanabe et al., 2008) and ES cells (Calabrese et al., 2007; Babiarz et al., 2008). Endogenous siRNAs do arise prominently from transposons and other repeat elements, but they also arise from regions known to transcribe both sense and antisense transcripts as well as from sequences having inverted repeat secondary structure (“hairpins”) within pseudogenes and protein-coding genes (reviewed in Golden et al., 2008; Ghildiyal and Zamore, 2009). Second, noncanonical RdRP enzymes were discovered in mammals (Maida et al., 2009). Third, numerous studies had shown that long dsRNA can be used for sequence-specific gene silencing even in cells capable of generating an interferon response (reviewed in Smalheiser et al., 2011a). Moreover, endogenously expressed dsRNAs differ from exogenous dsRNAs in many ways that might be distinguished by cells – in length, subcellular localization, 5′-end modifications, abundance, etc. (Wang and Carmichael, 2004; Schlee et al., 2006).

The first study to analyze small RNAs within a differentiated mammalian cell type was Kawaji et al. (2008), who examined the HepG2 liver cell line. They detected evidence for endogenous siRNAs that derive from loci expressing both sense and antisense transcripts (they were also the first to detect several novel classes of small RNAs derived from abundant noncoding RNAs, see below). Yi et al. (2009) detected low abundance endogenous siRNAs in developing skin, and confirmed that their expression is dependent on dicer but independent of DGCR8. Thus, the stage was set for carrying out deep sequencing of mammalian brain.

Sense–antisense transcript hybrids as a source of endogenous siRNAs

As mentioned above, there is strong circumstantial evidence that endogenous siRNAs are associated with mRNA loci known to express sense and antisense transcripts. However, an entirely different line of investigation has been concerned with whether sense and antisense transcripts are co-expressed within individual cells; whether (and where) they bind to each other to form double-stranded hybrids; and whether the hybrids are indeed processed by dicer to form endogenous siRNAs. Certainly, in the past decade, it has become well established that natural antisense transcripts are specifically induced in a number of physiologic and pathologic situations and regulate the expression of their sense counterparts (Faghihi et al., 2010; Werner and Swan, 2010). It has been demonstrated in numerous cases that sense–antisense hybrids can form within cells (e.g., Soldà et al., 2005; Faghihi et al., 2008). However, the relationship between antisense and sense transcript is not necessarily negative: often sense and antisense transcripts show a concordant, not discordant co-expression pattern, and hybrid formation sometimes has a stabilizing effect on the sense mRNA (e.g., Faghihi et al., 2008). It is likely that

hybrids are not efficiently processed by dicer in the cytoplasm under resting conditions (Carlile et al., 2008), although it is conceivable that RNAi may occur if dicer is activated or mobilized (Lugli et al., 2005). Numerous sense and antisense transcripts are co-expressed within isolated synaptic fractions in adult mouse forebrain (Smalheiser et al., 2008), some of which correspond to loci that give rise to small RNAs (see below).

On the other hand, sense–antisense transcript hybrids may be expected to form naturally within the nucleus. Several studies have demonstrated nuclear transport of Argonaute and other RNAi proteins as well as miRNAs and other small RNAs (e.g., Weinmann et al., 2009); indeed, RNAi is effective in silencing targets within the nucleus (e.g., Robb et al., 2005; Carlile et al., 2008), a compartment that is thought to be protected against eliciting the interferon response (Wang and Carmichael, 2004). Dicer, drosha and Ago are also involved in processing of pre-rRNAs, which is a nuclear event (Liang and Crooke, 2011). As discussed below, many novel small RNAs have been shown to derive from intronic elements and nuclear ncRNAs as well, suggesting that the nucleus may not be excluded, and may in fact be a preferred locus of small RNA biogenesis.

In summary, there is some evidence that endogenous siRNAs may arise from sense–antisense transcript hybrids, but it is unknown where this would occur within cells and it is not clear whether formation of the hybrids would automatically lead to their processing.

Endogenous siRNAs and noncoding RNA-derived small RNAs are expressed in adult mouse hippocampus and are up-regulated in olfactory discrimination training

To examine directly whether small RNAs having the characteristics of endogenous siRNAs could be detected within adult mouse hippocampus, we utilized tissue from mice that had been subjected to an olfactory discrimination training paradigm (Larson and Sieprawaska, 2002; Smalheiser et al., 2010). In this manner, we hoped to identify these and any other “interesting” small RNAs that showed large, specific changes with training (Smalheiser et al., 2011a).

Mice (male C57Bl/6 strain, 2 months of age) were first trained to execute nose-poke responses for water reinforcement in two 20-trial sessions per day. Mice were then randomly assigned to three experimental groups: the first group (“training”) received olfactory discrimination training. Mice were trained in a series of 20-trial sessions in which each trial began with the simultaneous presentation of two discriminative odors (S+ and S−) to the West sniff ports. The spatial position of the two odors on any given trial was randomly determined except that no more than three identical trials could occur in succession. A nose-poke response at the port carrying the S+ odor (l-carvone) terminated the trial, was scored as correct, and was rewarded with a drop of water; a response at the port carrying the S− odor (α-phellandrene) terminated the trial, was scored as incorrect, and was not rewarded. Each trial had a maximum duration of 60 s and was followed by a 10-s intertrial interval. The learning criterion was 14 or more correct trials in a 20-trial session, which is the earliest point at which learning differs significantly from random guessing at $p=0.05$. The second group (“pseudo-training”) received the same two odors and trial events as in the training group, except that rewards were not contingent upon responding at the correct odor port. A nose-poke response to either odor terminated the trial and was rewarded with a drop of water. Each mouse in the pseudo-training group was yoked to a mouse in the training group in terms of number of training sessions. The third group (“nose-poke”) simply continued nose-poke training and had no odors presented. Each mouse in this experiment was yoked to a mouse in the training group in terms of number of training sessions.

Hippocampal tissue from these mice had previously been measured individually with regard to microRNA expression using high throughput RT-PCR plates (Smalheiser et al., 2010). The most striking

finding was a global up-regulation of miRNA expression (by 9–12% across the population of miRNAs) that was observed in the training vs. pseudo-training comparison. As well, there was a reorganization of miRNA expression that was detected by identifying pairs of miRNAs that were highly correlated across individuals in the training group, but un-correlated among individuals in the pseudo-training or nose-poke groups (Smalheiser et al., 2010).

Total RNA from these mice were pooled such that each pool contained RNA from 3 to 4 mice of the same group, and each treatment group was represented by two pools. These samples were size-selected to obtain RNAs in the range of 18–30 nt., and adaptors were added using a strategy designed to selectively amplify RNase III products (i.e., RNAs having 5′-monophosphate groups and 3′-hydroxyl groups). cDNA libraries were made and sequenced on an Illumina Genome Analyzer II, giving 12–13 million raw sequence reads per pooled sample. We only analyzed sequences that aligned (“mapped”) exactly and uniquely to the reference mouse genome, and which mapped to exons or introns of Mouse Genome Informatics (MGI) annotated genes (consisting mostly of protein-coding genes). (Sequences that aligned to known miRNA genes were placed in a separate file and analyzed separately.)

In this fashion, we focused on putative endogenous siRNAs. However, note that this strategy may have under-detected a large proportion of endogenous siRNAs — namely, those that undergo RNA editing, those that derive from genomic repeat elements, and those which have 5′-triphosphate modifications (i.e. secondary siRNAs) or that have 3′ 2-O-methyl groups (which are characteristic of siRNAs in lower model organisms).

Across the filtered data set, a total of 65,516 unique RNA sequences were mapped uniquely and exactly to 14,583 known genes. These sequences exhibited a sharp peak in abundance at the 21- to 22-nt size class (Fig. 1), as expected for endogenous siRNAs. A 16% global elevation of expression with training was observed across all putative siRNAs (i.e., the population of 20–23 nt. small RNAs in the dataset), which was similar to that seen for the population of miRNAs as a whole (9–12%; Smalheiser et al., 2010, 2011a).

The mouse SynGAP1 locus gave rise to the most abundant set of siRNAs, about 50 unique sequences comprising several hundred counts in each sample, which mapped to both sides of an inverted repeat (“hairpin”) located within an intron (Fig. 2). This locus was actually somewhat complex, since both sense and antisense transcripts were detected in this region and both sense and antisense strands are predicted to fold separately into inverted repeats (Fig. 3) that are excellent substrates for dicer in vitro (Smalheiser et al., 2011a). Thus, a given small RNA processed at this locus will bind perfectly or near-perfectly to 4 different RNAs — the SynGAP1 pre-mRNA, the antisense transcript, the complementary small RNA arising from the sense hairpin, and the complementary small RNA arising from the antisense hairpin. This allows for quite sophisticated computation, since

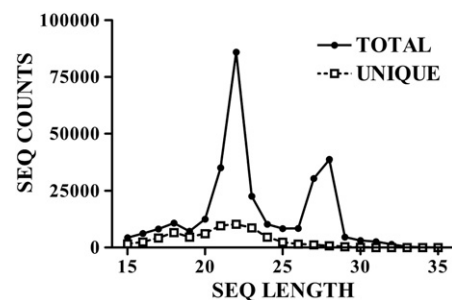


Fig. 1. Length distribution of small RNAs in the data set. Shown are the total number of sequence reads, and the total number of unique sequences, observed in the entire data set (across all samples and treatment groups). A more detailed breakdown of the data set is presented in Table 1.

All figures are reprinted from Smalheiser et al. (2011a) with permission.

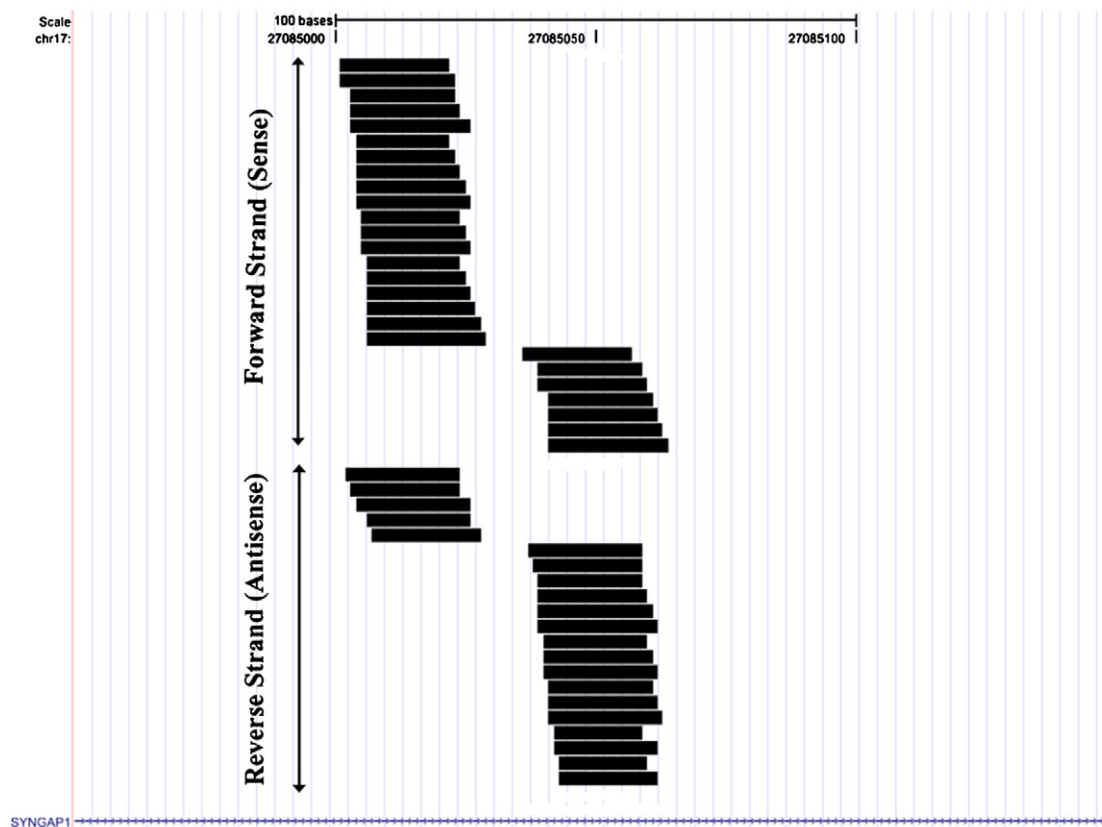


Fig. 2. Small RNAs aligned to the *SynGAP1* locus. Shown are all unique sequences that mapped to *SynGAP1*, including those that aligned to the forward or plus strand (placed on top) and to the reverse or minus strand (placed below the forward sequences).

the actions of a given small RNA may differ depending on the concentration of the sense and antisense RNAs, whether the sense and antisense RNA transcripts are present as hybrids, and the extent to which the transcripts have been processed to small RNAs. It has also not been excluded that a novel ncRNA may be present as an independent transcriptional unit within the *SynGAP1* intron.

The major *SynGAP1* siRNA is presumably involved in gene silencing since it is associated with Argonaute homolog proteins and FMRP (Fig. 4). The locus of siRNA biogenesis and action is still not entirely clear. Although the *SynGAP1* pre-mRNA is likely to be spliced predominantly within the nucleus, we have also detected transcripts in synaptic fractions containing the intronic inverted repeat (Lugli et al., in preparation), suggesting the possibility that a subset of *SynGAP1* mRNA containing retained introns may be transported into dendrites (Buckley et al., 2011) and processed by dicer (Lugli et al., 2005, 2008) to form *SynGAP1* siRNA locally in synapses.

A genome-wide examination of small RNAs that derive from inverted repeats revealed a total of eight gene loci (*Abca2*, *Arhgef17*, *Camk2a*, *Gap43*, *Rab40b*, *Slc17a7*, *Syn1*, and *SynGAP1*) that mapped to closely adjacent sites in sense orientation which were not annotated as being contained within ncRNAs or genomic repeats. Almost all (>99%) of the sequences mapping to these loci were 20–23 nt. in length. All of these mapped within introns, but they do not appear to represent intronic miRNAs, since the small RNAs did not map to ESTs or annotated transcripts of the size of pre-miRs, did not map to genomic regions that show high cross-species conservation between mouse and man, and did not map near any known miRNAs. Interestingly, half of the hairpin endo-siRNAs are major synaptic components and/or regulators of synaptic plasticity, including *SynGAP1*, *GAP43*, *CAMK2a*, and *synapsin I*, and several are regulators of signaling (*Arhgef17*, *Rab40b*, *Slc17a7*). When the set of hairpin endo-siRNAs (*Abca2*, *Arhgef17*, *Camk2a*, *Gap43*, *Rab40b*, *Slc17a7*, *Syn1*, and

SynGAP1) was pooled and tested as a group, a 22% increase was observed in the training vs. pseudo-training comparison that was highly significant ($P = 0.00012$); the pseudo-training and nose-poke control groups were not significantly different from each other.

We then looked for small RNAs that mapped to overlapping regions on both sense and antisense strands. One prominent example was found: more than fifty unique sequences mapped to *Ctnna2* (catenin [cadherin associated protein], $\alpha 2$) in both sense and antisense orientations (eight to 13 sequences were detected in each sample). The majority of these mapped to the *Lrrtm1* gene, which is encoded on the plus strand and lies entirely within an intron of *Ctnna2* encoded on the minus strand. Most importantly, 11 distinct sense and antisense sequences overlapped each other extensively, exhibited overhangs of 0–3 nt., and were co-expressed in three of the samples (Fig. 5). The *LRRTM* gene family (Laurén et al., 2003) has been identified as having roles as synaptic organizers (Linhoff et al., 2009), and *Lrrtm1* is a candidate gene for schizophrenia (Francks et al., 2007). Similarly, *Ctnna2* is a candidate gene for schizophrenia (Mexal et al., 2008) and α -N-catenin protein has been described as participating in the stabilization of dendritic spines in rodent hippocampal neurons (Abe et al., 2004).

Besides this “smoking gun”, many other small RNAs aligned to both strands of loci known to express both sense and antisense transcripts, including *Bdnf* and many of the loci reported in Smalheiser et al. (2008), such as beta-site APP cleaving enzyme (*Bace1*), sirtuin 3, *SNAP25*, *integrin-linked kinase*, and *activating transcription factor 5*.

Other small RNAs expressed within hippocampus

As expected, deep sequencing of the hippocampus revealed a wide variety of microRNAs and their variants (RNA editing variants, 5'-end and 3'-end variants, miR* sequences, offset miRNAs, antisense

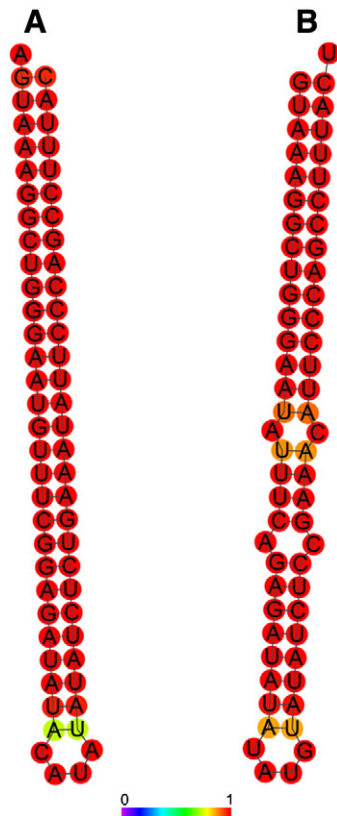


Fig. 3. Predicted secondary structure of RNA corresponding to the region within the *SynGAP1* locus that aligns with small RNAs. (A) The RNA encoded on the forward strand in the region covered by small RNAs (see Fig. 2) is predicted to form a perfect hairpin inverted repeat. (B) RNA encoded on the reverse strand forms an almost-perfect hairpin as well. Colors indicate the probability of base-pairing at each particular residue.

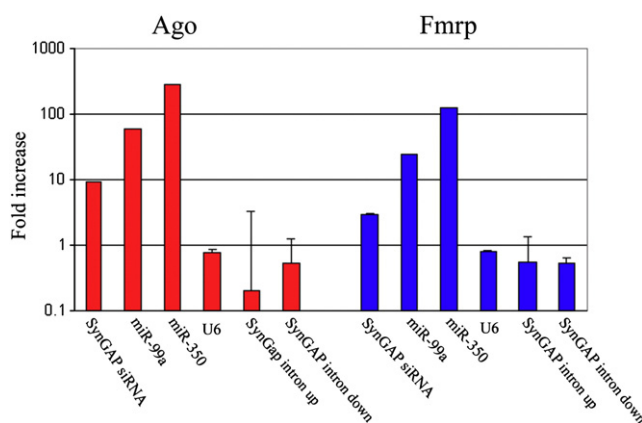


Fig. 4. Co-immunoprecipitation of *SynGAP1* siRNA with Argonaute homolog proteins and FMRP. The adult mouse forebrain S1 supernatants were immunoprecipitated using equal amounts of 4F9 anti-Ago antibody, anti-Fmrp antibody, or an irrelevant antibody against synapsin I. Equal fractions of the immunoprecipitates were measured for RNA content by qPCR as described in Smalheiser et al., 2011a. Each experiment was carried out on duplicate samples (error bars, SDs across duplicate samples), and each sample was assayed in duplicate. For each RNA, we plotted the ratio of the RNA abundance detected in the 4F9 or Fmrp immunoprecipitates relative to the synapsin I immunoprecipitates. *SynGAP1* siRNA binding to 4F9 was impressively almost 10 times above baseline, although not quite as enriched as several miRNAs (miR-99a and miR-350). In contrast, U6 RNA did not show any specific binding nor did *SynGAP1* intronic sequences derived from the sense strand just upstream or downstream from the intronic hairpin that gives rise to the siRNA. *SynGAP1* and miRNAs also showed detectable binding to Fmrp, which in brain is a RISC-associated protein (e.g., Lugli et al., 2005; data not shown).

miRNAs, etc.). We also detected many mirtrons (pre-miRs that are processed by splicing-out and trimming from short introns without the action of drosha, followed by dicer processing into small RNAs) (Berezikov et al., 2007). A few sequences were hard to classify; for example, a set of small RNAs was derived from the protein-coding region of *DGCR8* in sense orientation (Smalheiser et al., 2011a). Small RNAs were also detected arising from specific sites within abundant cellular noncoding RNAs including snoRNAs (C/D box and H/ACA box), 28S rRNA, 18S rRNA, Y1 RNA, Rmrp (Smalheiser et al., 2011a) as well as certain tRNAs and a mitochondrial noncoding transcript (Smalheiser et al., 2011b) [this list would likely be even longer if we had not excluded RNAs that align to multiple sites in the genome, since many ncRNAs are represented by multiple gene copies]. Some of the noncoding RNAs (e.g., Y1 RNA) fold into classical double-stranded regions that would be expected to be good dicer substrates, whereas others (e.g., most snoRNAs) show atypical precursor secondary structures. Nonetheless, others have shown that at least some of these noncoding RNA-derived small RNAs are formed in a dicer-dependent manner (e.g., Cole et al., 2009; Taft et al., 2009) and independent of drosha or *DGCR8* (e.g., Babiarz et al., 2011).

Unexpectedly, we observed that small RNAs deriving from mirtrons and cellular noncoding RNAs were expressed in a range of sizes. Sequences in the 20–23 nt. range were constitutively expressed in all treatment groups, showing only modest elevations with training as described for siRNA-like small RNAs. In contrast, longer sequences in the 25–30 nt. range were observed predominantly in the training group. These 25–30 nt. sequences shared the same precise 5′-end as the 20–23 nt. sequences, but had variable 3′-ends. Strikingly, the 25–30 nt. small RNAs as a class showed little expression in the pseudo-training or nose-poke groups and exhibited up to 100–200 fold elevations in the training group (Table 1). Neither putative siRNAs nor most microRNAs had associated sequences in the 25–30 nt. size range; thus, this phenomenon was restricted to small RNAs deriving from mirtrons and noncoding RNAs (Smalheiser et al., 2011a).

Recently, Lee et al. (2011) reported the existence of a subset of piRNAs that are expressed in hippocampus, which arise from unique genomic loci and which associate with the Argonaute homologue MIWI. These “piRNAs” actually derive from known noncoding RNAs and were included in our dataset – for example, the four most abundant sequences described in this study (DQ541777, DQ705026, DQ555094 and DQ719597) align to a Y1 RNA, a snoRNA, a rRNA, and a snoRNA, respectively. In our dataset, the piRNA sequences are overlapped by a variety of small RNA sequences ranging from 18 to over 30 nt., and as described above, those in the >25 nt. size range show large elevations in the training group (see Supplement 1 in Smalheiser et al., 2011a). Interestingly, Lee et al. (2011) showed that DQ541777 and MIWI are expressed within dendrites, and functional blockade of the piRNA in cultured hippocampal neurons affected dendritic spine area. This suggests that the 25–30 nt. size class of training-induced small RNAs may have functional effects within dendrites, but may differ from endogenous siRNAs, miRNAs and ncRNA-derived 20–23 nt. small RNAs in that they are associated with a different type of Argonaute family homologue (MIWI instead of Ago).

There are, indeed, many similarities between endogenous siRNAs and piRNAs in terms of being associated with Argonaute family homologues, sharing 3′ modifications, and forming a silencing complex that can target both repeat elements and cellular genes. However, it is important to distinguish the population of “piRNAs” that derive from abundant ncRNAs from the better characterized population of piRNAs, identified first in testes, which also have recently been detected and characterized within many other tissues including macaque monkey cortex (Yan et al., 2011). Typical piRNAs arise mainly from intergenic loci and show a very strong tendency (~80%) to have a U residue at the 5′-end; many of the sequences form by the so-called ping-pong pathway involving both MIWI and MILL. In contrast, only 24% of the ncRNA-derived piRNAs (27–28 nt.) detected in our

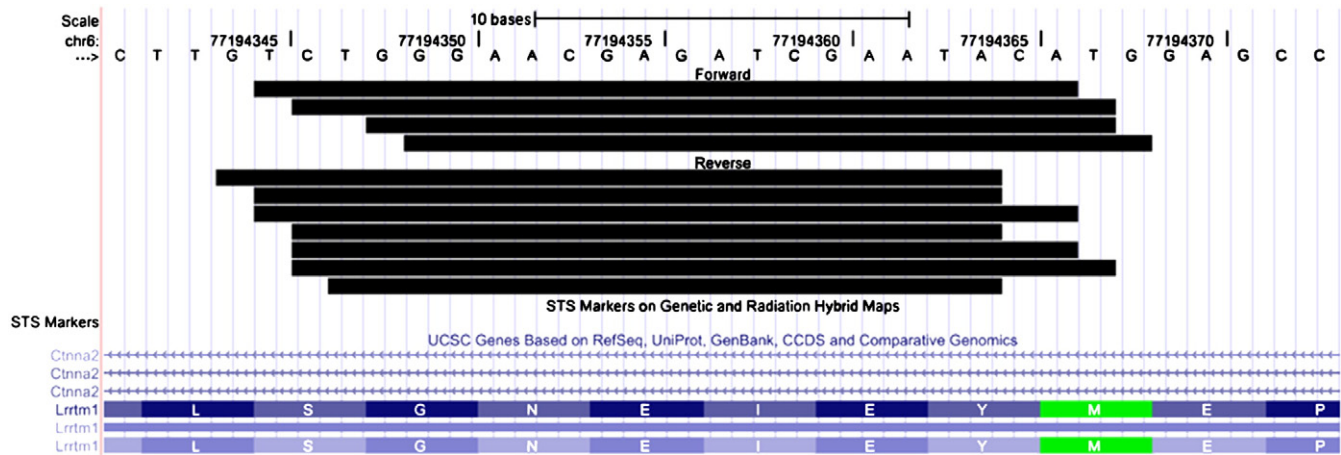


Fig. 5. Small RNAs aligned to the *Ctnna2* locus that putatively arise from processing of sense–antisense RNA hybrids. Multiple sequences align to a region of the *Ctnna2* gene that also encodes the *Lrrtm1* locus on the opposite strand. The small RNAs shown here align to both forward and reverse strands and exhibit a high degree of overlap.

mouse forebrain dataset expressed 5' U residues (Smalheiser et al., 2011a, supplementary data).

In contrast to the results of Smalheiser et al. (2011a) which examined B57Bl/6 mice at P60 or greater, Babiarz et al. (2011) did not detect significant expression of endogenous siRNAs in their study of P21 mouse hippocampus, although they did detect mirtrons and snoRNA-derived small RNAs and demonstrated that those RNA classes were DGCR8-independent/dicer-dependent. The reason for this discrepancy is unknown, although differences in RNA isolation methods, mouse age and strain, or different methods of sequence filtering and analysis may be involved.

Discussion. Where are we now?

Deep sequencing of adult mouse hippocampus has revealed a large population of small RNAs having characteristics of endogenous siRNAs. Moreover, the examples having the best documentation are derived from genes involved with synaptic proteins or signaling. Thus, these observations support our original hypothesis that RNA interference may regulate long-term gene expression in the brain. However, we have not yet proven that siRNAs arise from dicer processing of sense–antisense transcript hybrids and intronic hairpins in vivo.

Moreover, we did not originally anticipate that small RNAs would also be processed from abundant cellular noncoding RNAs, nor that longer 25–30 nt. RNA species would be formed specifically during training. In fact, the dramatic ~100-fold up-regulation of the 25–30

nt. small RNAs is much more striking and selective than the modest 10–20% increase that is observed in the 20–23 nt. siRNA/miRNA classes. (We are currently attempting to verify that this apparent increase in abundance is, indeed, due to an actual increase in sequence counts rather than to a selective, learning-specific loss of 3'-modifications which might cause more efficient detection in the deep sequencing pipeline.) The available evidence suggests that the siRNAs associate with Ago whereas the 25–30 nt. RNAs may associate with MIWI. Moreover, there is circumstantial evidence that at least some of the siRNAs and 25–30 nt. RNAs may be processed locally within dendrites, where they may regulate specific targets.

These findings suggest that endogenous siRNAs and ncRNA-derived small RNAs might be major regulators of synaptic plasticity and learning. The relatively low expression of siRNAs in deep sequencing studies should not be interpreted to mean that they are functionally unimportant – at least, not until further studies can be carried out to learn whether deep sequencing assays under-detect the class of siRNAs because they carry specific 5'- and/or 3'-end modifications (McCormick et al., 2011). As well, siRNAs are expected to be much more potent than miRNAs because they bind perfectly to their targets, so their levels should not (perhaps even *must* not) be as high as the high abundance miRNAs.

Small RNAs are currently thought to be associated with an Argonaute homologue that targets other RNAs to regulate their translation and/or stability. Unlike the case of miRNAs, which have multiple targets of relatively low affinity, siRNAs should silence one or a small number of perfect targets, though they probably show miRNA-like targeting of *trans* targets as well (Song et al., 2011). However, we know little about how (or where in the cell) small RNAs may function in the context of synaptic plasticity. For example, it is not clear whether siRNAs in mammalian brain utilize noncanonical RdRP enzymes to form secondary siRNAs, which may be expected to have long-lasting or self-amplifying effects. Besides the direct interactions of small RNAs with target RNAs, different classes of small RNAs might potentially compete with the entire population of miRNAs for binding to RISC (cf. Khan et al., 2009; Haussecker et al., 2010). In the nucleus, it is possible that small RNAs may have either enhancing or inhibitory effects on gene transcription in an Ago-dependent manner (Chu et al., 2010), or may control alternative splicing (Alló et al., 2009). At least in plants, yeast and *C. elegans*, siRNAs regulate DNA methylation of specific genes and heterochromatin domains, and there is increasing evidence that this may occur in mammals as well (Palanichamy et al., 2010).

It is also likely that small RNAs not only affect the translation of specific targets, but also have general effects on the protein synthesis machinery. For example, most of the noncoding RNAs that give rise to

Table 1

All RNAs in the dataset, divided by size class and treatment group. Reprinted from Smalheiser et al. (2011a) with permission.

Length	Group	Unique seq	Seq counts	p-value
15–17	Nose-poke	8244	2744.57	7.25E–08**
15–17	Pseudo-training	8244	2052.58	
15–17	Training	8244	1778.35	0.0069**
20–23	Nose-poke	34,801	14,820.52	0.0036**
20–23	Pseudo-training	34,801	20,440.43	
20–23	Training	34,801	23,633.06	4.59E–07**
25–30	Nose-poke	6410	703.23	0.436
25–30	Pseudo-training	6410	666.31	
25–30	Training	6410	43,269.34	7.99E–07**
31–35	Nose-poke	219	19.5	2.20E–05**
31–35	Pseudo-training	219	59.62	
31–35	Training	219	2153.03	0.017*

Shown are the total number of unique sequences and total number of normalized sequence counts in each size class for each treatment group. Training and nose-poke groups are each compared to the pseudo-training control group.

** p<0.01 by t-test.

* p<0.05 by t-test.

small RNAs are involved in protein synthesis and are induced during plasticity by stimulation of the mTOR pathway (Smalheiser et al., 2011a). Processing of pre-rRNAs has been shown to be dependent on drosha, dicer and Ago (Liang and Crooke, 2011). Thus, one function for the induction of ncRNA-derived small RNAs may be to support long-term protein synthesis and cellular growth following synaptic stimulation.

Conclusions. Where are we going?

The research agenda for the next few years is simple: perturb individual endogenous siRNAs and related small RNAs in neural systems, and learn how they regulate the expression of their target genes, as well as the read-out of neural development, synaptic plasticity, and behavior. As is the case with many of the miRNAs, individual siRNAs are likely to confer robustness on gene networks and their functions may be most apparent when organisms are subjected to environmental stressors (cf. Lucchetta et al., 2009).

To date, gene mapping and association studies in neuropsychiatric diseases have focused largely on exons of protein-coding genes, although several studies have sought to identify SNPs that occur in miRNAs and miRNA target sites. It will be important to confirm that endogenous siRNAs are expressed in human brain and to examine whether loci that are processed to form endogenous siRNAs and other small RNAs correlate with susceptibility to neuropsychiatric diseases.

Endogenous siRNAs are only one part of a larger revolution in our understanding of genomics. The number of genes encoding noncoding RNAs is now known to be ~4 times as great as the number of protein-coding genes in the human genome. Bidirectional transcription at promoters is now appreciated as the rule rather than the exception, and natural antisense transcripts are now known to be common regulators of protein-coding genes. MiRNAs, the best understood class of small RNAs, can arise from at least three different pathways of biogenesis in mammals (drosha dependent, drosha-independent mirtrons and Ago dependent). Besides endogenous siRNAs derived from protein-coding genes and those derived from abundant cellular noncoding RNAs, there are piRNAs (of several types), promoter-associated RNAs, splice-site RNAs, tRNA-derived small RNAs, vault-derived small RNAs, 3'-UTR derived small RNAs, transposon-derived small RNAs, centrosomal repeat RNAs, and so on. The implications of this revolution for neuroscience have only begun to be explored (Mercer et al., 2008; Mattick, 2011).

Finally, endogenous siRNAs may relate to three emerging new concepts that are likely to become prominent themes in neuroscience over the coming decade:

First, there is increasing recognition that genomic repeat elements (transposons and “junk” DNA) have physiologic roles in regulating normal gene expression, and that they may be major driving forces in evolution, including evolution of the human brain (Britten, 2010; Mattick, 2011). Genomic repeat elements can be a source of novel microRNA genes (Smalheiser and Torvik, 2005) as well as a source of miRNA target sites within mRNAs (Smalheiser and Torvik, 2006). Genomic repeats may act in real time within the life of an organism as well: transposition of LINE1 elements has been shown to occur within individual precursors of mammalian CNS neurons (Muotri et al., 2010), and cellular stresses cause the rapid, transient expression of Alu-containing transcripts (Liu et al., 1995). Although this review has emphasized the importance of endogenous siRNAs that target neuronal genes, in fact, the majority of endogenous siRNAs within cells are thought to target genomic repeats (Golden et al., 2008; Gildiyal and Zamore, 2009). Thus, endogenous siRNAs may be an integral part of gene networks that involve genomic repeats. Conditional dicer knockouts in mice

have produced neurodegeneration in several types of neurons, which has been assumed to reflect loss of miRNAs (e.g., Schaefer et al., 2007; Hébert et al., 2010). However, Kaneko et al. (2011) have shown that dicer knockout induced degeneration in retinal pigmented epithelial cells is actually due to accumulation of toxic Alu-containing transcripts, which are normally destroyed by direct dicer cleavage and/or by siRNAs arising from such cleavage.

Second, there is increasing awareness that cross-species conservation is not the only hallmark of functional transcripts. In fact, a large number of miRNAs and long ncRNAs are specific to the human lineage. Within the human genome, intronic inverted repeats are highly enriched in genes involved in synaptic functions (Wang and Leung, 2009), suggesting that many hairpin-derived endogenous siRNAs are likely to be human specific as well.

Third, there is extensive evidence for intercellular RNA transfer not only in lower model organisms (plants and *C. elegans*), but also in mammals: specifically, cells in the immune system can transfer miRNAs, mRNAs and other RNAs among themselves via exosomes and microvesicles (e.g., Théry et al., 2009) both at a distance as well as by local contact (Mittelbrunn et al., 2011). Since neurons and glial cells release exosomes which can have functional effects on recipient cells (e.g., Lachenal et al., 2011; Wang et al., 2011), it is likely that intercellular RNA transfer occurs within the nervous system as well (reviewed in Smalheiser, 2007). Thus, a small RNA made in one cell may have its functional target located in a different cell. Deep sequencing of glioblastoma microvesicles has revealed the existence of many different types of RNAs besides miRNAs, including high concentrations of genomic repeat (Alu and LINE1) containing transcripts (Balaj et al., 2011), suggesting that endogenous siRNAs may also participate in the regulation of intercellular RNA transfer.

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