Strand antagonism in RNAi: an explanation of differences in potency between intracellularly expressed siRNA and shRNA

Xin Jin, Tingting Sun, Chuanke Zhao, Yongxiang Zheng, Yufan Zhang, Weijing Cai, Qiuchen He, Kaz Taira, Lihe Zhang and Demin Zhou*

State Key Laboratory of Natural and Biomimetic Drugs, School of Pharmaceutical Sciences, Peking University, Beijing 100191, China

Received June 1, 2010; Revised and Accepted October 10, 2011

ABSTRACT

Strategies to regulate gene function frequently use small interfering RNAs (siRNAs) that can be made from their shRNA precursors via Dicer. However, when the duplex components of these siRNA effectors are expressed from their respective coding genes, the RNA interference (RNAi) activity is much reduced. Here, we explored the mechanisms of action of shRNA and siRNA and found the expressed siRNA, in contrast to short hairpin RNA (shRNA), exhibits strong strand antagonism, with the sense RNA negatively and unexpectedly regulating RNAi. Therefore, we altered the relative levels of strands of siRNA duplexes during their expression, increasing the level of the antisense component, reducing the level of the sense component, or both and, in this way we were able to enhance the potency of the siRNA. Such vector-delivered siRNA attacked its target effectively. These findings provide new insight into RNAi and, in particular, they demonstrate that strand antagonism is responsible for making siRNA far less potent than shRNA.

INTRODUCTION

RNA interference (RNAi) is an RNA-dependent gene-silencing phenomenon and is initiated by ∼20-bp double-stranded RNA in the cytoplasm (1–3). The trigger for RNAi can be exogenous, for example, a synthetic small interfering RNA (siRNA), or endogenous, for example, a pre-micro RNA (miRNA)-like shRNA or siRNA that is expressed from its respective gene within the cell (4–9). Endogenous short hairpin RNA (shRNA) and siRNA are transcribed in the nucleus and must be exported to the cytoplasm, where the characteristic stem–loop of shRNA is cleaved by Dicer (10,11). The pathways involving siRNA and its shRNA precursor converge at RNA-induced silencing complex (RISC), with subsequent removal of the sense strand from the siRNA duplex, presumably cleaved first and then degraded, so that the antisense strand within RISC can recognize sequence-homologous RNAs and mediate target specificity (Figure 1). The recruited RNA is cleaved and degraded without any effect on the antisense strand, such that the antisense-programmed RISC is able to identify and degrade multiple copies of the target RNA (1,12).

The selective and robust effect of RNAi on gene expression both in cell culture and in living organisms makes it a valuable research tool (10). Compared to exogenous siRNA, endogenous shRNA or siRNA, expressed via a plasmid or a viral vector, has enormous advantages in terms both of costless regeneration and long-term gene silencing (4–7,13–15). siRNA is generated via concomitant transcription of the integral sense and antisense strand from the respective coding sequences, which can be either a tandem or a convergent cassette (Figure 1); the latter system holds further promise for the construction of siRNA libraries for reasons both of convenience and of template stability (6–8). shRNA is transcribed from its unique template (16–19), a long and inverted-repeat DNA sequence (palindrome), and then it is translocated to the cytoplasm, where the hairpin loop is deleted to generate siRNA.

The broad applicability of shRNA renders it very attractive as a strong and versatile silencer of various genes both via transient transfection and via stable transduction (4,5,13–15). By contrast, expressed siRNA, even though it is the actual trigger and, theoretically, should be more efficient, is far less potent than its shRNA precursor (6–9). To date and to our knowledge, expressed siRNA delivered...
by viral vectors has never been shown to silence any target gene with useful efficiency. This problem remains a challenge to those researchers in the RNAi field and, especially to those who are using lentiviral siRNA and corresponding libraries for as potential biological and therapeutic tools (8).

The sequences of expressed siRNA and its shRNA precursor in this study are identical except a loop that links the sense and antisense duplexes in the latter case (Figure 1). Many potential factors, either related or unrelated to this loop, might reduce the potency of siRNA, such as poor transcription, due to potential interference between opposing promoters; poor nucleo-cytoplasmic translocation; and/or poor incorporation into RISC due to the absence of the loop. All these possibilities remain to be explored. Recently, Berkhout group has tested the impact of different hairpin loop sequences, varying in size and structure, and found that the nature of a shRNA has a rather major impact on the shRNA activity (20). In this report, we provide evidence to suggest yet another possibility, namely, that sense strand-mediated strand antagonism attenuates the potency of expressed siRNA. Moreover, we show that reduction of this negative effect via alterations in the relative levels of strands of siRNA duplexes during their generation significantly enhances the potency of siRNA, in particular, in cases of stable transduction. Our findings provide new insight into the pathway of RNAi and should help us to develop strategies for exploiting expressed siRNA as a more efficient tool in the future.

**MATERIALS AND METHODS**

**Construction of various shRNA- and siRNA-expression cassettes**

We constructed shRNA and siRNA, two p53-targeting siRNA-expression cassettes, by PCR ligation as described previously (21,22). We also constructed shRNA(0), siRNA(0), siRNA(O) and siRNA(O2), four shRNA- or siRNA-expression cassettes with one or two inducible U6 promoters (Figure 2a), by the same method. Additional four inducible siRNA expression cassettes targeting firefly luciferase were also constructed with the siRNA sequence as gtgcgctgctggtgccaaccc. We utilized a similar approach for construction of siRNA-antisense, siRNA-sense, shRNA-sense and shRNA-antisense, four siRNA- or shRNA-expression cassettes that allowed an additional antisense or sense strand to be generated, and hU6/U6-siRNA-mU6/U6, hU6/U6/O-siRNA-mU6/U6, hU6-siRNA-mU6/U6, hU6/O-siRNA-mU6/U6 and hU6-siRNA-O/mU6/U6, five siRNA-expression cassettes with one or two chimeric promoters. pSD31 was a lentivector...
derived from pHIV-7 that was used for transfection and transduction of siRNA, as reported previously (22).

Cell culture, transient transfection, stable transduction and packaging and titration of the lentivector

The mammalian cells used for most of this study were 293FT cells, cultured in Dulbecco’s modified Eagle’s medium supplemented with 10% fetal calf serum. The experimental protocols for expression of siRNA via transient transfection and stable transduction have been described previously (8,22). Experiments involving lentiviral packaging were performed by standard protocols (Invitrogen, San Diego, CA, USA). In brief, sub-confluent 293FT packaging cells were co-transfected with 20 \( \mu \)g of a recombinant lenti-plasmid, 15 \( \mu \)g of pcMV-DR8.91 and 5 \( \mu \)g of pMD2G-VSVG by calcium phosphate precipitation. Viral vectors were harvested 3 days after transfection. After filtration, the titer of the suspension of vector was determined as described by ‘Invitrogen’s’ protocol.

Western blotting analysis

Cells were washed with phosphate-buffered saline (PBS) buffer, lysed in lysis buffer for 5 min and passed through a 27-gauge needle. Lysates were cleared by centrifugation at 12,000g for 1 min, and the concentration of protein was determined with a protein assay kit from Bio-Rad with bovine serum albumin (BSA) as standard. Equal amounts of protein were fractionated by sodium dodecyl sulfate–polyacrylamide gel electrophoresis (SDS-PAGE; 4–20% polyacrylamide) before transfer to nitrocellulose membranes. Membranes were blocked with 3% BSA in TBST (10 mM Tris–HCl, pH 7.5, 150 mM NaCl, 0.1% Tween 20) for 1 h at room temperature. Primary and secondary antibodies were used according to the manufacturer’s instructions, with detection with an enhanced chemiluminescence kit (Amersham Biosciences, Piscataway, NJ, USA).

Quantitation of mRNA, expressed siRNA duplexes and shRNA by real-time reverse transcriptase-polymerase chain reaction (RT-PCR)

Total RNA was prepared from 293FT cells in TRIzol® reagents (Invitrogen, San Diego, CA, USA). Nuclear and cytoplasmic RNA were isolated as described previously (23). Standard quantitative real-time reverse transcriptase-polymerase chain reaction (RT-PCR) was performed to determine levels of expression of p53 mRNA, as described previously (22,24). Quantitative analysis of expressed siRNA duplexes and shRNA in transfected or transduced cells by real-time RT-PCR was based on methods developed by others groups (25–27). In brief, 1 \( \mu \)g of total RNA was polyadenylated by poly(A) polymerase plus adenosine triphosphate (ATP) at 37°C for 1 h in a 20-\( \mu \)l reaction mixture. After phenol-chloroform extraction and ethanol precipitation, the RNA was dissolved in diethylpyrocarbonate (DEPC)-treated water and reverse-transcribed with 200 U of SuperScript™ II reverse transcriptase (Invitrogen, San Diego, CA, USA) and 0.5 \( \mu \)g of poly(T) adapter according to the protocol from Invitrogen. For each real-time PCR, 1 \( \mu \)l of template cDNA, equivalent to \(~100 \mu\)g of total RNA, was mixed with 12.5 \( \mu \)l of 2 \( \times \) SYBR Green PCR master mix and

Figure 2. (a) Schematic representation of shRNA- and siRNA-expression cassettes with the U6 or an inducible U6 promoter. pSD31 is a DNA vector derived from pHIV-7 and pDual-Luci is a dual luciferase reporter system for simultaneous expression of firefly and renilla luciferase. (b) Western blotting analysis of p53 knockdown in 293FT cells transfected with pSD31-shRNA and pSD31-siRNA. (c) Western blotting analysis of p53 knockdown in 293FT cells transduced with pSD31-shRNA and pSD31-siRNA.
5 pmol each of the forward and reverse primers in a final volume of 25 μl. Programs for amplification by PCR were the same as those described elsewhere (25–27) and all reactions were run in triplicate. The variation among triplicate results did not exceed 15%.

Mapping of expressed siRNA and shRNA generated from various expression cassettes

In order to verify siRNA effectors generated from various expression cassettes were identical, the RNA transcripts were captured by reverse transcription and amplified by PCR. In brief, 1 μl of cDNA template from the reverse transcription of the total RNA, 47 μl of PCR SuperMix (Invitrogen, San Diego, CA, USA) and 1 μl of each forward and reverse primer with 200 nM as final concentration were mixed and then carried out PCR according to the manufacturer's instructions. The PCR products were purified by 2% agarose gel, cloned into TA vector and then harvested from TOP10 cells for sequencing.

Testing the quality of the nuclear–cytosol fractionation

The nuclear–cytosol RNA fractionation was carried out using Norgen’s Cytoplasmic & Nuclear RNA Purification Kit (Norgen, Ontario, Canada), which has been proved as a rapid and efficient method for the isolation of cytoplasmic and nuclear RNA from cultured animal cells and small tissue samples. According to the manufacturer’s instructions, a small nuclear RNA, U2 snRNA, and a house-keeping transcript in the cytoplasm, s14 RNA, were utilized as indicators via RT-PCR to demonstrate the quality of nuclear-cytoplasmic fractionation. The specific primers for U2 snRNA were 5'-CATCGGTTCTC GGCCTTTTG-3' (forward) and 5'-TGGAGGTACT GC AATACCAGG-3' (reverse). The primers for amplification of S14 were 5'-GGCA GACCGAGATGAATCCTC-3' (forward) and 5'-CAGGTCCAGGGGTCTTGGTCC-3' (reverse). In addition, ribosomal RNA 28S and 18S were also utilized as indicators to test the integrity and quality of the isolated RNA.

RESULTS AND DISCUSSION

Expressed siRNA was far less potent than the corresponding precursor shRNA

Unlike shRNA, siRNA expressed intracellularly has not been extensively exploited for inactivation of gene expression by either transient transfection or stable transduction. We chose the well-characterized p53 siRNA for our analysis (4,22) and cloned two forms of its DNA coding sequence (shRNA versus siRNA) into the vector pSD31 (Figure 2a). Then we compared their potency in the inactivation of the expression of the p53 gene. Transient transfection with pSD31-shRNA and pSD31-siRNA, in parallel, of 293FT cells indicated that expressed siRNA was far less potent than shRNA, when analyzed by western blotting: almost all expression of p53 was prevented by the shRNA, while the expressed siRNA was only moderately effective (Figure 2b). In stable transduction experiments with the lentiviral vector pSD31, siRNA was inactive, while shRNA was a strong silencer of its target gene (Figure 2c). The lower potency of expressed siRNA as compared to shRNA has been reported similarly by other groups who studied a variety of genes (6–8). To date siRNA delivered via a viral vector has not been shown to substantially disrupt the expression of any target gene. However, we do not know why expressed siRNA, the actual trigger of RNAi, is so much less effective than its shRNA precursor.

Comparisons of intracellular expression of siRNA versus shRNA

Many factors might be expected to affect the potency of siRNA. Transcription might be impaired as a consequence of opposing promoters, which might act in conflict with one another during convergent expression of the sense and antisense strands, with generation of fewer transcripts. In order to examine this possibility, we quantified the levels of siRNA and shRNA transcripts in transfected cells. Northern blotting analysis indicated that DIG-labeled probes were not sensitive enough to detect short RNA (Supplementary Figure 1). Moreover, even when detection was possible, quantitation of the tiny amounts of RNA and the variations in levels was very difficult, and the data were often unrepeatable (Supplementary Figure 1).

To overcome this problem, we used a previously reported real-time RT-PCR technique (25–27) to quantify expressed siRNA and shRNA (Supplementary Figure 2). The empty vector pSD31 was used as a negative control for comparisons of the relative levels of siRNA duplexes and shRNA generated in transfected and transduced cells. As shown in Figure 3a, we found that the sense and antisense strands of siRNA gave almost the same cycle threshold (Ct) values, namely 19.5 versus 19.4, indicating that the strands were generated with equal efficiency. After normalization (Supplementary Figure 2), the copy numbers of the sense and antisense strands of siRNA in each well of a 6-well plate (~0.25 × 10⁶ cells transfected with 2 μg of DNA with an efficiency of ~90%, as determined from a control with the gene for green fluorescent protein) were 7.1 × 10⁶ and 7.3 × 10⁶, respectively. In addition, shRNA generated in a parallel experiment had a Ct value of 19.2, which was very similar to that of siRNA (Figure 3a), indicating that the number of copies of shRNA in transfected cells was the same as that of siRNA (Figure 3a). On the basis of these results, we were able to predict that each transfected cell contained an average of ~300 copies of siRNA or shRNA transcripts. These results excluded the possibility of poor generation of siRNA, at least the concentration of siRNA detected, which is the sum of synthesis and degradation, was almost similar as that of shRNA. Those data also suggest that the opposing promoters within the siRNA cassette did not interfere with one another and transcription was efficient as from a single promoter.

siRNA transcripts were able to export from the nucleus into the cytoplasm

Export from the nucleus might also affect the potency of expressed siRNA. Both expressed siRNA and shRNA are
generated in the nucleus but function in the cytoplasm and, thus, must be exported across the nuclear envelope \((1,3,11)\). It has been demonstrated that shRNA, a structural homolog of pre-miRNA, exploits essentially the same nucleocytoplasmic shuttle protein, Exportin-5, as pre-miRNA. Exportin-5 recognizes the 3' two-nucleotide overhang of the pre-miRNA hairpin for transportation of this RNA into the cytoplasm \((28–31)\). The absence of a hairpin loop might impair the translocation of expressed siRNA, causing lower levels of siRNA in the cytoplasm, which is where RNAi is triggered.

To examine this possibility, we isolated nuclear and cytoplasm RNAs from transfected cells and quantified the respective levels of expressed siRNA and shRNA. We first tested the integrity and quality of the isolated RNA. Analysis of U2 snRNA by RT-PCR indicated that an intense product was observed when the nuclear fraction rather than the cytoplasmic fraction was used as the template (Supplementary Figure 3a). In contrast, the majority of the PCR product for S14 was from the cytoplasmic fraction rather than the nuclear as the template (Supplementary Figure 3b). In addition, the majority of ribosomal RNA (28S and 18S) was in cytoplasm rather than in nuclear as shown in Figure 3c, also indicating effective separation of cytoplasmic and nuclear RNA. Combination of these data indicated that the cytoplasmic and nuclear RNA were effectively separated.

As shown in Figure 3b, siRNA duplexes were detected in the cytoplasm and nucleus with Ct values of 21.4 versus 25.5 for the sense strand and 21.5 and 25.2 for the antisense strand, respectively. We also detected shRNA in both the cytoplasm and nucleus with Ct values of 21.4 and 24.4, respectively. These data indicate that the siRNA duplex, despite the absence of the hairpin loop, was able to transport into the cytoplasm just like shRNA. It remains unclear how siRNA, either as separate individual strands or as paired strands, is exported, but it was clearly not a difference in translocation that caused the difference in potency between siRNA and shRNA.

Expressed siRNA exhibited strand antagonism in triggering RNAi

In a previous study, we found that the lentiviral packaging system was an ideal model for elucidating the roles of individual strands of siRNA in triggering RNAi since the siRNA-delivering viral vector itself is an inherent target \((8)\). We found, previously, that blocking transcription of the antisense strand inactivated RNAi completely. By contrast, blocking transcription of the sense strand had almost no effect on the potency of expressed siRNA \((8)\). These observations let us to ask a fundamental question: is the sense strand really necessary for RNAi? In addition, we wondered whether ‘extra’ integral sense or antisense RNA might enhance the potency of siRNA. To answer these questions, we designed a series of experiments to detect the effects of changes in relative levels of the strands of siRNA duplexes on RNAi.

As reported previously \((8,21,22)\), an inducible U6 promoter with a tetracycline operator (TetO or O) reduced transcription of shRNA by \(~20\%\). Therefore, we replaced one of the two U6 promoters within the siRNA-expression cassette with the inducible promoter (Figure 2a), which reduced the expression of the antisense or sense RNA to the same extent \((20\%)\) as reported previously \((8,22)\). Map mapping data indicated that the sequences of siRNA duplexes generated from various siRNA-expression cassettes were identical (Supplementary Figure 4). Such a reduction in the level of the antisense RNA \(\text{pSD31-siRNA(O)}\) increased the titer of lentivector almost 2-fold (Figure 4a and b), suggesting the potency of RNAi decreased slightly since the siRNA-carrying viral RNA itself is an inevitable target of RNAi \((8,22)\). This result was consistent with the hypothesis that the antisense RNA is the predominant effective inducer of RNAi \((32–35)\). By contrast, reduction in the level of the sense RNA \(\text{pSD31-siRNA(O')}\) tended to increase RNAi with a lower titer of the lentivector being produced (Figure 4a and b), hinting that the sense component might act as an inhibitory factor. Consistently, the increase in potency caused by reduction in the level of the sense component vanished with a similar simultaneous reduction in the level of the antisense component \(\text{pSD31-siRNA(O2)}\). Together, these observations suggested that equivalent levels of the sense and antisense components rendered the siRNA less potent.

Confirmation of strand antagonism in RNAi

To confirm that the sense strand really reduced the potency of the siRNA, we expressed ‘extra’ sense RNA by ligating
a sense-expression cassette to the siRNA cassette (Figure 5a). As expected, this cassette engineering (siRNA-sense) eliminated the equivalence of the sense versus the antisense component, with the level of the former being close to twice that of the latter (Figure 5b). Generation of ‘extra’ sense RNA really did lower the level of the antisense RNA (i), in response to that of sense RNA (iii), in response to simultaneous reductions in levels of both sense and antisense RNA (v). The vector stocks were diluted 1000- and 3000-fold for titration. The effect of regular expression (+) and an ~20% reduction (−) in the level of the sense or the antisense RNA or both on production of the viral vector. The vector titer shown are derived from results of an experiment that was conducted in triplicate for each sample.

Disruption of molar equivalence rendered siRNA functional in stably transduced cell

Our group and others have demonstrated that opposing-promoter cassettes are very useful for the generation of siRNA libraries (6–8). When such a cassette is functional in stable transduction, it should have broad application in many contexts. Our discovery of strand antagonism suggested a potential strategy for enhancing siRNA potency via adjustment of the relative levels of the antisense and sense components during their generation. As reported previously, the combination of Pol II with a pol II promoter (36–38) or of Pol II with a pol III promoter (39) has a significant positive effect on RNA transcription. Therefore, we ligated a TATA box-deleted U6 promoter to an intact U6 promoter to generate a pol III/pol III chimeric promoter (Supplementary Figure 6a) and examined whether this combination enhanced the transcription of siRNA. Deletion of the TATA box from the upstream U6 promoter was designed to prevent
transcription of RNA other than siRNA duplexes (Supplementary Figure 6a). We constructed a siRNA-expression cassette with chimeric promoters, hU6/U6-siRNA-mU6/U6, with a human U6 chimeric promoter (hU6/U6) and a mouse U6 chimeric promoter (mU6/U6) to avoid long sequence repetition that destabilizes DNA (Figure 6a).

Analysis after transfection of 293T cells with chimeric hU6/U6-siRNA-mU6/U6 in parallel with regular hU6-siRNA-mU6 (Figure 6b), with ~50% more siRNA transcripts generated in the former case than in the latter (Supplementary Figure 6c). We then used the chimeric promoter to construct a variety of siRNA-expression cassettes, including symmetric hU6/U6-siRNA-mU6/U6 and hU6/U6-siRNA-O/mU6/U6 and asymmetric hU6-siRNA-O/mU6/U6 and hU6/O-siRNA-mU6/U6 (Figure 6a). In the various cassettes, the mouse U6 promoter (mU6) and the corresponding chimeric promoter (mU6/U6) drove transcription of the antisense strand, while the human promoter (hU6) and the corresponding chimeric promoter (hU6/U6) drove transcription of the sense strand. As shown in Figure 6b and c, stable transduction with the vector that harbored the symmetric hU6/U6-siRNA-mU6/U6 and hU6/U6-siRNA-O/mU6/U6 has almost no effect on the expression of p53, as was the case with hU6-siRNA-mU6, indicating that simultaneous increases in levels of both strands of siRNA duplexes had no significant effect on RNAi, at least in stable transduction experiments. By contrast, stable transduction with asymmetric hU6-siRNA-mU6/U6, hU6/O-siRNA-mU6/U6 and hU6-siRNA-O/mU6/U6, such that the chimeric promoter generated more antisense strand than sense strand (Supplementary Figure 6d), resulted in obvious knockdown of p53 at the level of both the protein (>50%; Figure 6b) and its mRNA (>70%; Figure 6c). To our knowledge, this is the first report of siRNA, delivered by a lentivector, having substantial ability to disrupt expression of a target gene, even though its potency remained much lower than that of shRNA.

Using asymmetric hU6/O-siRNA-mU6/U6 and hU6-siRNA-O/mU6/U6, we found that the former cassette, despite generation of more antisense RNA and less sense RNA than the latter, did not further enhance the potency of the siRNA (Figure 6b and c). This observation hints...
that the potential reward might not extend indefinitely with further alterations in the proportions of two strands. Prior to a given ratio of levels, there is enhancement of RNAi; beyond that point, the opposite occurs. This conclusion is consistent with the previous observation that the complete absence of the sense strand does not enhance RNAi (8). In an ongoing experiment aimed at further proving less sense RNA is beneficial, we co-transfected the antisense oligo at fixed concentration (15 nM) with the sense oligo varying at concentration from 5 to 40 nM. We found RNAi with the sense RNA at lower concentration than 15 nM was much potent that at higher concentration (Figure 7a and b). Combination of these data also supported the sense RNA and antisense RNA exerts strand antagonistic effect during RNA interference and less sense RNA is beneficial.

Mechanistic differences between the siRNA and shRNA in the induction of RNAi

The events that occur during RNAi, from incorporation of the siRNA duplex to degradation of the target mRNA, have been well studied (Figure 1). The key complex of antisense–RISC, after one round of activity, can be recycled, with multiple turnovers, to destroy all complementary RNAs (1,11). In the case of siRNA duplexes generated within cells, it is very possible that only part of the nascent sense RNA forms base pairs with the antisense RNA because of the cellular environment wherein various macromolecules interfere with one another. Unpaired sense RNAs might be diverted directly to the antisense–RISC complex and might, thus, compete with the real target (Figure 1). The strand antagonism observed in the present study strongly supports the possibility that sense RNAs do, indeed, reduce the levels of effectors of RNAi that are available for the real target, reducing the extent of RNAi. Our observations also help to clarify the fate of sense RNA in the initiation of RNAi. They appear to act as the first turned-over substrate, after cleavage within the loaded RISC complex (Figure 1). Then subsequent turnover of the true RNA substrates is triggered.

In the case of shRNA, the loop sequence linking the sense and antisense strand together lowers the kinetic barrier for duplex formation significantly (Figure 1). More importantly, the hairpin structure renders shRNA itself and other RNAs harboring shRNA structure poor targets for RNAi, as demonstrated previously (8,40–43). This scenario stands in significant contrast to that involving siRNA since the free sense RNA is an inevitable substrate of RNAi and, once recruited to the active antisense–RISC complex, it reduces the potency of RNAi. Thus, the present study provides new insight into RNAi, and in particular, into the way in which the sense RNA reduces the potency of siRNA.

The negative effect of the integral sense RNA is intrinsic and, even after further optimization, must always exist, preventing siRNA from being as effective as shRNA. However, by adjusting the molar ratio of antisense to sense RNA, namely, by over-expressing the antisense...
was varied from 5 to 40 nM. The level of the antisense oligomer was fixed at 15 nM and the level of the sense oligomer was varied from 5 to 40 nM. Supplementary Figures 1–6. Supplementary Data are available at NAR Online: Supplementary Figures 1–6.

strand of siRNA relative to the sense strand, we were able to enhance the activity of siRNA in cells to a significant extent. As a result, we were able, for the first time, to suppress expression of a target gene using siRNA-expression vectors in transduced cells. Our strategy, the over-expression of the antisense strand, might also be useful for enhancing the activity of widely used shRNA-expression vectors.

SUPPLEMENTARY DATA
Supplementary Data are available at NAR Online: Supplementary Figures 1–6.

FUNDING
Funding for open access charge: The National Basic Research Program of China (973 Program; grant no. 2010CB12300); and the National Natural Science Foundation of China (grant nos. 20932001 and 91029711).

Conflict of interest statement. None declared.

REFERENCES


