Strand selective generation of endo-siRNAs from the Na/phosphate transporter gene \textit{Slc34a1} in murine tissues

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ABSTRACT

Natural antisense transcripts (NATs) are important regulators of gene expression. Recently, a link between antisense transcription and the formation of endo-siRNAs has emerged. We investigated the bi-directionally transcribed Na/phosphate cotransporter gene (\textit{Slc34a1}) under the aspect of endo-siRNA processing. Mouse \textit{Slc34a1} produces an antisense transcript that represents an alternative splice product of the \textit{Pfn3} gene located downstream of \textit{Slc34a1}. The antisense transcript is prominently found in testis and in kidney. Co-expression of \textit{in vitro} synthesized sense/antisense transcripts in \textit{Xenopus} oocytes indicated processing of the overlapping transcripts into endo-siRNAs in the nucleus. Truncation experiments revealed that an overlap of at least 29 base-pairs is required to induce processing. We detected endo-siRNAs in mouse tissues that co-express \textit{Slc34a1} sense/antisense transcripts by northern blotting. The orientation of endo-siRNAs was tissue specific in mouse kidney and testis. In kidney where the Na/phosphate cotransporter fulfills its physiological function endo-siRNAs complementary to the NAT were detected, in testis both orientations were found. Considering the wide spread expression of NATs and the gene silencing potential of endo-siRNAs we hypothesized a genome-wide link between antisense transcription and monoallelic expression. Significant correlation between random imprinting and antisense transcription could indeed be established. Our findings suggest a novel, more general role for NATs in gene regulation.

INTRODUCTION

Natural antisense transcripts (NATs) represent a widespread phenomenon observed in all organisms (1). Sense-antisense transcript pairs comprise conventionally a protein coding sense mRNA, generally higher and more widely expressed and better characterized than the corresponding NAT, and a regulatory, often non coding antisense transcript (2). In prokaryotes NATs control plasmid copy numbers whereas NATs are involved in viral defense and stress responses in plants (3,4). In higher vertebrates, especially mouse and human, the biological role of NATs is controversial (5–7). There is clear evidence that NATs play an essential role in the epigenetic silencing of mono allelically expressed gene clusters such as parentally imprinted genes, immunoglobulin genes or odorant receptor genes (8,9). However, the total number of NATs exceeds those with an established function by more than an order of magnitude (10). This raises the question whether the myriad of uncharacterized NATs represent specific regulators for the related individual genes or whether a general regulatory concept for NATs remains to be established (11). There is increasing evidence that indeed both scenarios apply. The impact of NATs on the physiological regulation of the corresponding sense transcript and the encoded protein has been demonstrated for \textit{Mx1}, \textit{\beta} secretase and both thyroid and erythropoietin receptors to name just a few examples (12–15). This approach to gene regulation by NATs has been comprehensively reviewed by Beiter \textit{et al.} (1). Recently, a more general role of NATs in quality control of transcripts has been suggested (11).

Initial efforts to investigate the expression of NATs on a genome wide basis selected for spliced and/or polyadenylated transcripts in order to exclude wrongly oriented ESTs (16,17). The total number of antisense transcripts varied from study to study due to experimental differences; however, they all agreed on the fact that
sense-antisense transcript pairs with exonic complementarity are under represented on the X-chromosome as compared to autosomes. If transcript pairs with exonic complementarity were excluded from the analysis, the remaining sense transcript/NATs pairs were found to be distributed evenly throughout the genome (16,18). These hallmarks suggest that a significant group of NATs experience similar evolutionary constraints. The regulatory process related to this special group of NATs most likely relies on complementary RNA sequences (7,11).

Recently, a link between NATs expression and the formation of endogenous short interfering RNAs (endo-siRNAs) has been established. Both large scale sequencing and investigations into specific bi-directionally transcribed genes identified endo-siRNAs that matched the complementary regions of sense transcript/NAT pairs (19–21). In all cases, the orientation of the single-stranded endo-siRNAs was non-random. Watanabe et al. detected sense oriented endo-siRNAs (complementary to the NAT) in mouse oocytes (21). Carlile et al. reported a switch from antisense oriented to sense oriented siRNAs in zebrafish embryonic development between 48 and 72 h post fertilization (19).

We took an integrative approach with the aim of extrapolating the findings from a single bi-directionally transcribed gene, \textit{Slc34a1/Pfn3}, to a more general concept of gene regulation by NATs. Importantly, we could confirm the production of NATs-related endo-siRNAs and the non-random selection of endo-siRNA strands. Based on these findings we hypothesized and confirmed a general link between NATs and random monoallelic expression.

MATERIALS AND METHODS

Animals

BALB/c mice were bred in-house. Young male and female animals were killed by cervical dislocation according to the home office schedule 1 procedure. Tissues of interest were quickly removed, rinsed in ice cold PBS and frozen in liquid nitrogen. Frogs were obtained from the African Xenopus Facility (South Africa). Xenopus were anaesthetized by immersion into ice-cold tricaine solution (Sigma). The animals was killed by cervical dislocation according to the protocol. The brains and organs were removed by dissection under a binocular microscope and kept in modified Barth’s solution (NaCl 88 mM, KCl 2 mM, HEPES/Tris pH 7.5, 89 mM Tris-base, 2 mM EDTA-sodium salt, 89 mM boric acid, pH 8.5). This combination gave superior result as compared to TBE-urea gels. Gels were pre-run for 1 h prior to loading of the samples. Blotting was performed at constant 100 mA for 50 min. All steps were performed using precast gels and a Criterion midi gel system (Biorad). Hybridization was essentially done as above, however, the stringency was reduced. Hybridization was performed at 37°C and final washes were at room temperature in 0.1× SSC, 0.1% SDS.

Expression in Xenopus oocytes

cRNA was produced from \textit{HindIII} or \textit{EcoRV} linearized plasmids using the mMESSAGE mMACHINE kit (Ambion). Alternatively, RNA was synthesized directly from amplified DNA fragments that contained a T7-binding site added to one of the primers used for the PCR. The RNA was purified by LiCl precipitation and concentration was determined spectrophotometrically. Routinely, between 2 and 10 ng of cRNA in 50 nl of water were injected into oocytes. For nuclear injections, the injection volume was decreased to 10 nl without changing the amount of RNA. The oocytes were kept at 18°C in modified Barth’s solution up to 3 days before the assays. All experiments were done with oocytes from at least three different frogs with comparable results.

Isolation of nucleic acids

Mouse tissues (<100 mg) were ground to powder in liquid nitrogen and added to 1 ml of Tri-reagent (Sigma). Homogenization was completed by passing the slurry repeatedly through 21 and 25 G injection needles. RNA extraction was then performed according to the supplier’s protocol. The integrity of the RNA was checked by denaturing gel electrophoresis and concentration was determined as above. Total RNA was used for all PCR and cloning steps. Single oocytes were quickly homogenized in 100 μl of Tri-reagent using disposable plastic pestles. Thereafter, the supplier’s protocol was followed. The centrifugation times were increased for precipitation of nucleic acids for up to 1 h at 14000 g if short RNAs were to be detected.

Non-radioactive detection of nucleic acid

Assessment of RNA from injected oocytes was done using denaturing formaldehyde agarose gels (1.2%). RNA from single oocytes was separated and blotted by capillary force onto nylon membranes (Roche). After UV cross-linking the membranes were pre hybridized (>1 h) and hybridized over night in digoxigenin (DIG) EasyHyb solution (Roche). The DIG labelled probes were generated by \textit{in vitro} transcription using the mMESSAGE mMACHINE kit (Ambion) and DIG labelled nucleotides (Roche). Hybridization was carried out at 58°C. Membranes were washed at a final stringency of 0.5× SSC/0.1% SDS at 50°C followed by ECL detection (Roche). To assay short RNAs samples were mixed at 1:3 ratio with Ambion formaldehyde loading buffer and heated at 75°C for 15 min. RNA was separated on 4–12% Bis–Tris polyacrylamide gels using 1× TBE running buffer [89 mM Tris-base, 2 mM EDTA-sodium salt, 89 mM boric acid, pH 8.5]. This combination gave superior result as compared to TBE-urea gels. Gels were pre-run for 1 h prior to loading of the samples. Blotting was performed at constant 100 mA for 50 min. All steps were performed using precast gels and a Criterion midi gel system (Biorad). Hybridization was essentially done as above, however, the stringency was reduced. Hybridization was performed at 37°C and final washes were at room temperature in 0.1× SSC, 0.1% SDS.

PCR and cloning

PCR-related techniques were used for expression analysis, cloning purposes and probe generation. To detect Na-/phosphate transporter-related sense or antisense transcripts 0.1–0.5 μg of total RNA were reverse transcribed.
denatured at 70°C for 5 min in the presence of 0.1 µg/µl oligo-dT primer and cooled to 37°C. 15 µl of RT mix was added containing buffer, nucleotides (250 µmol each), 4 units reverse transcriptase (Qiagen) and 20 units RNase inhibitor (Promega). After 60 min incubation at 37°C the supplier’s protocol was downscaled and 2 µl of the RT reaction were used for hot start PCR with Taq polymerase and reagents from Qiagen. The final volume was 25 µl. For 3′ RACE an oligo dT adaptor primer (Sigma) was used to prime the reverse transcription. A first PCR was done as above including a gene-specific primer and the adaptor primer. A second, nested reaction was performed with 1 µl of the 1/2000 diluted first reaction, a second specific primer and the adaptor primer. PCR conditions were modified according to the annealing temperature of the primers and the length of the expected fragments. For 5′ RACE a kit from Invitrogen was used and the protocol was strictly followed. The sequences of the primers are given in the Supplementary Table 1. The two DNA fragments from 3′ and 5′ RACE were separated on agarose gels and purified. The entire fragment was amplified by overlapping PCR. One microlitre of each fragment was added to a PCR reaction (Qiagen). After four cycles at a low annealing temperatures (50°C) to allow hybridization of the overlapping DNA ends and extension of the full fragment the two adaptor primers were added and the cDNA was amplified. The resulting fragment was cloned into pCR2.1-TOPO using the TOPO cloning kit from Invitrogen according to the standard protocol. The cDNA was verified by sequencing.

Bisulfite treatment
Genomic DNA was isolated from adult mouse kidney, testis and skeletal muscle. The tissue was homogenized as above but omitting the step using the 25 G needle. The QIAamp DNA Mini Kit (Qiagen) was used according to the supplier’s protocol. Concentration was determined by spectrophotometry. Approximately 0.5 µg of DNA was bisulfite treated using the EZ DNA methylation gold kit (Zymo Research). Column purification of the DNA resulted in samples of 14 µl of which 3 µl were used for PCR in a 15 µl reaction (HotStarTaq Master Mix, Qiagen). The sequence of the primers specific for the sense and the antisense promoter as well as the sense/antisense overlapping region are given in the Supplementary Data. The resulting fragments were directly sequenced and checked for evidence of C/T bias in the context of CpG dinucleotides.

Bioinformatics
Probes from Affymetrix 430_2 arrays were mapped to the mouse genome using BLAT. The probes were correlated with exons and selected if they mapped to an exon on the opposite strand. The pipeline used the Affymetrix Mouse430_2 probe mapping generated in Ensembl v49 (http://Mar2008.archive.ensembl.org). Briefly, the Ensembl mapping pipeline retains genomic mappings with one mismatch regardless of the location on the genome, or multiple mappings. The probe mapping was done using exonerate (22). The antisense-specific probe coordinates represent about 3.5% of the total probes mapped to the genome. (The antisense probe sets are listed in Supplementary Table 2). The resulting probe set was used to assess datasets in the public repositories with emphasis on testis and embryonic stem cells. Other mouse tissues were included as controls and cross reference. The relevant GEO accession numbers are: GSE9954, different mouse tissues; GSE4193 spermatogenesis. Raw data was downloaded pre-processed with RMA and a per-gene normalisation applied in GeneSpring 7.3.1 (Agilent). Net expression levels were plotted for each probe and compared between the different tissues.

In order to assess a correlation between antisense transcription and random imprinting three published datasets were compared: Human antisense transcripts (16) were correlated with two compilations of monosnpially expressed human genes (23,24). HUGO gene names were used as common denominators for the three datasets. Genes were then identified that were present in both the antisense dataset and the imprinted genes pool. To assess significance of the overlap a random gene list of the same size as the imprinted gene set was compared to the antisense dataset over 100 000 permutations.

RESULTS
We compared the genomic organization of flounder and zebrafish Slc34a with the homologous gene encoding the Na/pH cotransporter Slc34a1 from mouse. The presence of an annotated gene Profilin 3, encoding the protein Profilin 3, closely downstream of the Slc34a1-3′ end strongly indicated overlapping transcription of the mouse locus (25). An additional gene encoding the coagulation factor F12 (F12) could lead to overlapping transcripts as well (Figure 1). We tested for the expression of antisense transcripts by RT-PCR using primers located in different exons of Slc34a1. Prof3 and F12. In Slc34a1 we focused on exons X and XIII based on structural information from the homologous zebrafish gene. Primers located in Slc34a1 exon X and the in the distal part of Prof3 in relation to Slc34a1) amplified specific fragments. Primers located in Slc34a1 exon XIII gave weak and unreliable signals and primers in the proximal part of Prof3 and F12 failed to amplify any DNA (Figure 2A and not shown). RNA was extracted from different mouse tissues and tested for integrity by gel electrophoresis. cDNA was amplified from testis and kidney RNA. Skeletal muscle did not express the antisense transcript (Figure 2B).

We cloned the Slc34a-related antisense transcript by RACE and overlapping PCR from mouse testis RNA. The predominant transcript contained 517 nucleotides with an open reading frame of 158 amino acids. The first 47 amino acids are identical with Profilin 3, the remaining 111 amino acids show no similarity to known proteins and lack structural motifs. Other splice forms were identified, based on the inefficient amplification of the corresponding fragments we assume that the additional isoforms represent splice byproducts. These results
indicate that evolutionary conservation of the antisense transcript does not follow rules for protein coding RNAs. Open reading frames may be present; however, little pressure seems to act on maintaining them.

The significant expression of the Slc34a-related antisense transcript in both mice and zebrafish testis (26) raised the question if this was a gene-specific feature or if antisense transcription was generally unregulated in testis (27). Tools to routinely assess antisense transcripts on a genome wide scale are not established. We took advantage of a small but representative number of Affymetrix probes that recognize the reverse strand of coding genes. The probes were selected to localize in exonic regions of annotated sense transcripts. This enabled us to screen specifically for a limited number of transcripts that fulfill hallmarks of NATs as outlined in the introduction. On the Affymetrix mouse 430_2 array, 14 101 probes map to exons predicted by Ensembl but on the opposite strand. Among those probes 10 420 mapped to the genome once. The antisense probes represent 2596 unique exons of 1977 different genes (Ensembl v49). The individual probes belong to 1630 probe sets according to the standard Affymetrix CDF file. In other words, the 1630 probe sets return a positive expression call if (i) a potential antisense transcript is complementary to this exon and (ii) the antisense exon covers enough individual probes to return an unambiguous call (this is not necessarily the case because the intron–exon structure refers to the sense transcript. The complementary exon(s) of the antisense transcript may only span a fraction of the individual probes that make up the entire probe set). We tested the expression of the corresponding transcripts in various mouse tissues using GEO datasets GSE9954 and GSE4193. In particular, antisense transcripts were assessed in a multi tissue experiment including testis, seminal vesicle, brain, kidney and embryonic stem cells. Datasets from spermatocytes at different stages of development were included. We found significant up regulation of antisense transcripts in testis and, to a lesser extend, in seminal vesicle. Increased NATs expression was observed specifically during the final stages of spermatogenesis (round stage, Table 1). Interestingly, kidney and ES cells also showed a slightly increased expression of NATs, whereas values from other tissues were in a comparable low range.

We have previously reported that co-expressed overlapping Slc34a sense-antisense transcripts from zebrafish are processed into endo-siRNAs after injection into the nucleus of Xenopus oocytes (19). We used a similar approach to demonstrate that the mouse NAT was processed accordingly. As shown in Figure 3A single transcripts remained stable in both nucleus and cytoplasm. Co-expression of sense and antisense cRNAs in the nucleus resulted in complete degradation of both transcripts, whereas the related signals remained detectable after cytoplasmic injections (Figure 3B, ‘full overlap’).
The mouse sense and antisense transcripts share a single exon with an overlap of 124 bp. We determined the minimal size of overlap that induced processing by gradually truncating the antisense transcript to 40, 31, 30, 29 and 20 bp of complementarity. All the transcripts were stable for days after co-injection into the cytoplasm (C) of Xenopus oocytes (Figure 3B). Upon co expression of sense-antisense pairs in the nucleus (N) RNA overlaps of 30 bp or longer were efficiently cleaved. Shorter duplexes were either poorly processed (29 bp) or were stable (20 bp) (Figures 3 and 4). The generation of endo-siRNAs from overlapping sense/antisense transcripts was demonstrated by RNA PAGE and northern blotting of samples from single oocytes. In accordance with conventional northern blots short RNAs of approximately 23 bases were detectable in samples that showed evidence of sense/antisense processing (Figures 3 and 4, left panel lanes 1–5).

If the processing observed in Xenopus oocytes was physiologically relevant one would expect the presence of endo-siRNAs in tissues that co express Slc34a1 sense and antisense transcripts [Figure 2B and (25)]. Total RNA samples from mouse kidney, testis and skeletal muscle were included into the PAGE northern experiments (Figure 4, right panel, lanes 9–11). Small RNAs are indeed present in both kidney and testis samples. Most interestingly, in testis both siRNA strands could be detected whereas in kidney only endo-siRNAs complementary to the antisense RNA were found. These results concur with published data from zebrafish Slc34a and other reports that showed accumulation of strand-specific endo-siRNAs (19–21). We concluded that strand selection of the endo-siRNAs was non-random. In the context of

**Table 1. Expression of NATs in mouse tissues**

| Tissue | ES cells | Brain | Kidney | Testis | Sem. vesicle | Sem. v. curated | Ovary | Placenta |
|--------|----------|-------|--------|--------|-------------|----------------|-------|----------|
| Tissue distribution of antisense transcripts (NATs) | | | | | | | | |
| Max value | 149.8 | 70.85 | 188.3 | 254.9 | 1843 | 128.1 | 80.13 | 22.26 |
| Min value | 0.049 | 0.043 | 0.234 | 0.059 | 0.09 | 0.09 | 0.11 | 0.21 |
| Mean | 1.56 | 1.28 | 1.55 | 2.34 | 2.45 | 1.32 | 1.05 | 1.09 |
| SD | 4.47 | 2.91 | 7.04 | 10.08 | 45.73 | 3.19 | 2.21 | 1.24 |
| Pfn3 | 1.07 | 0.77 | 1.06 | 18.75 | 1.39 | 0.66 | 0.80 |
| Slc34a1 | 0.94 | 0.82 | 274.6 | 1.09 | 1.47 | 0.74 | 0.96 |
| Slc34a-3’ | 0.99 | 0.75 | 49.49 | 1.46 | 1.62 | 0.72 | 0.84 |

| Spermatogenesis | | | | | | | | |
| Cell | A | B | | | | | |
| Max value | 4.07 | 3.50 | | 5.30 | 24.42 |
| Min value | 0.01 | 0.08 | | 0.10 | 0.11 |
| Mean | 0.98 | 1.00 | | 1.11 | 1.21 |
| SD | 0.33 | 0.32 | | 0.41 | 1.38 |
| Pfn3 | 0.33 | 0.36 | | 1.54 | 105.1 |
| Slc34a1 | 0.97 | 0.79 | | 1.04 | 1.06 |
| Slc34a-3’ | 0.98 | 0.95 | | 1.03 | 1.04 |

Datasets GSE9954 and GSE4193 were evaluated using the probe sets specific for NATs (Supplementary data 1). The normalized values for the probesets Pfn3 (1453962_at), Slc34a1 (1423279_at) and Slc34a-3’ (1427627_at) are included. The alternative splice product of Pfn3 is not represented in the database; therefore probe set Pfn3 (1453962_at) is included in the NAT’s probe compilation. The RT-PCR results indicate significant expression of the alternative splice form (Figure 2), however, the probe set will pick up the unspliced form as well.

The curated data from seminal vesicle lacks the value of a single probeset 1422515_at: the probes bind to a highly expressed protein coding transcript (Svs7) that is specifically expressed in seminal vesicle and complementary to another protein coding transcript (AC113081).
siRNA-induced gene silencing this implies that a downstream response can be directed either towards the sense or the antisense strand. We therefore hypothesized a connection between the expression of NATs and epigenetic gene silencing, for example random monoallelic expression.

Random monoallelic expression is experimentally approached by using polymorphisms to assess the allelic origin of transcripts. We argued that polymorphisms or mutations within a bi-directionally transcribed locus may skew or completely reverse the endo-siRNA strand selection process. This would result in reversed targeting of endo-siRNA-induced silencing. The sense transcript instead of the antisense transcript would become silenced on the allele that shows the polymorphism. The other allele, unaffected by the polymorphism, would show the ‘normal’ strand selection. As a consequence, mono-allelic expression of the polymorphic gene locus should be observed. To support this hypothesis we investigated whether a genome wide correlation between mono-allelic gene expression (i.e. random imprinting) and antisense transcription could be found. Both phenomena have been assessed in humans by other groups and the corresponding datasets are published (16,24). We used the datasets from Chen et al. for human NATs (2940) and Gimelbrant et al. for monoallelically expressed human autosomal genes (16,24). As a control group, the 25 157 HUGO genes were used. Matching the gene names of the three data sets resulted in 2772 NATs and 281 randomly imprinted genes with compatible annotations. The overlap between the NATs dataset and monoallelically expressed genes was 56, a figure in the 99th percentile when compared against the control of a randomly permuted list of 281 HUGO genes and the NATs. A similar evaluation was performed with an independent set of randomly imprinted genes (23) and (11) with comparable results (Table 2). These findings add weight to the argument that mutations may influence the orientation of endo-siRNAs.

To assess for short RNA-induced transcriptional silencing we checked for DNA methylation changes in the sense/antisense overlapping region (5 CpG dinucleotides in 274 bp) and the sense promoter (1 CpG in 374 bp) in DNA isolated from mouse kidney and muscle, respectively. Bisulfite treatment of the DNA and direct sequencing of the amplified fragments revealed complete CpG methylation and no difference between kidney and muscle. Therefore gene regulation by NATs may include other mechanisms such as histone modifications (28) to induce transcriptional silencing.

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**Table 2. Correlation between NATs and randomly imprinted genes**

| Monoallelically expressed genes | Antisense transcripts | HUGO genes | Overlap | Significance (%) |
|-------------------------------|----------------------|------------|---------|-----------------|
| 104 (23)                      | 2772 (16)            |            | 23      | >95             |
| 2772 (16)                     | 104 from 25 157      | 11 ± 3     |         |                 |
| 281 (24)                      | 2772 (16)            |            | 56      | >99             |
| 2772 (16)                     | 281 from 25 157      | 30 ± 5     |         |                 |

Two datasets that identified randomly imprinted human genes were compared to the human antisense transcripts (16,23,24). As a control the same comparison was done with 281 and 104 randomly selected genes from the HUGO database (100 000 times).
DISCUSSION

Our experiments addressed the phenomenon of antisense transcription at single gene and entire genome level. We aimed at correlating the data and suggest novel strategies to assess gene regulation by NATs. It is important to take into account that the conclusions from this approach only apply to processed NATs that show exon complementary with the corresponding processed sense transcript.

We report the cloning of a NAT related to the Na+/phosphate cotransporter gene Scl34a1 from mouse testis. The NAT represents an alternative splice product of Pfn3 that has not been reported previously in the database (EU375560). Our approach exemplifies the difficulties related to the cloning of a specific NAT. The poor phylogenetic conservation of NATs (Figure 1) and their often unreliable representation in the public databases complicate any cloning effort of a specific NAT. We were fortunate as the Pfn3 gene provided a promising starting point for a RACE approach. In addition, the Scl34a1 NAT contained an intron allowing for unambiguous annotation of PCR products. Without an intron, the confirmation of antisense orientation can be cumbersome and would rely on more error prone strategies such as strand-specific RT, oligo-dT priming, capping or transcript start site predictions. The generally low expression level and the restricted expression pattern of NATs add further complications to a targeted cloning approach. The general up regulation of NATs in testis [Table 1 and (27)] would now suggest using this tissue in relation with a NAT cloning effort. In addition, investigations into comprehensive antisense expression and transcript characterization may best focus on the testis transcriptome.

The expression pattern of NATs in testis is particularly intriguing with respect to the developmental stage at which overexpression occurs. During the early polyplody stages, types A, B and pachytene (Table 1), expression of NATs is low. It significantly increases during later stages of spermiogenesis in haploid cells. Widespread transcriptional repression is observed during this later stage of spermiogenesis (29).

We found a rather insignificant expression of NATs in other organs apart from testis whereas other reports find low but significant expression of NATs in other tissues. This discrepancy is most likely due to experimental constraints. We used stringent conditions when analyzing the DNA array data and may have excluded weak signals that were included in other reports (30,31). Transcripts specific to a very small number of cells in a heterogeneous tissue may have failed our detection limit. More sensitive experiments such as RT–PCR indeed confirmed the co expression of the complementary Scl34a transcripts [Figure 2 and (25,26)].

The cloned Scl34a1 NAT is processed into mRNA and displays exon complementarity with the corresponding sense transcript. There is compelling recent evidence that NAT/sense transcript hybrids may be cleaved into endo-siRNAs (19,21,32,33). The detection of Scl34a1-related endo-siRNAs in testis concurs with these previous findings (19,27). We also found that a 30 bp overlap of the two substrate RNAs represents the cut off for efficient processing (Figure 3B). Dicer accepts long double-stranded RNAs as substrates and produces short RNAs of variable size [19–30 bp (34)]. A significant decrease in dicer processivity between 30 and 29 bp double-stranded substrates was also reported by Elbashir et al. (35). These findings suggest that the short Scl34a1-related RNAs are indeed dicer processed endo-siRNAs. The tissue-specific orientation of the endo-siRNAs in testis and kidney (Figure 4) represents an exciting finding that corroborates previous observations in mouse and zebrafish. Watanabe et al. reported endo-siRNAs related to the Ppp4r1 gene that were all oriented in sense direction in mouse oocytes, thus reflecting a similar situation as reported for the Scl34a1 endo-siRNAs in mouse kidney. In zebrafish embryos, the orientation of Scl34a endo-siRNAs shows developmental regulation from antisense direction to sense orientation. Interestingly, the switch coincides with the physiological induction of the sense-encoded protein. These observations suggest that the orientation of the endo-siRNAs is somehow related to the expression of the sense transcript. The fact that northern blotting revealed different endo-siRNA patterns in testis and kidney (Figure 4) might relate to the transcriptional state of the relevant gene locus. In testis, a general up regulation of transcription would stimulate sense and antisense transcription at a similar scale leading to transient levels of both endo-siRNA strands (36). In kidney, the Scl34a1 sense transcript is activated in a gene-specific way. This could lead to either a short period of sense/antisense co-expression followed by sustained sense transcription or, alternatively, strong sense expression including stochastic antisense events at a low level. In both cases, it is conceivable that only the sense oriented endo-siRNAs (targeting antisense transcription) are pre-dominantly accumulated.

By comparing published datasets we found a significant correlation between NATs expression and monoallelically transcribed genes (16,23,24). The data sets, however, contain monoallelically expressed genes without NATs and vice versa. A better overlap between the datasets is likely to be achieved once the NAT transcriptome becomes systematically characterized. Random monoallelic expression of a gene is assessed using polymorphisms to determine the allelic origin of transcripts. On the other hand, we have shown that the probability of monoallelic gene expression increases with the expression of NATs and possibly endo-siRNAs. It is therefore tempting to speculate that the expression of NATs from a polymorphous locus, endo-siRNA strand selection and random allelic expression are connected phenomena. Such a link could, for example, explain the selection against NATs on the mammalian X chromosome because a NAT-induced silencing event would lead to a complete knock down of the relevant gene. In this context the identification of the factors that influence endo-siRNA strand selection would be of major interest (37).

We developed this idea further towards a concept which is outlined in Figure 5. The working model predicts that sense and antisense transcripts are co expressed during a limited window during cell development or differentiation. Our expression studies indicate that such co-expression...
could occur during late stages of spermiogenesis or in renal stem cells (Table 1). Production of endo-siRNA and possibly the concomitant accumulation of specifically oriented endo-siRNA strands involve fully processed mRNAs. Experimental evidence so far (19,21) predicts that the protein coding sense transcript dictates the strand selection. Features that differentiate sense and antisense transcripts and may affect endo-siRNA strand selection include, translatability (38), structure (39) or stability, for example. It is conceivable that polymorphisms or mutations in general alter these transcript features and skew endo-siRNA strand selection. As a consequence, the silencing response could become redirected and target the sense transcript (40–42,43). The entire process could be seen as a quality test for RNAs.

The proposed concept has different consequences if applied to the tissues testis and kidney that show increased NATs expression. In testis, male germ cells show significant up regulation of transcriptional activity including the expression of NATs (27,44). This will lead to a wide spread generation of endo-siRNAs, hence both endo-siRNA strands are detected on the northern blot in Figure 4. The concomitant RNA quality test will lead to the accumulation of sense oriented endo-siRNAs (complementary to the antisense transcript; quality test passes). If a specific gene is mutated the quality control potentially fails, endo-siRNA strand selection is reversed and the sense transcript becomes silenced. The haploid spermatids will not be able to compensate for the loss and face increased selective pressure. Significant levels of apoptosis are indeed detected during spermatogenesis (45). The process may therefore remove cells that carry deleterious mutations and eventually result in a purified population of spermatozoa.

In kidney, the RNA quality control would apply as above, however with slightly different consequences. Under physiological conditions, the endo-siRNA complementary to the antisense RNA is selected and the sense transcript is expressed. If one allele is mutated and shows reversed strand selection only one allele would become silenced and the other one stays active. Allele specificity may be achieved simply by the timing of transcription from the two alleles. The specific cell may still function normally but show ‘random’ monoallelic expression of the corresponding gene.

To conclude, we suggest that NATs are a significant source of endo-siRNAs. We hypothesize that these endo-siRNAs act as molecular switches responsive to mutations/polymorphisms. Such a biological role may explain the under representation of NATs on mammalian X-chromosomes and the phenomenon of mono-allelic gene expression.

SUPPLEMENTARY DATA

Supplementary Data are available at NAR Online.

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