The exonuclease Nibbler regulates age-associated traits and modulates piRNA length in Drosophila

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Summary

Nibbler (Nbr) is a 3′-to-5′ exonuclease that trims the 3′ end of microRNAs (miRNAs) to generate different length patterns of miRNAs in Drosophila. Despite its effect on miRNAs, we lack knowledge of its biological significance and whether Nbr affects other classes of small RNAs such as piRNAs and endo-siRNAs. Here, we characterized the in vivo function of nbr by defining the Nbr protein expression pattern and loss-of-function effects. Nbr protein is enriched in the ovary and head. Analysis of nbr null animals reveals adult-stage defects that progress with age, including held-up wings, decreased locomotion, and brain vacuoles, indicative of accelerated age-associated processes upon nbr loss. Importantly, these effects depend on catalytic residues in the Nbr exonuclease domain, indicating that the catalytic activity is responsible for these effects. Given the impact of nbr on miRNAs, we also analyzed the effect of nbr on piRNA and endo-siRNA lengths by deep-sequence analysis of libraries from ovaries. As with miRNAs, nbr mutation led to longer length piRNAs—a effect that was dependent on the catalytic residues of the exonuclease domain. These analyses indicate a role of nbr on age-associated processes and to modulate length of multiple classes of small RNAs including miRNAs and piRNAs in Drosophila.

Key words: aging; endo-siRNA; miRNA; Nibbler; piRNA.

Introduction

microRNAs (miRNAs) are 20–24nt small RNAs that regulate diverse biological processes, such as development and age-associated diseases (Bartel, 2009; Ambros, 2011; Kato & Slack, 2012). Since the discovery of the first miRNA, lin-4 and the second miRNA, let-7 as developmental timing genes, hundreds of miRNAs have been identified across species. The canonical biogenesis pathway of animal miRNAs starts with the transcription of the primary miRNA (pri-miRNA) from the miRNA-coding genes by RNA polymerase II in the nucleus (Bartel, 2004; Czech & Hannon, 2011). Pri-miRNAs are then cleaved by two distinct RNase III/RNA-binding protein complexes. Drosha/Pasha (Drosha/DGCR8 in mammals) cleaves pri-miRNAs to generate precursor-miRNAs (pre-miRNAs) in the nucleus. After the export of pre-miRNAs to the cytoplasm by Exportin-5, Dcr-1/Losq-PB (Dcr/TRBP in mammals) cleaves the pre-miRNAs to generate mature miRNA/miRNA* duplexes. One of the strands of the miRNA duplex is preferentially retained in miRISC containing Ago1 (Ago2 in mammals), which targets mRNAs through the partial complementarity between the seed sequence (nucleotides 2–8 at the 5′ end of miRNA) and the miRNAs to induce translational repression and mRNA decay (Bartel, 2009; Fabian & Sonenberg, 2012).

Initial efforts to identify novel miRNAs relied on computational prediction of miRNA genes followed by Northern blots (Lai et al., 2003). However, development in high-throughput sequencing techniques enabled discovery of small RNA species across different biological contexts (Ruby et al., 2006, 2007; Landgraf et al., 2007; Morin et al., 2008; Burroughs et al., 2010; Westholm et al., 2012). The general conclusion from these profiling studies is that miRNAs are heterogeneous at the 5′ end, 3′ end, and even in internal sequence (Neilsen et al., 2012). In addition, the 3′ end of miRNAs is more variable compared to the 5′ end. There are a few known mechanisms by which such heterogeneity is generated. For example, Drosha and Dicer cleavages define the 5′ end and 3′ end of miRNAs, but the cleavages could be imprecise such that they generate 5′ end and 3′ end variations (Calabrese et al., 2007; Wyman et al., 2011). In line with this, the cleavage position by Dicer is controlled by its partner protein Losq-PB in Drosophila and TRBP in mammals, to generate miRNA isoforms that are overlapping, but with distinct seed sequences due to a differential 5′ end (Fukunaga et al., 2012; Lee & Doudna, 2012). In addition to Drosha and Dicer cleavages, 3′ end heterogeneity of miRNAs is subject to nucleotide addition, such as adenylation and uridylation (Jones et al., 2009; Kato et al., 2009; Burroughs et al., 2010). Intriguingly, the loss of such heterogeneity leads to a change in specificity and efficacy of target silencing, underscoring the functional significance of controlling end heterogeneity. Despite the accumulating evidence of miRNA heterogeneity and the identification of the enzymes to generate such heterogeneity, however, we still lack clear knowledge of the biological impact of such heterogeneity at the organismal level.

Study of Drosophila miR-34-5p shows that miR-34-5p displays a pattern of different length isoforms due to 3′ end heterogeneity and that the short isoform accumulates with age (Liu et al., 2012). Loss of miR-34 leads to accelerated aging in Drosophila. Screening defined a 3′-to-5′ exonuclease, Nbr, which is responsible for the isoform pattern of miR-34-5p: upon knockdown of nbr, the long isoform accumulates, while the short isoforms decline (Han et al., 2011; Liu et al., 2011). A subset of Drosophila miRNAs are subject to length pattern control by Nbr; moreover, recent data have shown that the pattern may reflect differential loading into the miRISC and siRNA RISC complexes with age (Abe et al., 2014). Disruption of the process, by knockdown of the genes Hen1 and Ago2, leads to shorter lifespan and neurodegeneration. It is unknown whether Nbr impacts the length of classes of small RNAs beyond miRNAs, such as piRNAs and endo-siRNAs, and a detailed characterization of the nbr loss of function phenotype has not been
performed. Here, we characterize loss-of-function effects of the \textit{nbr} gene on the animal, and effects on piRNAs and endo-siRNAs. These analyses indicate that \textit{nbr} loss results in accelerated age-associated defects, as well as impacting the length of piRNAs. Importantly, these effects depend on the catalytic residues of the Nbr exonuclease domain, suggesting that the processing of RNA substrates by Nbr is critical for these effects. Together, this study reveals new insight into the importance of controlling length heterogeneity of small RNAs.

Results

Expression pattern of Nbr \textit{in vivo}

Nibbler is a 3’-to-5’ exonuclease whose function is critical for trimming the 3’end of miR-34-5p in Drosophila (Han et al., 2011; Liu et al., 2011). Upon \textit{nbr} loss, a subset of Drosophila miRNAs show accumulation of long isoforms. To understand the biological role of \textit{nbr} \textit{in vivo} in more detail, we first assessed the expression pattern of the Nbr protein. We developed a rabbit polyclonal antibody against the N-terminus of Nbr (see Methods). By Western immunoblot, Nbr was enriched in ovary and then heads, followed by the body (Fig. 1A). Temporally, Nbr showed little change in level with age in the adult head (Fig. 1B), despite the fact that the lower isoform of miR-34-5p accumulates with age (Liu et al., 2011). Nuclear/cytoplasmic fractionations revealed that Nbr was enriched in the cytoplasm (Fig. 1C), consistent with its role in a complex with Ago1 to process the 3

Gene on the animal, and effects on piRNAs and endo-siRNAs. These analyses indicate that \textit{nbr} loss results in accelerated age-associated defects, as well as impacting the length of piRNAs. Importantly, these effects depend on the catalytic residues of the Nbr exonuclease domain, suggesting that the processing of RNA substrates by Nbr is critical for these effects. Together, this study reveals new insight into the importance of controlling length heterogeneity of small RNAs.

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Generation of \textit{nbr} loss-of-function mutants

Previous studies suggested lethality and sterility upon \textit{nbr} knockdown (Han et al., 2011; Liu et al., 2011). To rigorously examine whether these effects were indeed associated with loss of \textit{nbr} function, we crossed the \textit{nbr}^{Df(2L)BSC312} allele to a deficiency line (\textit{Df(2L)BSC312}) that deletes a ~60 kb region that includes the \textit{nbr} gene (Fig. 2A,B). We refer to the \textit{nbr}^{Df(2L)BSC312} heterozygotes as ‘\textit{nbr} null’ because we cannot detect the Nbr protein (Fig. 2C), although we cannot rule out that some level of protein is expressed that is below the level of detection in our assays. We found that this allelic combination was viable and fertile. Thus, the previously observed lethality and sterility appear unlinked to \textit{nbr} (Han et al., 2011; Liu et al., 2011). miR-34-3p trimming was compromised in the \textit{nbr} null combination, and the Nbr protein level and miR-34-3p trimming pattern were fully rescued by introducing the wild-type genomic \textit{nbr} transgene (Fig. 2C). Importantly, rescue of miRNA trimming activity was dependent on the catalytic residues of the Nbr exonuclease domain: mutating catalytic residues (D435A,E437A) within the genomic transgene (referred to as ‘cat-dead \textit{nbr}’) failed to rescue

Fig. 1  Expression pattern of the Nbr protein. (A) Western immunoblot showing Nbr protein expression in head, ovary, and body (without ovary). Left panel: Nibbler (Nbr) is enriched in the head relative to the body. Right panel: Nbr protein expression is highest in the ovary. (B) Western immunoblots of Nbr expression with age show little change between 3d and 30d. Mean±SD (n = 4), P = 0.76 (Student’s t-test). (C) Western immunoblot of fractionated protein from heads of controls (Bloomington line 5905) shows Nbr protein (Fig. 2C), although we cannot rule out that some level of protein is expressed that is below the level of detection in our assays. We found that this allelic combination was viable and fertile. Thus, the previously observed lethality and sterility appear unlinked to \textit{nbr} (Han et al., 2011; Liu et al., 2011). miR-34-3p trimming was compromised in the \textit{nbr} null combination, and the Nbr protein level and miR-34-3p trimming pattern were fully rescued by introducing the wild-type genomic \textit{nbr} transgene (Fig. 2C). Importantly, rescue of miRNA trimming activity was dependent on the catalytic residues of the Nbr exonuclease domain: mutating catalytic residues (D435A,E437A) within the genomic transgene (referred to as ‘cat-dead \textit{nbr}’) failed to rescue...
miR-34-5p trimming, despite robust protein expression (Fig. 2C). These data indicate that the lethality and sterility effects, previously thought to be associated with nbr, are instead independent of nbr function, and rather that the nbr null genetic combination yields viable and fertile adults.

nbr mutants show accelerated age-associated effects

Using the nbr null chromosomal combination (nbr\textsuperscript{D42257}/Df(2R)BSC312), we assessed the effect of the loss of nbr function to the animal. Although Nbr was highly expressed in the ovary, we saw no effect on ovary development in nbr null animals (Fig. S1A) and were able to obtain viable eggs from nbr null females. In addition, the number of eggs laid per day did not differ significantly between nbr null and wild-type rescued females with age (Fig. S1B).

We then examined the adult animal for effects. Intriguingly, nbr null animals showed an age-associated held-up wing phenotype (Fig. 3). At the time of emergence of the adult (eclosion), nbr null animals showed normal wing posture. However, by 20d, >90% of nbr mutants showed held-up wings (Fig. 3C). This effect was fully rescued by wild-type, but not the cat-dead, nbr genomic transgene (Fig. 3C). Together, these results suggest that nbr loss is associated with early onset of several age-associated effects in Drosophila.

Nbr affects the length of piRNAs

Nbr has been shown to impact the length of a subset of miRNAs in Drosophila (Han et al., 2011; Liu et al., 2011). However, it is unknown whether other classes of small RNAs, such as Piwi-interacting RNAs (piRNAs) (Guzzardo et al., 2013) and endogenous siRNAs (endo-si RNAs) (Czech & Hannon, 2011), are also affected by nbr. piRNAs are ~24-30nt small RNAs that are bound to Piwi-clade proteins of the Argonaute family, and are derived from heterochromatin, 3'UTRs of protein-coding genes, and euchromatic transposable elements. Endogenous siRNAs are ~21nt small RNAs identified in Drosophila, as well as C. elegans and mammals (Czech & Hannon, 2011). In Drosophila, endo-siRNAs are bound to Ago2, an siRISC component. Like piRNAs, endo-siRNAs are also derived from transposable elements, as well as other overlapping and hairpin RNA sources. Both piRNAs and endo-siRNAs are suggested to silence transposable elements, indicating the importance of these two classes of small RNAs to maintain genome integrity in the animal.

Given the high expression level of Nbr in the ovary, we examined the effect of nbr loss of function on piRNA and endo-siRNA length in the ovary libraries. We deep-sequenced and analyzed small RNA libraries from ovaries of wild-type, nbr del/wild-type (Df(2R)BSC312/+), nbr null, nbr null with pCaSpeR-nbr (WT), and nbr null with pCaSpeR-nbr (D435A,E437A) (‘rescue (WT nbr’) and nbr null with pCaSpeR-nbr (D435A,E437A) (‘rescue (cat-dead nbr’) . Because none of these genotypes had defects in ovary development (see Fig. S1 and data not shown), none of the effects on the length of endo-siRNAs and piRNAs were likely due to loss of specific tissue or cell types in the ovary.

We first confirmed the effects of Nbr on miRNAs, such as miR-34-5p and miR-305-5p in the ovary libraries. These miRNAs showed a higher portion of longer isoforms in the nbr null, which was rescued by the wild-type, but not by the cat-dead nbr transgene (Fig. S2A-D). We also...
piRNAs are predominantly derived from germline cells and associated with Aub, Ago3, and Piwi (Brennecke et al., 2007). However, piRNAs are also expressed in somatic cells of the ovary, which are predominantly derived from the flamenco locus (Malone et al., 2009). To examine whether the effect of Nbr on piRNAs was tissue specific, we mapped small RNA reads to the flamenco locus as well. This analysis indicated that Nbr loss did not lead to accumulation of long forms of flamenco piRNAs (data not shown). Thus, Nbr predominantly affects the length of piRNAs from germline cells and not somatic cells of the ovary of *Drosophila*.

We next examined individual endo-siRNA loci. Among the 49 endo-siRNA loci identified in *Drosophila* ovaries (Czech et al., 2008), none of the loci appeared to be modulated by nhr as defined by our statistical threshold (see Methods).

**Discussion**

Here, we have characterized the biological function of the nhr gene to the organism in *Drosophila* and found that loss of nhr leads to age-associated defects of brain degeneration, declining locomotion, and wing postural defects. Although previous studies suggested lethality and sterility were associated with nhr, in the studies here we used a combination of the original nhr allele in trans to a deficiency for the locus. In addition, we rescued the effects of this nhr null combination with genomic nhr expression transgene, but not by a catalytically dead transgene, confirming association with nhr function, and indicating that these defects are indeed associated with the enzymatic activity of Nbr. Some of these defects associated with nhr overlap with those of miR-34-5p (brain degeneration, loss of climbing ability, shorter lifespan); however, whether these phenotypes depend on the loss of 3’end trimming of miRNAs and notably miR-34-5p, or other functions of Nbr on small RNAs, awaits further study. We also observed that the nhr null animals rescued with the catalytically mutated genomic nhr transgene showed a consistent and striking lifespan reduction of ~50% (M. Abe and N. M. Bonini, unpublished data), suggesting potentially broader roles of Nbr. We note that this effect and the effect on climbing (see Fig 4C) are worse with the catalytically dead genomic transgene compared to the null situation. This indicates that there may be residual nhr activity for those functions that is worse with the catalytically dead form or that nhr functions in a complex with a more severe effect when a catalytically compromised protein is expressed.

Given that Nbr affects the length of not only miRNAs, but also piRNAs, Nbr could potentially trim the 3’ends of a much broader species of RNA substrates, including other long and short noncoding RNAs and miRNAs. It is worth-noting that the potential homologues of the Nbr exonuclease domain in mammals include EXD3 and Werner syndrome protein (WRN) (Liu et al., 2011), the latter of which is associated with a premature aging disorder. Even though it is not yet clear whether mammalian WRN impacts 3’end heterogeneity of small RNAs, future studies in mammalian systems might reveal a link between the control of 3’end heterogeneity of small RNAs and aging processes across species.

Ours and others’ studies suggest a model of how Nbr impacts the length of miRNAs (Han et al., 2011; Liu et al., 2011). In this model, Nbr interacts with Ago1 (miRISC) to trim the 3’end of miRNAs. The findings we present here indicate that Nbr also impacts the length of select piRNAs, leading to their shortening at the 3’end. The current model for piRNA biogenesis suggests that the primary biogenesis starts with the transcription of the piRNA clusters (Guzzardo et al., 2013). The 3’S’end of piRNAs is thought to be defined by an endonuclease Zucchini (Zuc) (Ipsaro et al., 2012; Nishimasu et al., 2012). Following the loading of the
piRNA intermediates into Piwi proteins, a Mg²⁺-dependent 3' trimming activity is required to generate mature lengths of piRNAs (silkworm in vitro assay (Kawaoka et al., 2011)). Based on this model, one possibility is that Nbr, a predicted Mg²⁺-dependent 3’-to-5’ exonuclease, might trim the end of piRNA intermediates to generate different length piRNAs. Our finding that loss of nbr gene function affects the length of piRNA reads with the same 5’ start site is consistent with a model in which trimming of the piRNA 3’ end occurs after the 5’ end has been defined. In considering this model, it is of note that piRNAs and endo-siRNAs are protected at the 3’ end by 2’-O-methylation, in contrast to miRNAs that are typically unmodified at the 3’ end (Czech & Hannon, 2011). Given that 2’-O-methylation of small RNAs at the 3’ end is protective from 3’ end trimming, by this model, Nbr likely trims the 3’ end of piRNAs prior to the protection by 2’-O-methylation. Alternatively, Nbr might affect the length of piRNAs in a more indirect manner. It is intriguing that the three Drosophila Piwi-clade proteins, Piwi, Aub, and Ago3, are loaded with slightly different length piRNAs: Piwi is bound by the longest piRNAs, followed by Aub and Ago3 (Brennecke et al., 2007). Given this observation, the change in the length of piRNAs upon nbr loss might instead reflect a change in the loading pattern of piRNAs among these different Piwi-clade proteins. Further studies are required to reveal additional mechanistic detail into nbr modulation of the length of piRNAs.

Despite the effect of nbr on the length of piRNAs, nbr loss did not lead to an obvious developmental defect in the ovary or a change in fertility with age, in contrast to other mutations with severe effects on piRNA biogenesis (Lin & Spradling, 1997; Cox et al., 1998; Harris & Macdonald, 2001). Rather, our analysis indicates that Nbr has a subtle impact on shaping the piRNA population. This fine-tuned role of nbr explains why screens for components of the primary piRNA biogenesis pathway did not identify nbr as a candidate (Czech et al., 2013; Handler et al., 2013; Muerdter et al., 2013), as such screens have been focused on genes with dramatic effects. The role of trimming by Nbr on miRNA function has been assessed with the study of miR-34 upon expression of a catalytically mutant form of nbr in cultured cells, where miR-34 silencing was compromised by ~20% (Han et al., 2011). The functional impact of nbr on piRNA length for their activity may also be similarly fine-tuned; our attempts to define an impact on transposon activity in the ovary failed to reveal an effect (M. Abe and N. M. Bonini, unpublished data). However, it is intriguing that transposons have recently been shown to become mobilized in the adult fly brain with age (Li et al., 2013; Perrat et al., 2013), and our other studies have indicated a shift with age in the loading of miRNAs between the miRNA RISC and the

Fig. 4 nbr null animals show age-associated defects. Paraffin sections of wild-type, nbr del/+ (Df(3L)BSC312/+), nbr null (nbr50257/Df(3L)BSC312), rescue (WT nbr) (nbr null; pCaSpeR-nbr (wild-type))+, and rescue (cat-dead nbr) (nbr null; pCaSpeR-nbr (D435A,E437A)+) heads at 3d and 30d. Scale bar in top left panel, 0.1 mm for all panels. (B) Quantification of brain vacuolization at 3d and 30d. nbr null shows an increase in vacuoles with age that is rescued by WT nbr transgene but not cat-dead nbr. (C) Climbing ability of animals with age shows that nbr null displays rapid loss of climbing that is rescued by WT nbr, but is worse with cat-dead nbr. Values in B and C are mean ± standard error of the mean of three independent experiments. *P < 0.01 compared to wild-type control using one-way ANOVA followed by Dunnett's test.

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Fig. 5 nbr affects the length of piRNAs with the same 5’end. A–D. Abundance of piRNA reads with the indicated length relative to the total number of reads originating from that specific piRNA locus and start site. Graphs for piRNA locus 1, start sites (A) 2175279 and (B) 2328563, and piRNA locus 6, start sites (C) 23299704 and (D) 23299198, are highlighted with red dots and arrows in E and F. Insert shows abundance of the specific reads plotted, which is not consistently different for the different genotypes. Start sites are numbered according to the position of the first nucleotide of the reads in the reference chromosome sequence (dm3 Drosophila genome assembly). E,F. Density plots of piRNA loci 1 (E) and 6 (F) for wild-type (top panels) and nbr null (bottom panels) flies. We observed no significant difference in genomic location of origin or overall read abundance of piRNA loci between the genotypes. The start positions for the piRNA reads that are of different length in nbr vs control in A–D are noted with red dots and highlighted with red arrows. Genotypes: wild, wild-type (w1118°), def: nbr deficiency/+ (Df(3L)BSC312/+), null: nbr null (nbrP02257/Df(3L)BSC312). rescue: nbr null with genomic rescue of wild-type nbr (nbr null; pCaSpeR-nbr (D435A,E437A)+). cat: nbr null with genomic rescue with catalytically dead nbr (nbr null; pCaSpeR- nbr (D435A,E437A)+/v). The t-statistic describing the ratio of departure in the abundance of piRNA reads compared to the wild-type control was calculated for each specific piRNA locus, start site, and read length. The t-statistic was then converted to the corresponding P-value using the sum total of reads being considered as the number of degrees of freedom, and it was adjusted for multiple comparisons using the false discovery rate (FDR). In addition, we computed Cohen’s d to indicate the effect size. **P < 0.05 compared to wild-type and Cohen’s d ≥ 0.6. ***P < 0.01 compared to wild-type and Cohen’s d ≥ 0.6. Detailed information on all piRNAs with significance is listed in Table S1 (Supporting information).

siRNA RISC (Abe et al., 2014), coupled with age-associated defects at the organismal level if the integrity of small RNAs that are loaded into siRISC is compromised. Given the impact of nbr on age-associated biological processes and the modulation of small RNA loading with age revealed by our earlier study of trimmed RNAs (Abe et al., 2014), there may be additional roles of nbr on small RNA populations in the brain with age.

Materials and methods

Fly stocks

Flies were grown in standard cornmeal molasses agar medium at 25 °C. nbrP02257 (FlyBase ID: FBti0050491) and nbr deficiency line (Df(3L)BSC312/CyO) (FlyBase ID: FBst0024338) were obtained from the Bloomington Stock Center. nbrP02257 line was backcrossed into a homogenous wild-type background (Bloomington Stock Line 5905 (BL5905), FlyBase ID: FBst0005905, w1118°) for five generations. All lines used were generated or crossed into the same wild-type background, to maintain a homogenous and consistent background for all assays.

Genomic nbr transgenic flies

Wild-type, HA-tagged (C-terminus of Nbr), and the catalytically mutated (D435A,E437A) nbr transgenics, which include ~650 bp upstream and ~150 bp downstream of nrb ORF, were generated by PCR and cloned into pCaSpeR4 vector. Because of unanticipated difficulties on amplifying the entire region of nbr locus with a single PCR reaction, we amplified the genomic nbr region with the combination of regular PCR from genomic DNA (BL 5905) and overlapping PCR to eventually amplify the whole genomic region (~3.2 kb) using the primers, 5’-TAAGAAGCCGATCTGCAGGAAT-3’ and 5’-TGCCGTTCCTCGTCCCT-GAT-3’. The concept of overlapping PCR is described in Young & Dong (2004) and Xiong et al. (2006). Based on this wild-type genomic nbr sequence, we inserted 1 × HA tag sequence at the C-terminus, as well as inserted mutations (D435A,E437A) at the exonuclease domain by additional FCRs. The genes were then subcloned into pCaSpeR4. Constructs were sequence-verified. Genomic constructs were prepared by maxi-prep (Qiagen, Germantown, MD, USA) and injected into BL5905 (w1118°) (Genetic Services, Cambridge, MA, USA), and transgenic flies were selected and maintained over the TM6C,Sb balancer chromosome.

Nbr antibody

A rabbit polyclonal antibody against the Nbr protein was developed using a synthetic peptide of residues 10-23 (C-APIPAGEFESDEENME) (ProSci Incorporated, Poway, CA, USA). The serum was affinity-purified to enrich for IgG directed to the Nbr peptide antigen. For Western immunoblots, the purified antibody was used at 1/2000.

Western immunoblots

Fly tissues were resuspended in RIPA buffer, followed by grinding and centrifugation to remove debris. The supernatant was measured by Bradford assay, and 25–50 µg of protein in NuPAGE LDS sample buffer (4x) (NP0007, Life Technologies, Carlsbad, CA, USA) was loaded in each lane. NuPAGE Novex 4-12% Bis-Tris gel (#NP0321BOX, Life Technologies, Carlsbad, CA, USA) were loaded and run in 1xNuPAGE MES SDS Running Buffer (#NP00002, Life Technologies, Carlsbad, CA, USA). Western transfer was performed on PVDF membrane, followed by blocking in 5% milk/TBST for 1 h at 4 °C. The membrane was incubated with primary antibody (anti-Nbr, 1/2000) at 4 °C overnight. After washing the membrane in TBST buffer 3 times (5 min each), the membrane was incubated with secondary antibody (goat anti-rabbit IgG-HRP, #sc-2030, Santa Cruz Biotechnology, Inc., Dallas, TX, USA) at 4 °C for 2 h. The membrane was washed in TBST 3 times (5 min each), followed by signal development by Pierce ECL plus Western Blotting Substrate (#32132, Thermo Fisher Scientific, Waltham, MA, USA). The image was scanned by Fujifilm LAS-3000 Imager (Fujifilm, Tokyo, Japan).

Immunohistochemistry

Ovaries were dissected in PBS, followed by fixation in 4% paraformaldehyde in PBS for 20 min at room temperature. After washing with PBST (PBS + 0.2% Triton X-100) twice, the ovaries were permeabilized in PBST-5 (PBS + 0.5% Triton X-100 with 5% goat serum). After washing once with PBST-B (PBS + 0.2% Triton X-100 + 1% BSA), the ovaries were incubated with primary antibody (1:150, rat monoclonal anti-HA: 3F10, #11867423001, Roche, Indianapolis, IN, USA) and rabbit anti-Ago3 (1:1000) (Brennecke et al., 2007)) in PBST-B at 4 °C overnight. Washing was performed in PBST 3 times, 2 min each at room temperature, followed by 20 min wash in PBST 3 times and 2 min wash in PBST-B once at room temperature. The ovaries were incubated with secondary antibody Alexa Fluor 488 goat anti-rat IgG (H+L) (1:100, #A-11006, Life Technologies) in PBST for 2 h at 4 °C. After secondary antibody incubation, washing was performed in PBST 3 times, 2 min each at room temperature, followed by 20 min wash in PBST 3 times and 2 min wash in PBST-B once at room temperature. After washing, the ovaries were carefully separated on slides by fine forceps and mounted.
with Vectashield mounting medium with DAPI (#H-1200; Vector laboratories, Burlingame, CA, USA).

**Small RNA Northern hybridization**

Total RNA was extracted from fly tissues using Trizol Reagent (#15596-018, Life Technologies), following the manufacturer’s protocol. Total RNA of 3–10 μg depending on the experiment were loaded per lane onto 15% TBE-era-urea gels (#EC6885BOX, Life Technologies Carlsbad, CA, USA), and run for 90 min at 180 V, followed by the transferring to nylon membrane (Hybond N+, GE Healthcare, Piscataway, NJ, USA). After UV cross-linking and prehybridization (50 °C, 1 h), the membranes were hybridized with \(^{32}P\)-labeled probes overnight at 50 °C. Two DNA oligonucleotides were annealed to obtain the template for each RNA probe. The DNA oligonucleotides used to make probe templates were miR-34-5p (5'-GAT ACG ACT CAC TAT AGG GAG A-3', 1 h), and catalytically dead rescue (ntr null; pCaSpeR-ntr (WT)), and catalytically dead rescue (ntr null; pCaSpeR-ntr (D435A,E437A)), using Trizol Reagent (#15596-018, Life Technologies Carlsbad, CA, USA) following the manufacturer’s protocol. The small RNAs between ~16 and ~29 nt in size were purified from 15% TBE-era-urea gel (#EC6885BOX, Life Technologies Carlsbad, CA, USA). Small RNA libraries were prepared using Illumina’s TrueSeq small RNA sample preparation kit (#RS-200-0012, Illumina, Inc. San Diego, CA, USA), following the manufacturer’s protocol. The libraries were sequenced on HiSeq2000 platform (Illumina, San Diego, CA, USA).

**Brain paraffin sections**

Adult female heads (3d and 30d) were used for paraffin sections as described (Liu et al., 2012; Abe et al., 2014). Brain vacuoles were counted in the whole area of each brain section except retina, through five continuous frontal sections, starting from the center section (defined as the section in which the brain occupies the largest region, and the esophagus is obvious) toward posterior direction.

**Computational analyses**

**Alignment**

Trimming of the adapter sequences from the obtained reads was performed by an in-house script (S. Fisher and J. Kim). The trimmed reads were then aligned to the dm3 (BDGP Release 5) genome assembly of *Drosophila melanogaster* using the RUM pipeline (Grant et al., 2011). We set RUM to use 0 mismatches while aligning using Bowtie (Langmead, 2010) and 100% identity for Blat (Kent, 2002). GEO number for libraries is GSE50055.

**Mapping to small RNAs**

miRNA stem-loop sequences were obtained from miRBase. Genome coordinates of piRNA loci in *Drosophila* ovaries were obtained from Brennecke et al. (2007). Endogenous siRNA loci in *Drosophila* ovaries were obtained from Czech et al. (2008). Only the uniquely mapped reads with no mismatches and length ranging from 19 to 31 nt that mapped to each small RNA locus were counted. To control for sequencing depth, the read counts for each locus were normalized by dividing them with the total small RNA read number in each library after trimming. In addition to enumerating the total number of reads mapping to each small RNA locus, we also quantified the read counts for each unique isoform.

**Length distribution and density plot of piRNAs and endo-siRNAs**

We only considered the small RNA loci that were expressed in all of the five genotypes and comprised of reads belonging to two or more length categories (19–31 nt) with a total read count of ≥5 in at least one of the genotypes. Then for each of the genotypes, for each small RNA locus, and for each origin position within that locus, we computed the t-statistic for every length category present to measure the departure of the fraction of reads of a given length from that of wild-type. The t-statistic is the ratio of the difference between the observed value and the expected value to the standard error. The t-statistic was converted to the P-value, and we then identified significant upward and downward peaks in the distribution (FDR ≤ 0.05 and effect size indicated by Cohen’s d ≥ 0.6 which corresponds to a moderate-to-large effect (Cohen, 1988)). Small RNAs whose long isoforms significantly increased in abundance in ntr null and catalytically dead ntr rescue genotypes compared to wild-type control, and whose long isoforms did not increase significantly in ntr del/+ and ntr wild-type rescue genotypes compared to wild-type control, were considered to be affected by ntr. A detailed list of start positions, the effect of increase length or decreased length, Cohen’s d value, and P-values are given in Table S1 (Supporting information).

**miRNA ratio plot**

For generating miRNA ratio plot, the most abundant isoform from each 5p and 3p arm of each miRNA stem-loop was first identified. The fraction of the most abundant isoform among all the isoforms starting
with the same 5' nt position was calculated in wild-type and nbr null. Finally, the ratio of the wild-type and nbr null fractions was calculated by dividing nbr null/wild-type fraction (‘Ratio nbr null/wild-type’, y-axis of Figure S2). Only miRNA isoforms with > 70 raw reads in both wild-type and nbr null are shown in the graph (Figure S2).

Egg-lay count

The effect of nbr loss-of-function mutation versus nbr wild-type rescue on female fecundity was examined by counting eggs laid each day by single females over a 40-day time course. A standard cornmeal/molasses medium was poured into lids of 35 × 10 mm tissue culture dishes which served as egg-laying plates that were taped to the bottom of cages made from Drosophila culture bottles with multiple small holes punched in to provide ventilation. Single females of the nbr null genotype (nbr
\textsuperscript{702257/DF(2)UB5C312} and nbr wild-type rescue (nbr
\textsuperscript{702257/DF(2)UB5C312}, pCaSpeR-nbr) were placed in cages with the plates sprinkled with active yeast to promote egg laying. The plates were replaced every day with active yeast to promote egg laying over 24-h periods were counted.

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Conflict of interest

None declared.

References


Supporting Information

Additional Supporting Information may be found in the online version of this article at the publisher’s web-site.

Table S1. piRNA lengths affect by nbr.

Fig. S1. Nbr null females have normal ovaries and normal fecundity with age.

Fig. S2. Length distribution of select miRNAs in ovary deep-sequencing libraries.