Arginine methylation of Aubergine mediates Tudor binding and germ plasm localization

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ABSTRACT

Piwi proteins such as Drosophila Aubergine (Aub) and mouse Miwi are essential for germline development and for primordial germ cell (PGC) specification. They bind piRNAs and contain symmetrically dimethylated arginines (sDMAs), catalyzed by dPRMT5. PGC specification in Drosophila requires maternal inheritance of cytoplasmic factors, including Aub, dPRMT5, and Tudor (Tud), that are concentrated in the germ plasm at the posterior end of the oocyte. Here we show that Miwi binds to Tdrd6 and Aub binds to Tudor, in an sDMA-dependent manner, demonstrating that binding of sDMA-modified Piwi proteins with Tudor-domain proteins is an evolutionarily conserved interaction in germ cells. We report that in Drosophila tud1 mutants, the piRNA pathway is intact and most transposons are not de-repressed. However, the localization of Aub in the germ plasm is severely reduced. These findings indicate that germ plasm assembly requires sDMA modification of Aub by dPRMT5, which, in turn, is required for binding to Tudor. Our study also suggests that the function of the piRNA pathway in PGC specification may be independent of its role in transposon control.

Keywords: Argonaute; Aubergine; piRNA; Piwi; Tudor; miRNA

INTRODUCTION

Ribonucleoprotein complexes composed of Argonaute proteins bound to small RNAs form the essential effector complexes of RNA silencing (Liu et al. 2008). Argonaute proteins contain two characteristic domains termed PAZ and PIWI and are divided into two subclades: Ago and Piwi (Carmell et al. 2002). Ago proteins are typically expressed in most cell types and bind to microRNAs (miRNAs) and short interfering RNAs (siRNAs) (Liu et al. 2008). Piwi family proteins are expressed in the germline and bind to piRNAs that consist of 25–31 nucleotides (nt) (Klattenhoff and Theurkauf 2008; Ghildiyal and Zamore 2009; Kim et al. 2009). The PIWI domain of Ago and Piwi proteins is an RNase H protein domain that may display endonucleolytic activity toward RNAs that are complementary to bound miRNAs or piRNAs (Ghildiyal and Zamore 2009; Kim et al. 2009).

Piwi proteins are essential for germline development and germ cell specification. Drosophila melanogaster expresses three Piwi proteins termed Aubergine (Aub) (Harris and Macdonald 2001), Piwi (Cox et al. 1998), and Ago3 (Brennecke et al. 2007; Gunawardane et al. 2007; Li et al. 2009). Mice express three Piwi proteins known as Mili (Kuramochi-Miyagawa et al. 2004), Miwi (Kuramochi-Miyagawa et al. 2001; Deng and Lin 2002), and Miwi2 (Carmell et al. 2007; Girard and Hannon 2008). The sequence diversity of piRNAs is immense, and hundreds of thousands of unique piRNAs have been described in diverse species (Aravin et al. 2003, 2006; Girard et al. 2006; Grivna et al. 2006; Lau et al. 2006; Ruby et al. 2006; Saito et al. 2006; Watanabe et al. 2006; Brennecke et al. 2007; Houwing et al. 2007; Kirino et al. 2009). piRNAs originate from piRNA clusters but also from many other genomic areas, including intergenic and genic regions. Many piRNAs are derived from transposable and repetitive elements and also target transposons (Malone and Hannon 2009). However, large classes of piRNAs in different...
species (for example, pachytene piRNAs [Girard et al. 2006] in mice or 21U piRNAs in Caenorhabditis elegans [Ruby et al. 2006]) do not appear to be derived from or to target transposons, and their targets and functions remain unknown.

Arginine methylation is an important post-translational modification that is catalyzed by protein methyltransferases (PRMTs) and occurs either as asymmetric arginine dimethylation (aDMA) or symmetric arginine dimethylation (sDMA) (Krause et al. 2007). PRMT5 and its cofactor MEP50/WD405 form the methylosome (Friesen et al. 2001, 2002; Meister et al. 2001) and deposit sDMAs in diverse proteins, such as the Sm proteins, components of small nuclear ribonucleoproteins (snRNPs) (Friesen et al. 2001, 2002; Meister et al. 2001), and histones (Zhao et al. 2009). Methylated arginines, and in particular sDMAs, bind to Tudor domains and regulate protein–protein interactions (Bedford and Richard 2005; Cote and Richard 2005). For example, sDMA modification of Sm proteins promotes their binding to the Tudor domain of the survival of motor neurons (SMN) protein (Selenko et al. 2001), and this interaction facilitates snRNP assembly in mammals (Friesen et al. 2001; Meister et al. 2001; Boisvert et al. 2002; Gonsalvez et al. 2007).

Specification of primordial germ cells (PGCs) in the developing Drosophila embryo requires maternal inheritance of cytoplasmic factors that are concentrated in the posterior pole in an area known as the pole or germ plasm (Ephrussi and Lehmann 1992; Jongens et al. 1992; Williamson and Lehmann 1996; Houston and King 2000; Mahowald 2001; Strome and Lehmann 2007; Bastock and St Johnston 2008; Dansereau and Lasko 2008). Pole plasm contains electron-dense granules and related amorphous material that is rich in ribonucleoproteins and mitochondria; it is related to nuage, which surrounds the nurse cell nuclei and contains some of the same components (Dansereau and Lasko 2008; Chuma et al. 2009). Similar electron-dense amorphous material often in close apposition to mitochondria is found in the cytoplasm of germ cells in various species and is known as P granules in C. elegans, germinal granules in Xenopus, and intermitochondrial cement and chromatoid bodies in mice (Dansereau and Lasko 2008; Chuma et al. 2009). Similar electron-dense amorphous material often in close apposition to mitochondria is found in the cytoplasm of germ cells in various species and is known as P granules in C. elegans, germinal granules in Xenopus, and intermitochondrial cement and chromatoid bodies in mice (Dansereau and Lasko 2008; Chuma et al. 2009). A set of maternally expressed genes (often referred to as posterior group or grandchildless genes) are required for PGC specification (Schupbach and Wieschaus 1986), and invariably the protein or RNA products of these genes are concentrated in the pole plasm and are incorporated in PGCs (Ephrussi and Lehmann 1992; Williamson and Lehmann 1996; Houston and King 2000; Mahowald 2001; Strome and Lehmann 2007; Bastock and St Johnston 2008; Dansereau and Lasko 2008). Loss-of-function mutations of grandchildless genes lead to offspring that do not form PGCs and are thus sterile (Williamson and Lehmann 1996; Houston and King 2000; Mahowald 2001; Strome and Lehmann 2007; Bastock and St Johnston 2008; Dansereau and Lasko 2008).

Among these genes are aub, which encodes the piRNA-binding protein Aub (Harris and Macdonald 2001; Brennecke et al. 2007; Gunawardane et al. 2007); csul/dart5, the Drosophila homolog of PRMT5 (dPRMT5) (Gonsalvez et al. 2006; Anne et al. 2007); valois, the Drosophila homolog of MEP50 (dMEP50) (Anne and Mechtler 2005; Cavey et al. 2005); and tudor (Boswell and Mahowald 1985; Thomson and Lasko 2004, 2005; Arkov et al. 2006). In valois-null mutants, dPRMT5 is destabilized, resulting in a loss of sDMA modifications of target proteins, indicating that dMEP50 is required for sDMA production in concert with dPRMT5 (Gonsalvez et al. 2006). Piwi family proteins, including Aub, from diverse species, contain sDMAs, and the sDMAs in Drosophila are catalyzed by dPRMT5 (Kirino et al. 2009). These findings explain the genetic relationship between aub, csul, and valois by demonstrating that Csul/dPRMT5 (and presumably its Valois/dMEP50 cofactor) methylate Aub (Kirino et al. 2009).

Tudor is an ~285-kDa protein that contains 11 Tudor domains (Boswell and Mahowald 1985; Thomson and Lasko 2004, 2005; Arkov et al. 2006). Tudor domains of other proteins have been shown to be bound to methylated amino acids and specifically to sDMAs, suggesting that an important function of Tudor domains is to bind to sDMA-containing proteins (Selenko et al. 2001; Bedford and Richard 2005; Cote and Richard 2005). In mice, several Tudor-domain-containing proteins (Tdrd1, Tdrd4, Tdrd5, Tdrd6, and Tdrd7) are expressed in the germline (Smith et al. 2004; Hosokawa et al. 2007). Genetic disruption of Tdrd1 leads to arrest in spermatogenesis and male sterility (Chuma et al. 2006). In Tdrd1-null spermatocytes, there is a strong reduction of the intermitochondrial cement, but the chromatoid body shows a milder disruption of its architecture (Chuma et al. 2006). Tdrd1 contains four Tudor domains and associates predominantly with Miwi (Reuter et al. 2009; Vagin et al. 2009; Wang et al. 2009). It was recently shown that sDMA modifications in Miwi are required for binding to Tdrd1, and in the absence of Tdrd1, there is up-regulation of L1 retrotransposons (Reuter et al. 2009; Vagin et al. 2009). Tdrd6 is the mouse homolog of Drosophila Tudor; it contains seven Tudor domains and associates predominantly with Miwi (Vagin et al. 2009; Vasileva et al. 2009), and also with Miwi (Vagin et al. 2009; Vasileva et al. 2009). Interestingly, in Tdrd6-null mice, the architecture of the chromatoid body is severely disrupted (Vasileva et al. 2009). In contrast to the transposon up-regulation that is seen in Tdrd1-null mice, Tdrd6-null mice do not show any de-repression of transposons (Vasileva et al. 2009), and the piRNA profile of Tdrd6-null spermatocytes is not altered (Vagin et al. 2009).

Here we demonstrate that Aub binds to Tudor and that the sDMAs of Aub are essential for this binding. We also show that Miwi binds to Tdrd6 and sDMAs of Miwi mediate Tudor binding in vitro. Thus, the binding of sDMA-modified Piwi family proteins with Tudor-domain-containing proteins is an evolutionarily conserved interaction in germ cells.
Furthermore, we report that in Drosophila tud1 mutants, neither the levels of Piwi proteins nor of piRNAs are affected in the female germline. However, the localization of Aub in the pole plasm is severely reduced. These findings indicate that pole plasm assembly requires arginine methylation of Aub by dPRMT5, which, in turn, is required for binding to Tudor. The finding that loss of Tudor results in only very mild transposon de-repression suggests that the function of the piRNA pathway in PGC specification may be independent of its function in transposon control.

RESULTS

We have previously shown the presence of symmetrically dimethylated arginines (sDMAs) in the amino termini of Piwi proteins from diverse species, including Drosophila Aubergine (Aub) and mouse Miwi, and we hypothesized that sDMAs might mediate interaction with Tudor-domain-containing proteins. To identify proteins that bind specifically to sDMAs of Aub and Miwi, we performed binding experiments using biotinylated peptides derived from the amino termini of Aub and Miwi that contain sDMAs (Fig. 1A). As controls, we used peptides with the same sequence but containing either unmodified arginines or arginines containing asymmetrical dimethyl groups (aDMAs) (Fig. 1A). We immobilized equal amounts of each biotinylated peptide on streptavidin-Sepharose and then incubated the Miwi peptides with mouse testis lysates and the Aub peptides with Drosophila ovary lysates. After extensive washes, we analyzed bound proteins with NuPAGE and silver staining. As shown in Figure 1B, Miwi peptide containing unmodified arginines bound numerous proteins. In contrast, very few proteins bound to sDMA or aDMA Miwi peptides (Fig. 1B). Two prominent bands at ~200 kDa were specifically bound to the sDMA-Miwi peptide (Fig. 1B), and they were identified as Tdrd6 by mass spectrometry (see Supplemental Table). The upper band corresponded to full-length Tdrd6, and the lower band corresponded to a naturally found C-terminally truncated form of Tdrd6 (known as ΔC-Tdrd6) (Vasileva et al. 2009). To confirm the results of the mass spectrometry analysis, we performed Western blotting on the eluates of the Miwi peptides, and we detected Tdrd6 and ΔC-Tdrd6 only in the eluates of sDMA-Miwi peptides (Fig. 1B).

We performed a similar experiment and analysis with Aub peptides. As shown in Figure 1C, a >200-kDa protein band was specifically seen in eluates from sDMA-Aub and was identified by mass spectrometry as Drosophila Tudor protein (Supplemental Table). Although the calculated molecular weight of Tudor is ~285 kDa, its mobility is faster in NuPAGE. Western blot analysis of the eluates with anti-Tudor antibody confirmed the presence of Tudor in sDMA-Aub eluates. These findings show that Drosophila Tudor protein binds specifically to sDMA-Aub, and Tdrd6, the mouse homolog of Tudor, binds to sDMA-Miwi. It is interesting to note that numerous proteins bind to Aub and Miwi peptides with unmodified arginines, while far fewer proteins bind to aDMA-, or sDMA-modified Aub and Miwi peptides, and only Tudor or Tdrd6 binds specifically to sDMA-Aub and sDMA-Miwi, respectively.

We next performed immunoprecipitations using an antibody against Tdrd6 or non-immune rabbit serum (NRS, negative control) from mouse testis, and we probed the immunoprecipitates with Tdrd6 and Miwi antibodies. The properties of our anti-Miwi antibody are shown in Figure 2A. As shown in Figure 2B, Miwi was present in Tdrd6 immunoprecipitates, consistent with recent reports of Miwi–Tdrd6 interaction (Vagin et al. 2009; Vasileva et al. 2009). We also performed immunoprecipitations using anti-Tudor or NRS from wild-type (wt) and dPRMT5/csul-null Drosophila ovary lysates, and we probed the immunoprecipitates with anti-Tudor or anti-Aub antibodies. csul-null flies cannot produce symmetrical methylation on arginines, and we have previously shown that Aub does not contain sDMAs in ovaries of csul-null flies. As shown in Figure 2C, Aub was found in the anti-Tudor immunoprecipitates from wild-type (wt) but not...
Tudor termed Tudor-modified to sDMAs are required for this interaction. with Tudor and that the four arginines that can be shown in Figure 3B (upper panel), Tudor bound to Aub-WT or mutant Aub-4K expressed stably in Drosophila S2 cells (which express dPRMT5), and equivalent amounts of S2 lysates prior to immunoprecipitation are shown. (C) Tudor or NRS immunoprecipitates from mouse testis were probed with indicated antibodies; total lysates prior to immunoprecipitation are shown. (Fig. 3B, bottom panel) were used in binding experiments with in vitro translated and radiolabeled Tudor protein. As shown in Figure 3B (upper panel), Tudor bound to Aub-WT but not Aub-4K, indicating that Aub protein interacts with Tudor and that the four arginines that can be modified to sDMAs are required for this interaction.

Previous work has shown that a deletion mutant of Tudor termed Tud-Δ3, expressing Tudor domains 1 and domains 7–11, rescues germ cell formation in a strong loss of function tud1 mutant background (Fig. 3C). In contrast, deletion mutants of Tudor domains 7–11 (Fig. 3C, Tud-Δ1) and deletion of domains 1–9 (Fig. 3C, Tud-Δ2) were unable to rescue germ cell formation in strong loss-of-function tud alleles, indicating that domains 7–11 of Tudor are critical for germ cell formation (Arkov et al. 2006). We tested the ability of these deletion mutants to interact with Aub protein using in vitro binding experiments. As shown in Figure 3D, Tud-Δ3 but not Tud-Δ2 bound specifically to Aub-WT. We observed a strong, nonspecific binding of Tud-Δ1 to the beads (that we did not observe with full-length Tudor) (Fig. 3B), suggesting that the protein produced from the Tud-Δ1 construct might be misfolded and prone to nonspecific binding. Overall, these binding experiments suggest that Tudor domains 7–11, which are required for germ cell formation in vivo, interact with Aub.

Next, we analyzed Piwi proteins and the piRNA pathway in tud1 mutant ovaries. tud1 is a strong loss-of-function mutant allele (K1036UAG) that encodes a prematurely truncated form of Tudor that is not detectable in immunoblots (Fig. 4A; Arkov et al. 2006). However, the levels of all three Drosophila Piwi proteins (Piwi, Aub, and Ago3) and of the miRNA-binding Ago1 protein were the same between wild-type and tud1 ovaries. Similar amounts of Aub and Piwi proteins were immunoprecipitated between wild-type and tud1 ovaries (Fig. 4B), and the amount of bound piRNAs was the same between wild-type and tud1 ovaries (Fig. 4C). We have previously reported a reduction of Aub and Ago3 protein levels in csul ovaries (Kirino et al. 2009). We have found that there is variability in the levels of Aub in csul ovaries that may correlate with culture conditions. It is also possible that loss of dPRMT5 may affect an as-yet-unidentified factor(s) that leads to reduction of Aub protein levels.

We also tested the levels of several transposon transcripts, whose expression is sensitive to mutations that disrupt piRNA-mediated transposon silencing (Vagin et al. 2006; Li et al. 2009) in csul (dPTMT5-null) and tud1 ovaries. As shown in Figure 4D, transcript levels of Diver, HeT-A, Accord2, and Blood were clearly up-regulated in csul ovaries. However, in tud1 ovaries, only the Blood retrotransposon was up-regulated. Next, we analyzed by confocal microscopy the localization of Aub in wild-type and tud1 ovaries. As shown in Figure 4E, the levels and localization of Aub were the same between wild-type and tud1 early egg chambers. However, there was a marked reduction of Aub that is localized in the pole plasm in tud1 ovaries (Fig. 4F). Collectively, these findings indicate that in the absence of Tudor, neither the levels of Piwi proteins nor piRNAs are affected in the female germline, and silencing of most transposons is intact. However, the localization of Aub in the pole plasm is severely affected.

**DISCUSSION**

We have recently shown that dPRMT5 (Csul/dart5) catalyzes sDMA modifications of Aub (Kirino et al. 2009). We predict that a similar requirement for dMEP50/Valois in Aub methylation is required since dPRMT5 stability and function require dMEP50. In this study, we identify that an important and evolutionarily conserved function of sDMA modifications of Piwi family proteins is to direct their binding to Tudor-containing proteins. One such interaction is between sDMA-modified Aub and Tudor in Drosophila oocytes. Collectively these findings provide an explanation for the relationship between the protein products of four posterior-group genes that has been previously elusive: dPRMT5 and dMEP50 produce sDMAs in Aub, which, in turn, are required for binding to Tudor (Fig. 5).

A general role of Tudor-domain-containing proteins and Piwi family proteins in germline development is now
becoming apparent. Mouse Tdrd1 binds to Mili (Reuter et al. 2009; Wang et al. 2009), and this interaction is dependent on sDMA modifications of Mili (Reuter et al. 2009; Vagin et al. 2009). Although the levels of Mili protein and bound piRNAs are not changed in Tdrd1-null spermatocytes (Reuter et al. 2009; Wang et al. 2009), the identity of the Mili-bound piRNAs is altered with over-representation of genic piRNAs at the expense of transposon-derived piRNAs (Reuter et al. 2009). This shift correlates with L1 transposon de-repression (Reuter et al. 2009; Vagin et al. 2009) and DNA demethylation (Reuter et al. 2009), which is similar to the phenotype observed in mili-null spermatocytes (Aravin et al. 2007). Furthermore, in the absence of Tdrd1 or Mili, Miwi2, which is normally a nuclear protein, delocalizes to the cytoplasm (Reuter et al. 2009; Vagin et al. 2009), and in the absence of Mili, the cytoplasmic Miwi2 is devoid of piRNAs (Aravin et al. 2007). Miwi2 also associates with Tdrd1 (Vagin et al. 2009). These findings indicate that the function of Tdrd1 is closely related to Mili and Miwi2, and Tdrd1 has an important role in specifying the piRNA content of Mili (Reuter et al. 2009) and the operation of the ping-pong cycle of piRNA amplification (Vagin et al. 2009).

Mouse Tdrd6 interacts with Miwi and Mili (Vagin et al. 2009; Vasileva et al. 2009), and we show in this study that Tdrd6 binds to sDMA-modified peptide of Miwi. In contrast to the Tdrd1-null mice, transposons are not de-repressed in Tdrd6-null spermatocytes (Vasileva et al. 2009), and the piRNA profile of Tdrd6-null spermatocytes is not altered (Vagin et al. 2009). This is consistent with our finding that most transposons are not up-regulated in tud1 Drosophila ovaries, with the exception of the Blood transposon. This may indicate that Tudor is required directly or indirectly for the biogenesis or function of a subset of piRNAs that may target Blood. Future deep sequencing studies of tud1 piRNAs will be required to address whether Blood derepression correlates with loss of cognate piRNAs. However, we note that the relationship between transposon derepression and loss of piRNAs is complex and not well understood. For example, despite widespread changes in the content and levels of piRNAs in Aub-null and Ago3-null ovaries, there is only partial overlap between the altered piRNAs and the de-repressed transposons (Li et al. 2009; Malone et al. 2009). It is also possible that piRNAs and piRNA-associated proteins target and regulate the expression of mRNAs whose protein products are important for the specification of germ cells. For example, the Drosophila AT-chX-1 and AT-chX-2 piRNAs are antisense to Vasa mRNA and down-regulate the expression of Vasa protein, which is essential for germ cell specification (Nishida et al. 2007; Li et al. 2009). An important goal of future studies will be to identify RNAs that are bound by piRNPs in the germ plasm.

It appears that specific members of the Piwi family of proteins function together with Tudor-domain-containing proteins. In that regard, Ago3 and Piwi will likely interact with specific Tudor-domain-containing proteins. It is interesting to note that Spindle E contains a Tudor domain along with an RNA helicase domain and is an important factor for piRNA biogenesis in Drosophila (Savitsky et al. 2006; Vagin et al. 2006; Malone et al. 2009). The mouse homolog of Spindle E is Tdrd9 and shows weak association...
with Miwi and Miwi2 (Vagin et al. 2009). Krimper, which is also required for piRNA biogenesis in Drosophila, contains a Tudor domain (Lim and Kai 2007). Interactions between these proteins and Piwi family proteins will be interesting to elucidate. At the same time, the occurrence of multiple Tudor domains in Tudor and other Tdrd’s suggests that they may form landing pads for additional DMA-containing or other proteins. It is likely that Tudor has multiple binding partners. The functions of Tudor with regard to germ cell specification and posterior patterning appear to involve different regions of the protein (Arkov et al. 2006), and ME31B, eIF4A, Aub, and TER94 have been identified as components of Tudor complexes (Thomson et al. 2008), although direct binding to Tudor has not been demonstrated for any of these proteins other than Aub. Further analysis of Tudor-binding proteins will be important to future studies of germ cell specification and will shed additional light on its function.

**MATERIALS AND METHODS**

**Analysis of the proteins interacting with peptides containing arginine methylations**

Miwi and Aub peptides (Fig. 1A) were synthesized by Millipore. Each peptide was immobilized on Streptavidin Sepharose High Performance (GE Healthcare) and incubated in the lysate produced from mouse testis (Pel-Freez Biologicals) (Miwi peptide) or Drosophila ovary lysate (Aub peptide) for 1.5 h at 4°C in a lysis buffer (20 mM Tris-HCl at pH 7.5, 200 mM NaCl, 2.5 mM MgCl₂, 0.5% NP-40, and 0.1% Triton X-100 in the case of Miwi peptides and complete EDTA-free protease inhibitors [Roche]; and the same buffer but containing 150 mM NaCl in the case of Aub peptides). After extensive washings, bound proteins were resolved by NuPAGE and visualized by silver staining.

**Western blots and immunoprecipitations**

Western blots and immunoprecipitations were performed as described (Kirino et al. 2009). Anti-Mili (17.8) (Kirino et al. 2009), anti-Flag M2 (Sigma), and anti-β-tubulin (E7; Developmental Studies Hybridoma Bank) were used in this study. Antibodies against the Drosophila Ago1, Aub, Piwi, and Ago3 were gifts from M.C. Siomi and H. Siomi (Keio University) (Miyoshi et al. 2005; Saito et al. 2006; Gunawardane et al. 2007). Drosophila Tudor antibody was described by Thomson et al. (2008). Anti-Tdrd6 antibodies were gifts from R. Jessberger (Mount Sinai School of Medicine) (Vasileva et al. 2009), and S. Chuma (Kyoto University) (Chuma et al. 2006). Anti-Miwi antibody was prepared by immunizing rabbits with a synthetic peptide coupled to KLH (C-ERGGRRRDFHD; Genscript); sera were affinity-purified over a column containing immobilized peptide.

**In vitro binding experiments**

Drosophila full-length Tudor and mini-tud constructs Δ1, Δ2, and Δ3 carrying an HA epitope at the N terminus cloned into
p[CaSpRe-2] (gifts from A. Arkov, Murray State University) (Arkow et al. 2006) were used as templates for the amplification of the four coding sequences (CDS) by PCR with Pfu Turbo polymerase (Stratagene), following the manufacturer’s instructions. PCR primers were:

Forward: 5’-CTCGAGACCATGTAACCGTGATGTCG-3’; and Reverse: 5’-TCACAGCTTCCTCAGGCT-3’.

After the addition of 3’ adenosine overhangs by incubation with 
Taq DNA polymerase and dATP, the CDS were cloned into pCR-XL-TOPO vector (Invitrogen). Recombinant plasmids were selected for same-strand orientation of CDS with vector T7 RNA polymerase promoter by restriction analysis and were verified by DNA Sequencing. One microgram of recombinant plasmid from each construct, linearized ~100 bases downstream from the stop codon, was used for in vitro translation using TNT reticulocyte lysate system in the presence of 35S-methionine in a 50 μl reaction for 2 h at 30°C. Recombinant wild-type and mutant Flag-Aub were produced in S2 cells and immunoprecipitated using M2 anti-Flag agarose as previously described (Kirino et al. 2009). Fifteen microliters of either wild-type or mutant Aub-bound beads were incubated for 1 h with 15 μl of reticulocyte reaction containing 35S-labeled Tudor in RSB-150 buffer (20 mM Tris-HCl at pH 7.5, 150 mM NaCl, 5% glycerol, 2.5 mM MgCl2, 0.05% NP-40) at 4°C and washed three times with the same buffer. Proteins bound on the beads were analyzed on NuPAGE 3%–8% Tris-Acetate gels.

Drosophila stocks

Tudor mutant flies (yw; tudB/CyO) were a gift from A. Arkov (Murray State University) (Arkow et al. 2006).

RNA isolation and labeling, and quantitative RT-PCR analysis

RNA isolation from Drosophila ovaries or immunoprecipitates, 5’-end labeling of piRNAs, and quantification of the transposon transcript by quantitative RT-PCR were performed as previously described (Kirino et al. 2009). Fifteen microliters of either wild-type or mutant Aub-bound beads were incubated for 1 h with 15 μl of reticulocyte reaction containing 35S-labeled Tudor in RSB-150 buffer (20 mM Tris-HCl at pH 7.5, 150 mM NaCl, 5% glycerol, 2.5 mM MgCl2, 0.05% NP-40) at 4°C and washed three times with the same buffer. Proteins bound on the beads were analyzed on NuPAGE 3%–8% Tris-Acetate gels.

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**SUPPLEMENTAL MATERIAL**

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**ACCEP TED AUGUST 6, 2009; ACCEPTED OCTOBER 5, 2009.**

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**ACKNOWLEDGMENTS**

We are grateful to A. Arkow (Murray State University) for tud flies and Tudor cDNA constructs; to M.C. Siomi and H. Siomi (Keio University) for Aub and Piwi antibodies and Aub cDNA construct; to S. Chuma (Kyoto University) and R. Jessberger (Mount Sinai School of Medicine) for Tdrd6 antibodies; to S. Kuramochi-Miyagawa and T. Nakano for Miwi and Mili cDNA constructs; to R. Beerman for help with fly methodology; and to members of the Mourelatos laboratory for discussions. This work was supported by a Human Frontier Science Program Long Term Fellowship to Y.K.; and GM072077, NS056070, UL1RR024134, and in part by ITMAT-PENN and SOM-PENN grants to Z.M.; and by HD036631 to P.L.

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