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Functions of PIWI proteins in gene regulation: new arrows added to the piRNA quiver

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Abstract

piRNAs and PIWI proteins play key functions in a wide range of biological and developmental processes through the regulation of cellular mRNAs, in addition to their role in transposable element repression. Evolutionary studies indicate that these PIWI functions in mRNA regulatory programs, occurring in both germ and somatic cells, are ancestral. Recent advances have widely expanded our understanding of these functions of PIWI proteins, identifying new mechanisms of action and strengthening their importance through their conservation in distant species. In this review, we discuss the latest findings regarding piRNA/PIWI dependent mRNA decay in germ cells and during the maternal-to-zygotic transition in embryos combined with new modes of action of PIWI proteins in mRNA stabilization and translational activation, and piRNA-independent roles of PIWI proteins in cancer.

The piRNA pathway and the range of its functions

Piwi-interacting RNAs (**piRNAs**; see **Glossary**) are a class of small non-coding RNAs expressed mainly in animal germlines. They are primarily a defense mechanism for the germline genome against transposable element (TE) mobilization and invasion (reviewed in [1-4]). piRNAs are 21 to 32 nucleotides in length and associate with specific ARGONAUTE proteins of the **PIWI** clade: MIWI, MILI and MIWI2 in the mouse; PRG-1 in *Caenorhabditis elegans*; Piwi, Argonaute 3 (Ago3) and Aubergine (Aub) in *Drosophila*. In mice and *Drosophila*, a large proportion of piRNAs originate from arrays of defective TEs assembled in loci that have originally been called "piRNA clusters". These clusters adapt by insertion of newly invading transposons, producing new piRNAs that repress cognate active TEs [5, 6]. The biogenesis of piRNAs is tightly intertwined with their role as TE silencer. A unified model of piRNA biogenesis has recently been reported, which explains piRNA production in most species, indicating an evolutionary conservation for about 800 million years [7] (**Box 1**).

Beside this well documented role in TE repression, functions of PIWI proteins and piRNAs in the regulation of gene expression have also been described early. Cellular mRNA regulation by piRNAs and PIWI proteins contribute to various cellular and developmental processes, such as embryonic patterning in *Drosophila* and spermatogenesis in the mouse, through the decay of large numbers of mRNAs [8-11]. PIWI proteins were first discovered based on their conserved functions in germline stem cell self-renewal [12], and these functions were shown more recently to involve cellular mRNA regulation [13, 14]. These proteins are found in a variety of stem cells, including somatic stem cells, and required for stem cell stemness in primitive species, such as planaria, which are known to be associated with high regenerative capacity (reviewed in [15]). In these species a large proportion of piRNAs are produced from genes (genic piRNAs) suggesting functions of the piRNA pathway in gene regulation. In fact, genic piRNAs are abundant in many species, consistent with conserved functions of PIWI proteins in post-transcriptional regulation of developmental programs, with recent evolutionary studies proposing that these PIWI/piRNA functions could be ancestral [16, 17].

In this Review, we focus on recent advances made in uncovering both the biological functions of PIWI proteins, and their mechanisms of action. While PIWI proteins act mostly by mRNA **slicing** (or cleavage) through their endonuclease activity, upon base-pairing of target mRNA with piRNAs, novel mechanisms of action of PIWI proteins in mRNA stabilization and translational activation have been identified. Recent studies have also revealed the conserved function of the piRNA pathway in maternal mRNA decay during the maternal-to-zygotic transition, and established piRNA-independent roles of PIWI proteins in tumorigenesis and metastasis. These new findings largely expand the breadth of piRNA and

PIWI protein functions in healthy development and pathological processes, through a variety of molecular mechanisms.

Degradation of cellular mRNAs by piRNAs and PIWI proteins

Since PIWI proteins cleave TE mRNAs, they can be easily considered as being able to degrade cellular mRNAs. This would require either the insertion of TE-related sequences into mRNA untranslated regions (UTRs), the production of piRNAs from genes with similar sequence (e.g. pseudogenes), or a low complementarity-based targeting of mRNAs with piRNAs produced from TE or repeated sequences. These different modes of cellular mRNA recognition by piRNAs have indeed been described in various contexts and species (reviewed in [15]).

One such example has been the cause of experimental troubles for decades with *UAS* transgenes in the *Drosophila* germline but has only been identified recently as ensuing from piRNA-mediated regulation (**Box 2**). Beyond this technical example, piRNA-mediated degradation of cellular mRNAs regulates a whole cohort of genes essential for various developmental programs. Mouse spermatogenesis is one of those. In mouse testes, whereas fetal piRNAs are produced from TE sequences and regulate TEs, pachytene piRNAs that are produced in adults at the pachytene stage of meiosis are unrelated to TEs. Pachytene piRNAs are mostly loaded into MIWI, a cytoplasmic PIWI protein. CLIP (crosslinking and immunoprecipitation) assays of MIWI revealed its bindings to a large repertoire of cellular mRNAs pointing to a role in post-transcriptional regulation of gene expression [11, 18]. Different modes of MIWI-dependent mRNA decay have been reported. piRNAs produced from ancient TEs target the same TEs inserted into long noncoding RNAs or mRNA 3'UTRs, leading to mRNA cleavage by MIWI slicer activity [19]. piRNAs produced from pseudogenes present in piRNA clusters were also proposed to repress their cognate mRNAs [19]. However, a recent evolutionary study revealed a lack of functional constraint upon pseudogene-derived piRNA targeting, suggesting a minimal contribution of pseudogene piRNAs in mRNA regulation [20]. Finally, incomplete base-pairing of mRNAs with pachytene piRNAs was shown to lead to either mRNA slicing by MIWI, generating genic piRNAs by **ping-pong**, or mRNA decay by **deadenylation** through the recruitment by MIWI of the CAF1 deadenylase [9, 11, 21] (**Key Figure: Figure 1A**). These two outcomes depend on the level of base-pairing between piRNAs and their target mRNAs, and on the formation of the MIWI-CAF1 complex taking place specifically in late spermatids. Importantly, both piRNA cluster gain-of-function and lack-of-function approaches showed that defects in mRNA regulation by pachytene piRNAs lead to mouse male sterility, demonstrating the key role of this regulatory mechanism in sperm maturation [21, 22]. Removal of piRNAs produced from different piRNA clusters does not systematically lead to phenotypic defects,

possibly due to redundancy. In addition, a small number of piRNAs within a piRNA cluster are actually responsible for mRNA cleavage and sperm defects, consistent with the high level of base-pairing required for slicing [21].

A recent study in the planarian *Schmidtea mediterranea*, revealed that one of the three PIWI proteins also targets a large repertoire of mRNAs leading either to their decay through ping-pong, or to binding without degradation [23]. Again mRNA slicing by PIWI depends on the level of piRNA complementarity: a strong base-pairing in particular across nucleotides 10-11 leading to mRNA cleavage, whereas uncleaved mRNAs show a lack of base-pairing at nucleotides 10-11 and after nucleotide 16 [23].

The piRNA pathway is rather different in *C. elegans* in that mRNA targeting by piRNAs (called 21U-RNAs) induces the production from target mRNAs of secondary antisense small RNAs (called 22G-RNAs), that loaded into other ARGONAUTE proteins (WAGOs or CSR-1) are the actual effectors of mRNA target regulation (reviewed in [3]). In this species, piRNAs target most germline mRNAs through partial complementarity similar to microRNA **seed**-based interactions [24, 25]. This leads to transcriptome-wide mRNA regulation by piRNAs, whereas their role in regulating TEs remains modest [26, 27].

Strikingly, the silencing of a specific *C. elegans* mRNA, *xol-1* by an X-linked piRNA plays a key role in sex determination and dosage compensation [28]. This piRNA developmental function is remarkable because it appears to be conserved in a distant species of nematode, *C. briggsae*, and more surprisingly, a similar regulation also takes place in the silk worm *Bombyx mori* that is separated from nematodes by 700 million years. Indeed in *B. mori*, a female specific piRNA represses through ping-pong, the *Masculinizer* mRNA that controls sex determination and dosage compensation in males [29]. This piRNA-mediated regulation is essential for female differentiation. Therefore, mRNA degradation by piRNAs has crucial functions in various developmental processes related to sexual reproduction such as germ cell development, sex determination and dosage compensation.

Another important role of piRNA-mediated mRNA decay has been recently reported in reproductive isolation between species. In *Drosophila* testes, the most abundant piRNAs are unrelated to TEs and originate from repeated sequences: the *Suppressor of Stellate* (*Su(Ste)*) and *AT-chX loci* located on the Y and X chromosomes, respectively [30-33]. Deletion of the *Su(Ste)* locus leads to significant increase of *Stellate* (*Ste*) mRNA and protein levels, abnormal spermatocyte development and male sterility, thus revealing the biological importance of *Ste* mRNA repression by *Su(Ste)* piRNAs [30, 34]. However, *Ste* and *Su(Ste)* are not conserved in related *Drosophila* species. On the other hand, *AT-chX* piRNAs show sequence similarity with *vasa* mRNA that encodes a key determinant of germ cell specification [33]. *vasa* is not highly regulated by *AT-chX* piRNAs though, due to low complementarity. Unexpectedly, *AT-chX* piRNAs show stronger base-pairing with *vasa*

mRNA from a closely related species, *D. mauritiana* [31]. Interspecies crosses between *D. melanogaster* and *D. mauritiana* produce males with reduced number of germ cells and meiotic failure, resulting in part from repression of *D. mauritiana vasa* mRNA by *AT-chX* piRNAs, and derepression of *Ste* mRNA due to the lack of *Su(Ste)* piRNAs [31]. Therefore, the repression of cellular mRNAs by piRNAs and PIWI proteins is not only involved in germline development and sexual reproduction, but also appear to contribute to reproductive isolation between closely related species. Intriguingly, a recent study revealed the high divergence of pachytene piRNAs between placental mammals and even within the human population, and proposed that piRNA diversity might act in reproductive isolation [35].

A key role of piRNAs and PIWI proteins in the maternal-to-zygotic transition

In most species, the zygotic genome is silent in the early embryo, therefore, maternally deposited mRNAs orchestrate the first steps of development. Maternal mRNAs are then progressively eliminated, and the zygotic genome starts to be expressed taking control of development, in a process called the **maternal-to-zygotic transition (MZT)**. Maternal mRNA decay is accomplished by two pathways that are maternally and zygotically encoded (reviewed in [36]). Recent data have highlighted the conservation of piRNA and PIWI protein function in maternal mRNA decay during the MZT (**Figure 2**).

The role of piRNAs in maternal mRNA degradation in *Drosophila* has been the first clear example of a cellular mRNA regulation by piRNAs with a role in development. *nanos (nos)* mRNA is one of the maternal mRNAs that gets degraded in the early *Drosophila* embryo. It encodes a key determinant of posterior patterning and germ cell development. *nos* mRNA regulation involves a complex interplay between degradation, stabilization and translational control allowing the distribution of Nos protein as a gradient emanating from the posterior pole of the embryo. *nos* mRNA is initially present in the whole embryo, with about 4% being localized and stabilized at the posterior pole, in the so-called **germ plasm** [37, 38]. The rest of *nos* mRNA in the somatic part of the embryo is degraded by both the maternal and zygotic pathways of mRNA decay [39]. The cytoplasmic PIWI protein Aub loaded with piRNAs is provided maternally to the embryo and contributes to *nos* mRNA decay; it is therefore a component of the maternal pathway of mRNA decay [10] (**Figure 2**). Aub cooperates with two other components of this pathway, the RNA binding protein Smaug and the CCR4-NOT deadenylation complex. *nos* mRNA decay by Aub does not involve its endonuclease activity but rather deadenylation by CCR4-NOT. piRNAs produced from two TEs, *roo* and *412*, target *nos* 3'UTR with partial base-pairing. piRNA target sites in *nos* sequence, as well as the piRNAs themselves are necessary for *nos* mRNA decay and embryonic development, revealing an intriguing role of TEs in this developmental process [10]. Aub CLIP assays in *Drosophila* embryos have identified more than 600 mRNAs bound

by Aub in a piRNA-dependent manner [8]. Aub is involved in the decay of germ cell mRNAs that, similarly to *nos*, are unstable in the soma and accumulate in the germ plasm to participate in germ cell development. Interestingly, some of these mRNAs produce genic piRNAs with ping-pong signatures, indicating cleavage by Aub. Thus, Aub degrades maternal mRNAs by two mechanisms: cleavage and recruitment of the CCR4-NOT complex [8, 10].

A recent study revealed a similar piRNA-mediated maternal mRNA decay in the mosquito *Aedes Aegypti* [40]. In this system, piRNAs are not produced from TE sequences but from satellite repeats that have been conserved in mosquitos for more than 200 million years. Two piRNAs derived from satellite repeats associate with the PIWI protein Piwi4 and degrade maternal mRNAs in mosquito embryos. Injection of oligonucleotides antisense to piRNAs in early embryos leads to early developmental arrest and increased levels of target mRNAs. These two piRNAs are not maternally deposited but expressed from the zygotic genome. Therefore, in *Aedes Aegypti*, piRNAs are part of the zygotic pathway of maternal mRNA decay. These piRNAs act similarly to specific microRNAs in *Drosophila* and zebrafish, which are also expressed zygotically and target a large number of maternal mRNAs to induce their decay during the MZT [41, 42]. Analysis of base-pairing requirement of mosquito piRNAs have shown the implication of the seed and additional base-pairing either directly following the seed, or in the 3' part of the piRNA. However, complementarity at the potential cleavage site -positions 10/11 of the piRNA- was dispensable, indicating a cleavage-independent mode of mRNA decay [40].

Remarkably, in *C. elegans* a role for 22G-RNAs produced from mRNA targeting by piRNAs has also been reported in maternal mRNA decay during the MZT. 22G-RNAs loaded into the Argonaute protein CSR-1 are provided maternally to the embryo and initiate the degradation of complementary mRNAs through CSR-1 cleavage activity [43].

These studies point to a widespread role amongst animals of the piRNA pathway in the MZT, a key developmental program driving early embryogenesis. How did piRNAs become players of this developmental process? Various mechanisms contribute to mRNA clearance during the MZT [36]. As an efficient system to degrade mRNAs, the piRNA pathway might have been coopted to provide an additional level of mRNA decay during the MZT and increase the robustness of the process.

piRNAs and PIWI proteins in stabilization of cellular mRNAs

Low base-pairing between piRNAs and their target mRNAs does not allow slicing by PIWI proteins, but rather the recruitment of regulators such as the CCR4-NOT complex [9, 10]. Recruitment of different regulators would mediate various outcomes in mRNA regulation, including positive regulation.

In the early *Drosophila* embryo, Aub and piRNAs are part of the developmental program leading to germ cell mRNA decay in the soma [8], but Aub is also a core component of germ granules that compose the germ plasm, where these mRNAs are stabilized [38, 44]. These conflicting data were analyzed using *nos* mRNA as a paradigm. Aub and piRNA target sites in *nos* 3'UTR were shown to be required for *nos* mRNA stabilization in the germ plasm [45]. At the mechanistic level, Aub directly interacts with the germline specific cytoplasmic poly(A) polymerase Wispy that accumulates in the germ plasm, inducing mRNA **polyadenylation** and stabilization (**Key Figure: Figure 1B**). In line with this positive role of Aub and piRNAs, Aub was reported to be involved in anchoring germ cell mRNAs to the germ plasm during late oogenesis [46]. The molecular basis of the switch in Aub function between soma and germ plasm remains unknown, although additional factors, in particular specific components of the germ plasm such as Oskar or Tudor, a direct Aub interactor, are likely to be involved.

Germ granules are conserved structures in germ cells of many species. They contain mRNAs required for germline specification and development, as well as PIWI proteins, suggesting that this role of PIWI proteins in mRNA stabilization and storage in germ granules might be conserved. Consistent with this, recent studies in *C. elegans* have revealed that piRNA/PIWI-mediated mRNA accumulation in germ granules prevent their silencing [47, 48].

Translational activation: a new mode of action of piRNAs and PIWI proteins

Early reports pointed toward a role of PIWI proteins in the regulation of translation. Both MIWI and MILI were found to associate at different steps of mouse spermatogenesis with the mRNA cap-binding complex that is required for translation activation [49, 50]. More recently, Aub was shown to regulate protein levels without affecting cognate mRNA poly(A) tail length in germline stem cells of *Drosophila* ovaries, indicating a potential role in translational regulation [14]. A link was also reported between Aub and eIF4 translation initiation factors in *Drosophila* cultured cells [13].

Two recent studies have established the role of PIWI proteins in translational activation and revealed the underlying mechanisms, in mouse spermatids and *Drosophila* embryos [51, 52]. While analyzing pachytene piRNA-induced mRNA decay in a spermatocyte-derived cell line, an increase in protein levels without affecting mRNA levels was found instead for specific piRNAs, suggesting a role in translational activation [51]. This positive effect was shown to require MIWI, and a combination of CLIP assays and ribosome profiling identified a large group of mRNAs potentially regulated by MIWI. AU-rich elements (AREs) in 3'UTRs were found as the common element in these mRNAs, and indeed the insertion of an ARE was sufficient to switch the regulation of an mRNA from decay to

translational activation. The HuR protein, known to bind AREs, associated with MIWI-activated mRNAs and contributed to translational activation (**Key Figure: Figure 1C, Figure 3**). Importantly, many mRNAs subject to MIWI-dependent translational activation are involved in spermatid development, and the regulation of two such mRNAs by MIWI was demonstrated to play a crucial role in acrosome formation [51].

In the *Drosophila* embryo, translational regulation of germ cell mRNAs is intimately linked to their stability. These mRNAs are translationally repressed and unstable in the soma, whereas they are stabilized and translated in the germ plasm. Consistent with this, the *nos* translational repressor complex contains components involved in both translational repression and mRNA decay such as Smaug and the CCR4-NOT deadenylation complex [53]. Aub being involved in *nos* mRNA stabilization in the germ plasm [45], its potential role in translational activation was analyzed. Because Oskar protein drives germ plasm assembly at the posterior pole of embryos, overexpression of Oskar in the whole embryo was used to mimic the germ plasm. In this context, Aub is indispensable for *nos* mRNA translation [52]. piRNAs are also involved in this Aub function as Nos protein levels depends on both piRNA biogenesis and the presence of piRNA target sites in *nos* 3'UTR. Polysome profiling revealed the role of Aub at the initiation step of translation [52].

These two studies identify a new function of PIWI proteins in promoting translation and strongly suggest an evolutionary conservation of this function. Remarkably, several aspects of this PIWI mode of action show striking similarities in mouse and *Drosophila*. First, both MIWI and Aub activate translation at the level of initiation, by directly recruiting the translation initiation complex eIF3 [51, 52] (**Figure 3**). Recent data have highlighted regulatory functions of eIF3, in addition to its role in basal translation [54-56]. MIWI and Aub bind eIF3 through the eIF3f and eIF3d subunits, respectively. eIF3d plays an especially important role in the varied modes of eIF3-based regulation, involving both cap-dependent and -independent translation [57-59]. Second, both MIWI and Aub directly associate with the poly(A) binding protein (PABPC1 in the mouse, PABP in *Drosophila*), another actor in translation initiation [51, 52, 60]. Third, the localization of PIWI protein interaction with eIF3 was also similar in mouse and *Drosophila*. In both cases, immunostaining revealed eIF3 foci in close proximity to, rather than inside, PIWI-containing germ granules [51, 52], suggesting that PIWI-dependent active translation takes place at the edge of germ granules (**Figure 3**). These data reveal a high level of conservation of PIWI-dependent translational activation, adding a new fundamental PIWI mechanism of action in mRNA regulation, which might be conserved in other animal species.

piRNA-independent functions of PIWI proteins

PIWI proteins are mostly specific to the germline, however, *PIWI* genes are aberrantly expressed in different types of human cancers, and are part of cancer-testis antigens that are testis-restricted genes induced in somatic cancers [61, 62]. The mechanisms of action of PIWI proteins in cancers have remained puzzling because their expression is not linked to the presence of large amounts of piRNAs [63]. A recent study identified the function of PIWIL1 (the homologue of mouse MIWI) independent of piRNAs in pancreatic cancer metastasis [64]. Unloaded PIWIL1 was shown to interact with the anaphase promoting complex/cyclosome (APC/C) that is involved in protein homeostasis through the ubiquitin-proteasome system. This interaction activates APC/C-dependent degradation of the cell adhesion-related protein Pinin, contributing to cancer cell migration and metastasis [64] (**Key Figure: Figure 1D**). A function of MIWI independent of piRNAs in protein regulation has also been described in mouse spermatogenesis. MIWI sequesters in the cytoplasm and inhibits the activity of the E3 ubiquitin ligase RNF8 known to play a role in histone ubiquitylation and degradation. The timely degradation of MIWI in late spermatids leads to RNF8 nuclear translocation and histone degradation and replacement by protamines, a process essential for chromatin compaction and spermatid maturation [65] (**Key Figure: Figure 1D**). Although MIWI loading is not required for its interaction with RNF8, MIWI does associate with piRNAs in late spermatids and its loading is necessary for its degradation via APC/C [66]. This PIWI function is relevant to human male fertility since mutations producing undegradable PIWIL1 were found in patients with azoospermia [65].

Finally, another piRNA-independent function of PIWIL1 was recently reported in gastric cancer. Although mRNA binding by PIWI proteins without piRNAs has been previously proposed in germ cells [13, 18], this PIWI protein mode of action has not been formally demonstrated in germ cells and was not confirmed in following studies [9, 11, 14]. piRNAs are not present in gastric cancer cells and PIWIL1 was shown to bind mRNAs independently of piRNAs and repress them through the recruitment of nonsense-mediated mRNA decay components, promoting cancer cell proliferation, migration, and metastasis [67]. How PIWIL1 directly binds mRNA without piRNAs remains to be analyzed.

These studies reveal emerging roles of PIWI proteins independent of piRNAs. More examples of such PIWI mechanisms of action remain to be discovered in the future in particular within pathological contexts, where PIWI proteins are expressed independently of the whole cohort of genes required for piRNA biogenesis.

Concluding remarks

Since their discovery as a germline-specific defense mechanism against TEs, piRNAs and PIWI proteins have been involved in a wide range of regulatory processes through the regulation of non-TE mRNAs. Because they were shaking up a "dogma", these PIWI/piRNA

functions unrelated to TEs have been reluctantly accepted. However, it is not surprising that, as an efficient system for mRNA decay, the piRNA pathway has been repurposed to cellular mRNA regulation. It is striking that the same developmental programs are regulated by piRNAs and PIWI proteins in very distant species. Biological functions of piRNA/PIWI-dependent mRNA regulation include germline development and specific processes linked to sexual reproduction such as sex determination and dosage compensation [28, 29]. Massive maternal mRNA decay during the MZT in early embryos also depends on piRNAs and PIWI proteins in both *Drosophila* and *Aedes* whose lineages separated 260 million years ago. Evolutionary studies are required to understand whether the regulation of these developmental programs by the piRNA pathway is conserved or was repeatedly co-opted for during evolution. Nonetheless, the presence of genic piRNAs across a wide range of species, including primitive bilaterian and non-bilaterian species, such as planarians and cnidarians, indicates that mRNA regulation by piRNAs and PIWI proteins is evolutionary ancient and conserved [8, 11, 16, 17, 20, 23, 68]. Many questions remain to be solved and a challenge for future studies is to understand how mRNA regulation by piRNAs and PIWI proteins is conserved, although not at the sequence level (see **Outstanding Questions**). Indeed, in contrast to microRNAs whose sequences are conserved through evolution, those of the piRNA are not- even between closely related species. piRNAs are extremely diverse and their pool can evolve rapidly within a species (**Box 1**). In addition, the low level of base-pairing required to target mRNAs indicate that most mRNAs might potentially be regulated by piRNAs. How is selectivity achieved? Cooperation with other regulatory pathways, e.g. RNA binding proteins, mRNA modifications, are likely to contribute strongly. Consistent with this, piRNA-based regulation is often redundant with other regulatory mechanisms and involved in fine-tuning developmental processes [15]. Increasing the piRNA repertoire also provides novel opportunities for mRNA regulation that may be fixed (or discarded) by natural selection, leading to new piRNA biological functions. This capacity of piRNAs to evolve rapidly might also participate in speciation through reproductive isolation between related species mediated by both detrimental piRNA-dependent mRNA regulation, and de-repression of transposable elements in interspecies crosses.

Positive mechanisms of action of piRNAs and PIWI proteins in mRNA stabilization and translational activation have been discovered. Again, the parallels in the underlying mechanisms seems remarkable with PIWI proteins recruiting the same translation initiation factors across very distant species. In addition, PIWI proteins act independently of piRNAs in cancer progression and metastasis. These studies reveal the high versatility of PIWI proteins in gene regulation and highlight the importance of these PIWI functions in developmental and pathological processes. Future analyses are likely to identify additional biological functions of piRNAs and PIWI proteins, particularly ones linked to germline development and

sexual reproduction. They might also reveal new mechanisms of action of PIWI proteins and should allow for a better understanding of their connection with other regulatory mechanisms.

Box 1. piRNA biogenesis and function in transposable element repression

The unified model of piRNA biogenesis proposes that piRNA production involves two interconnected mechanisms: phasing and **ping-pong** amplification. Interestingly, these two mechanisms are physically separated in the cell, ping-pong taking place in nuage composed of membrane-less ribonucleoprotein granules localized at the periphery of germ cell nuclei, and phasing occurring at the mitochondrial outer membrane [69-73]. First, piRNA cluster genes [74] are transcribed into long noncoding transcripts by RNA polymerase II via specific transcription factors or chromatin regulators [2, 3] (**Key Figure: Figure 1**). The piRNA precursor transcript is then exported at the periphery of the nucleus in the nuage, with a specific export complex containing the Nuclear export factor 3 (Nxf3) in *Drosophila* [75, 76]. There, *Drosophila* Ago3 associated with a maternally-inherited piRNA recognizes and cleaves a complementary piRNA precursor transcript, generating a 5' monophosphorylated RNA that interacts with Aub. New piRNAs can then be produced either by ping-pong or phasing. In the ping-pong cycle, the piRNA precursor is cleaved again further downstream by Ago3 to generate the piRNA 3' end. This new piRNA loaded into Aub targets and drives slicing of complementary TE transcripts, generating piRNAs that are loaded into Ago3. In turn, piRNA-loaded Ago3 binds to and slices piRNA precursor transcripts to generate piRNAs that associate with Aub. This reciprocal cleavage by Aub and Ago3 results in the production of complementary piRNAs with an overlap of ten nucleotides, a signature of the ping-pong amplification cycle (reviewed in [1]). For piRNA generation by phasing, the cleaved piRNA precursor transcript interacting with Aub travels with the RNA helicase Armitage to the mitochondrial outer membrane [70]. The endonuclease Zucchini (MitoPLD in the mouse) directed by Aub cleaves the piRNA precursor transcript generating the 3' end of a new piRNA loaded into Aub. The rest of the piRNA precursor transcript is repeatedly bound at its 5' end by Piwi and cleaved by Piwi-guided Zucchini, generating a phased production of Piwi-loaded piRNAs towards the 3' end of the piRNA precursor transcript [77-81]. While the phased piRNA production generates *de novo* piRNAs increasing piRNA diversity, the ping-pong amplification cycle increases the pool of pre-existing piRNAs.

In addition to this post-transcriptional silencing of TEs, piRNAs also repress TEs transcriptionally. piRNAs produced by phasing and loaded into nuclear PIWI proteins (Piwi in *Drosophila*, MIWI2 in the mouse) travel to the nucleus where they interact with TE nascent transcripts. PIWI proteins then establish repression through a complex network of chromatin remodelers [82-87].

Box 2. Repression of *UAS* transgenes by *Hsp70* piRNAs in *Drosophila* germ cells

In *Drosophila* developmental genetics, the *UAS/Gal4* inducible expression system set up in the 90's has been unavoidable [88]. This yeast-derived system involves the transcriptional activator Gal4 and its binding sequence *UAS* upstream of a minimal *Hsp70* promoter. Localized Gal4 expression allows spatial and temporal expression of a cDNA cloned downstream of *UAS-Hsp70* promoter. It soon became evident that the system was working in somatic tissues, but not in germ cells [89], although the reason was not understood. A recent study investigated this question and showed that the piRNA pathway is responsible for *Hsp70*-driven repression of *UAS* transgenes in the germline [90]. Indeed, the *Hsp70* gene clusters produce germline specific piRNAs that target the *Hsp70* sequence present in *UAS* expression vectors. Furthermore, the presence in the genome of a *Hsp70*-containing transgene stimulates cleavage of endogenous *Hsp70* transcripts, increasing the amount of *Hsp70* piRNAs [91]. Reducing *Hsp70* regions in new *UAS* vectors results in high expression in germ cells, clearly demonstrating that piRNA base-pairing with a cellular mRNA can efficiently induce its repression [90].

Glossary

Deadenylation: the process of poly(A) tail shortening where adenosine nucleosides are removed from the 3' end of mRNAs by a poly(A)-specific 3' exonuclease. The CCR4-NOT complex that is conserved from yeast to human, is the predominant deadenylase. It is composed of eight proteins including two deadenylases CCR4 and CAF1/POP2. Deadenylation triggers full mRNA decay.

Germ plasm: specialized cytoplasm present at the posterior pole of *Drosophila* oocytes and embryos. It is composed of germ granules in which germ cell mRNAs are stored and tightly regulated to participate in the formation of posterior embryonic structures and germ cell development.

Maternal-to-zygotic transition (MZT): period at the beginning of embryonic development during which the control of development switches from the maternal to the zygotic genome: maternal mRNAs are massively degraded and transcription of the zygotic genome is activated.

PIWI proteins: *P*-element-induced wimpy testis (Piwi), the first PIWI protein was identified genetically in *Drosophila* from its role in germline stem cell self-renewal. PIWI proteins form a specific family among ARGONAUTE proteins, based on phylogenetic analyses.

Ping-pong: mechanism of piRNA biogenesis leading to piRNA amplification and achieved through reciprocal cleavage of piRNA-targeted transcripts by PIWI proteins. Due to cleavage by PIWI proteins after nucleotide 10 of piRNAs, ping-pong produces piRNA pairs that are complementary over 10 nucleotides.

PIWI-interacting RNAs (piRNAs): small RNAs defined by their ability to associate with PIWI proteins. They are 21 to 32 nucleotides long depending on species, and present a 2'-O-methylation at their 3' end.

Polyadenylation: the process of poly(A) tail lengthening, where a poly(A) polymerase adds adenosines to the 3' end of the mRNA. Cytoplasmic polyadenylation involves specific proteins different from those required for nuclear polyadenylation.

Seed: the seed sequence has been defined for microRNAs and corresponds to nucleotides 2 to 7 from the microRNA 5' end, where perfect complementarity with the target mRNA is

required for regulation. Additional complementarity in the microRNA 3' region is also generally necessary to achieve regulation.

Slicing or cleavage: ARGONAUTE-mediated cleavage of target mRNAs, occurring between nucleotides 10 and 11 from the 5' end of the complementary piRNA.

Spermiogenesis: complex differentiation program at the end of spermatogenesis where spermatids differentiate and mature into spermatozoa. This program includes chromatin compaction leading to transcription repression, and thus depends, after this step, on regulation of stored mRNAs.

Transposable elements (TEs): DNA sequences that have the ability to move into a genome. They lead to various types of genomic alterations and rearrangements that may be deleterious. However, they also increase genome diversity and thus play a major role in genome dynamics and evolution.

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Conflicts of Interest

The authors declare no conflicts of interests.

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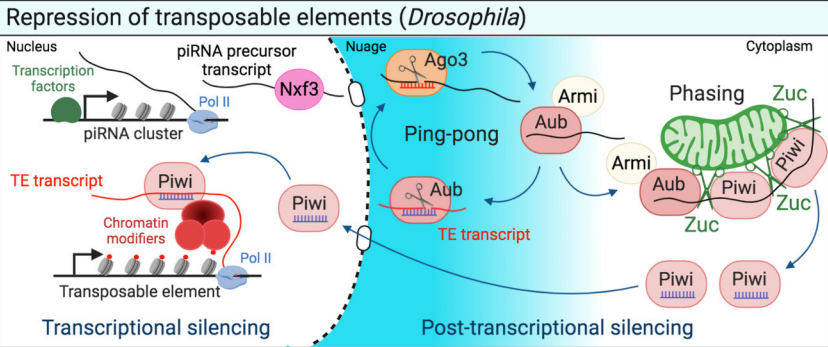
Figure legends

Figure 1 (Key Figure): The different mechanisms of action of PIWI proteins. (**Top panel**) Transcriptional (left) and post-transcriptional (right) repression of TEs by piRNAs and PIWI proteins. piRNA precursor transcripts are produced by the RNA polymerase II from piRNA cluster genes and exported to the nuage (blue). Here, piRNA-loaded Ago3 slices a complementary piRNA precursor transcript, generating a cleaved RNA with a new 5' end that is bound by Aub. This RNA fragment is cleaved into piRNAs either via phasing, by the Zucchini endonuclease (Zuc) at the mitochondrial outer membrane, or via ping-pong in the nuage. In the second part of the ping-pong cycle, piRNA loaded-Aub targets and cleaves a complementary TE mRNA, generating piRNAs loaded into Ago3. Reciprocal cleavage by Aub/Ago3 contributes to TE post-transcriptional repression and amplification of the piRNA pool. Piwi loaded with piRNAs during phasing translocates to the nucleus, associates with TE nascent transcripts and recruits chromatin remodelers, inducing transcriptional silencing through histone modifications (red dots). (**Bottom panel**) Molecular mechanisms of PIWI and piRNA functions in the regulation of gene expression. (**A**) PIWI-dependent cellular mRNA degradation. PIWI proteins promote mRNA decay through either the recruitment of deadenylation factors -the CAF1 deadenylase or the CCR4-NOT complex- or mRNA cleavage, depending on the level of base-pairing between piRNAs and target mRNAs. (**B**) PIWI-dependent mRNA stabilization. In *Drosophila* oocytes and early embryos, Aub binds germ cell mRNAs through piRNA base-pairing. Whereas in the soma, Aub binding leads to the decay of these mRNAs (**A**), in the germ plasm (green) Aub accumulates through direct interaction with Tudor and contributes to localization of the same mRNAs. Aub directly recruits the cytoplasmic poly(A) polymerase Wispy, leading to polyadenylation and stabilization in the germ plasm. Components of germ granules such as Tudor, Vasa and Oskar, are likely to participate in the switch in Aub function from mRNA decay to stabilization between soma and germ plasm. (**C**) PIWI-dependent translational activation. PIWI proteins directly recruit the eIF3 translation initiation factor and the poly(A) binding protein (PABP), thus contributing to mRNA 5'-3' end interactions and leading to translational activation. (**D**) piRNA-independent functions of PIWI proteins. PIWI proteins interact with the APC/C complex acting either as an activator (in cancer cells), or a target (in spermatids) of APC/C-mediated protein degradation. (**Left panel**) In cancer cells, unloaded-PIWI bound to APC/C triggers the ubiquitylation and degradation of the tumor suppressor Pinin, facilitating cancer cell migration and metastasis. (**Right panel**) In elongated mouse spermatids, timely APC/C-dependent degradation of PIWI allows the release and nuclear translocation of the ubiquitin ligase RNF8, essential for histone exchange with protamines.

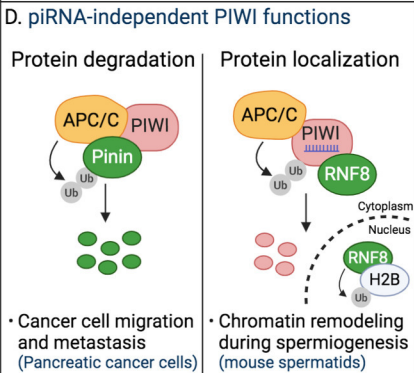
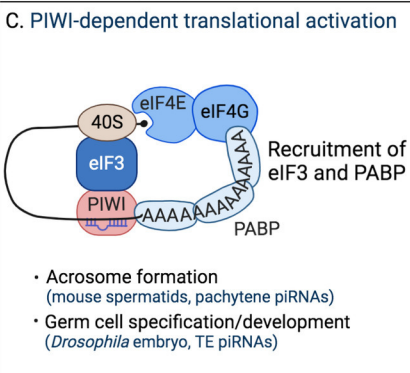
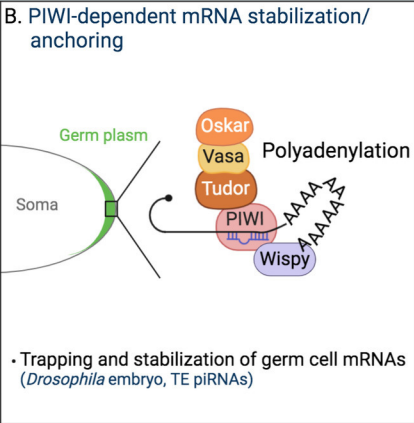
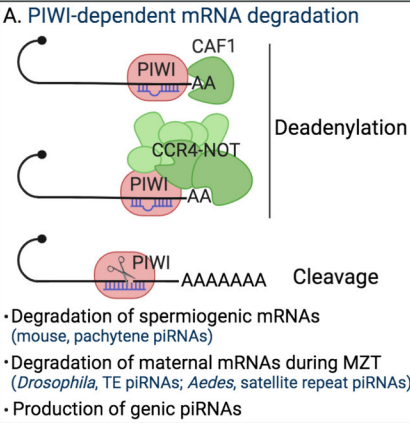
Figure 2: Function of piRNAs and PIWI proteins during the MZT. (**Top panel**) Profiles of maternal unstable mRNAs (blue lines) and of zygotic mRNAs (red line) are shown. Both maternal and zygotic factors contribute to maternal mRNA decay leading to a sequential degradation. The dashed line indicates the start of the bulk of zygotic transcription. (**Bottom panels**) In *Drosophila*, Aub and TE piRNAs are part of maternal factors required for maternal mRNA decay, together with Smaug and the CCR4-NOT complex. Aub promotes maternal mRNA clearance by deadenylation or cleavage. In *Aedes*, Piwi4 is provided maternally, whereas satellite repeat piRNAs that target maternal mRNAs are expressed by the zygotic genome. Therefore, Piwi4/piRNAs are part of the zygotic pathway of mRNA decay. Satellite repeat piRNAs target maternal mRNAs with loose base-pairing and contribute to their clearance by an unknown mechanism (indicated by a question mark).

Figure 3: Translational activation by piRNAs and PIWI proteins. (**Left panel**) Temporal mRNA regulation by MIWI/piRNAs during mouse spermiogenesis. MIWI and piRNAs are key factors of mRNA regulation during spermiogenesis. They are involved in mRNA decay by MIWI-dependent cleavage in spermatocytes and round spermatids, and by deadenylation through the recruitment of CAF1 in elongating spermatids. In addition, MIWI and HuR activate translation of ARE-containing mRNAs in round spermatids. MIWI recruits the eIF3 translation initiation factor through direct interaction with eIF3f; it also directly associates with PABPC that coats the mRNA poly(A) tail. On the other hand, HuR bound to the mRNA through ARE motifs recruits eIF4G3 known to bridge the cap-binding protein eIF4E and PABPC, a process facilitating translation initiation. These protein interactions activate cap-dependent translation. The temporal regulation depends in part on stronger MIWI/eIF3f/HuR interactions in round spermatids, and on stronger association between CAF1 and MIWI in elongating spermatids. (**Right panel**) Spatial mRNA regulation by Aub/piRNAs in the *Drosophila* embryo. *nos* maternal mRNA translation is repressed in the somatic part of the embryo and its targeting by piRNA/Aub contributes to its decay. In contrast, in the germ plasm (green), Aub promotes *nos* mRNA stabilization and translational activation. Aub recruits PABP by direct interaction, and eIF3 at least via its association with the eIF3d subunit. Aub activates translation initiation, possibly by a cap-independent mechanism, bypassing the repression imposed by the eIF4E-binding protein Cup. The poly(A) polymerase Wispy that directly associates with Aub, might also participate in translational activation through polyadenylation. In both the mouse and *Drosophila* systems, PIWI interactions with the translation machinery take place at the periphery of germ granules, suggesting actual localized translation at the edge of germ granules.

Mechanisms of action of PIWI proteins



Regulation of gene expression



Key Figure, Figure 1

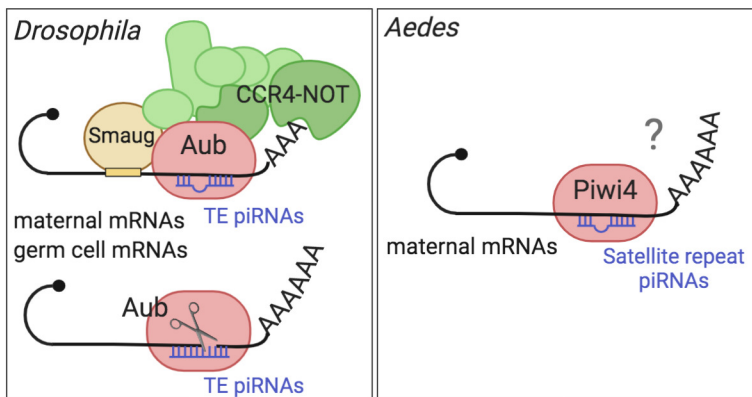
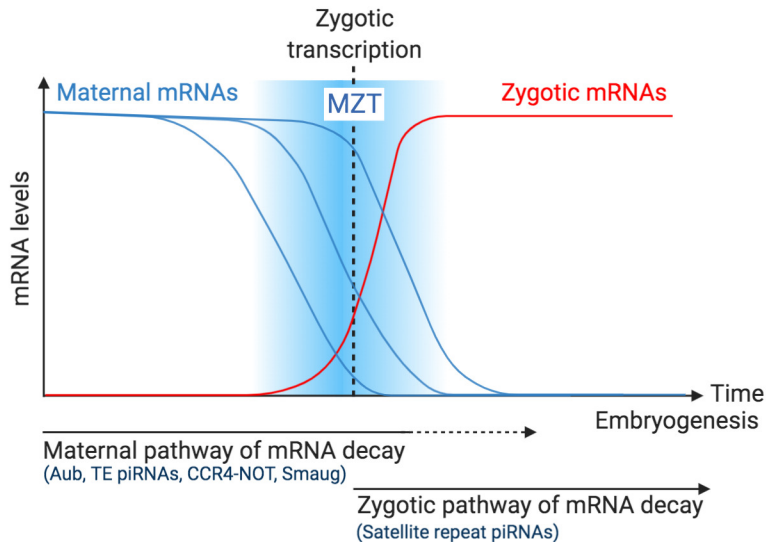
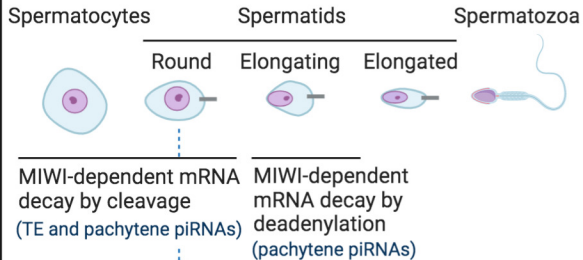


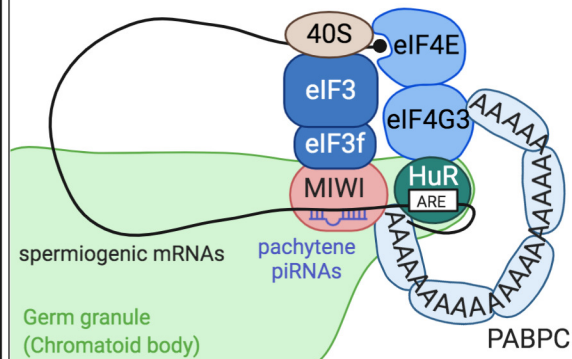
Figure 2

Mouse spermiogenesis

Temporal mRNA regulation by MIWI/piRNAs

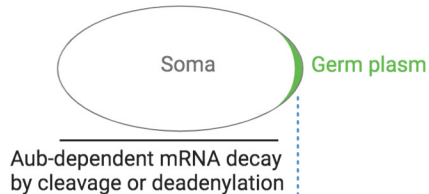


MIWI-dependent mRNA translational activation



Drosophila embryo

Spatial mRNA regulation by Aub/piRNAs



Aub-dependent mRNA stabilization and translational activation

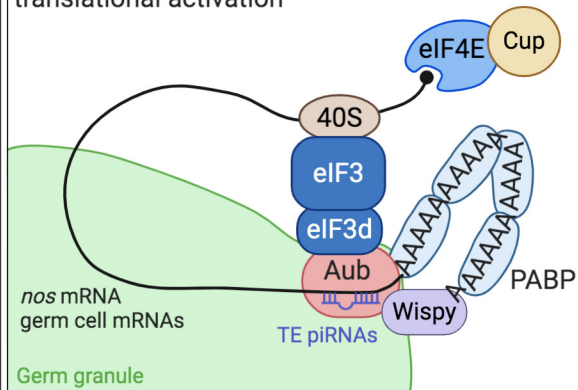


Figure 3