

organism	RNA signal:	Effector:	chromatin/DNA modification:	Outcome:
<i>A. thaliana</i>	sRNA →	Ago/Piwi	↔ histone H3K9me ↔ DNA 5mC	→ TGS
<i>S. pombe</i>	sRNA →	Ago/Piwi	↔ histone H3K9me	→ TGS, CTGS
<i>C. elegans</i>	sRNA →	Ago/Piwi	→ histone H3K9me	→ TGS, CTGS
<i>Drosophila</i> (germline)	sRNA →	Ago/Piwi	↔ histone H3K9me	→ TGS
<i>M. musculus</i> (germline)	sRNA →	Ago/Piwi	→ histone H3K9me → DNA 5mC	→ TGS
<i>T. thermophila</i>	sRNA →	Ago/Piwi	→ histone H3K9me	→ DNA elimination
<i>S. pombe, M. musculus</i>	lncRNA mRNA →	RBD	→ histone H3K9me	→ TGS, CTGS

Supplementary information S1 (figure). Conservation and divergence of RNA silencing pathways. RNA silencing mechanisms are usually composed of an RNA signal (sRNA or sequence within lncRNA) that recruits an effector protein. For sRNAs, the effector is a member of the conserved Argonaute/Piwi (Ago/Piwi) family of proteins, whereas for lncRNAs it is an RNA-binding protein (RBD). The effector then recruits enzymes that either methylate histone H3 on lysine 9 (H3K9) or cytosine in DNA (5mC) resulting in transcriptional gene silencing (TGS) and in some cases also co-transcriptional gene silencing (CTGS), involving degradation of targeted nascent transcripts. In *S. pombe* and *A. thaliana*, sRNA amplification and the downstream histone or DNA methylation events are interdependent and form self-reinforcing positive feedback loops (denoted by forward and reverse arrows).