PIWI-interacting RNA (piRNA) biogenesis

European Bioinformatics Institute, New York University Langone Medical Center, Ontario Institute for Cancer Research, Oregon Health and Science University.

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**Introduction**

Reactome is an open-source, open-access, manually curated, and peer-reviewed pathway database. Pathway annotations are authored by expert biologists, in collaboration with Reactome editorial staff and cross-referenced to many bioinformatics databases. A system of evidence tracking ensures that all assertions are backed up by the primary literature. Reactome is used by clinicians, geneticists, genomics researchers, and molecular biologists to interpret the results of high-throughput experimental studies, by bioinformaticians seeking to develop novel algorithms for mining knowledge from genomic studies, and by systems biologists building predictive models of normal and disease variant pathways.

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**Literature references**


Reactome database release: 79

This document contains 1 pathway and 16 reactions (see Table of Contents)
In germ cells of humans and mice, precursors of PIWI-interacting RNAs (piRNAs) are transcribed from a few hundred sequence clusters, as well as individual transposons, intergenic regions, and genes in the genome. These longer transcripts are processed to yield piRNAs of 26-30 nucleotides independently of DICER, the enzyme responsible for microRNAs (miRNAs) and small interfering RNAs (siRNAs) (reviewed in Girard and Hannon 2008, Siomi et al. 2011, Ishizu et al. 2012, Pillai and Chuma 2012, Bortvin 2013, Chuma and Nakano 2013, Sato and Siomi 2013). The initial step in processing long transcripts to piRNAs is cleavage by PLD6 (MitoPLD), which generates the mature 5′ end. The cleavage products of PLD6 are bound by either PIWIL1 (HIWI, MIWI) or PIWIL2 (HILI, MILI) in complexes with several other proteins. The 3′ end is trimmed by an unknown exonuclease to generate the mature piRNA. PIWIL1:piRNA complexes appear to be involved in post-transcriptional silencing in the cytosol while PIWIL2:piRNA complexes generate further piRNAs from transposon transcripts and other transcripts in the cytosol. Cleavage products from PIWIL2:piRNA may be loaded into either PIWIL2 or PIWIL4 (HIWI2, MIWI2). Loading into PIWIL2 forms a step in a cytosolic amplification loop called the "ping-pong cycle" which yields further PIWIL2:piRNA complexes from cleaved precursor RNAs. Loading into PIWIL4 yields a complex also containing TDRD9 that translocates to the nucleus and directs DNA methylation of cognate loci, causing transcriptional silencing during spermatogenesis. Transcriptional silencing by piRNAs is necessary to limit transposition of endogenous transposons such as L1 elements in the genome.

Literature references


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RNA polymerase II polymerizes primary piRNA transcript

Location: PIWI-interacting RNA (piRNA) biogenesis

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