GENETICS

Spotlight

A showcase of research and scholarship
in selected articles from 2016

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Multitasking of the piRNA Silencing Machinery: Targeting Transposable Elements and Foreign Genes in the Bdelloid Rotifer *Adineta vaga*

Fernando Rodriguez and Irina R. Arkhipova

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> **EDITORS' NOTE** The genome of the bdelloid rotifer *Adineta vaga* is characterized by massive horizontal gene transfer, low transposon content, and highly diversified RNA-mediated silencing machinery. The authors investigated genome-wide distribution of *A. vaga* piRNAs and found that an unexpectedly large fraction matches foreign genes. Small-RNA covered genes have a higher frequency of nearby telomeric repeats and transposons, indicating that gene acquisition occurs largely at the genome periphery, where it can be affected by RNA-based silencing.

ABSTRACT RNA-mediated silencing processes play a key role in silencing of transposable elements, especially in the germ line, where piwi-interacting RNAs (piRNAs) are responsible for suppressing transposon mobility and maintaining genome integrity. We previously reported that the genome of *Adineta vaga,* the first sequenced representative of the phylum Rotifera (class Bdelloidea), is characterized by massive levels of horizontal gene transfer, by unusually low transposon content, and by highly diversified RNA-mediated silencing machinery. Here, we investigate genome-wide distribution of pi-like small RNAs, which in *A. vaga* are 25–31 nucleotides in length and have a strong 5′-uridine bias, while lacking ping-pong amplification signatures. In agreement with expectations, 71% of mapped reads corresponded to annotated transposons, with 93% of these reads being in the antisense orientation. Unexpectedly, a significant fraction of piRNAs originate from predicted coding regions corresponding to genes of putatively foreign origin. The distribution of piRNAs across foreign genes is not biased toward 3'-UTRs, instead resembling transposons in uniform distribution pattern throughout the gene body, and in predominantly antisense orientation. We also find that genes with small RNA coverage, including a number of genes of metazoan origin, are characterized by higher occurrence of telomeric repeats in the surrounding genomic regions, and by higher density of transposons in the vicinity, which have the potential to promote antisense transcription. Our findings highlight the complex interplay between RNA-based silencing processes and acquisition of genes at the genome periphery, which can result either in their loss or eventual domestication and integration into the host genome.