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The role of the *rhino* gene in the transcriptional regulation of different piRNA clusters

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Motivation and Aim: piRNA silencing is one of major ways of retrotransposon activity suppression in eukaryotes. Nowadays this system is thoroughly explored in *Drosophila melanogaster* and in other model objects, including nematode and mouse. But regardless of description of this mechanism in details, many questions are still unsolved.

piRNAs can beprocessed from satellite retrotransposon transcripts or from extended accumulations of transposons known as piRNA clusters. In *D. melanogaster* these clusters are classified into two types: uni-strand (*20A* and *flamenco*) and dual-strand (*42AB* and *38C*). Most of them are expressed in the germ line, and transcripts are processed in the special area Nuage on the out surface of nucleus and interact with transposable elements' mRNAs. It is strongly believed that proteins coded by the *del (deadlock)*, *rhino (rhi)* and *cutoff (cuff)* genes help RNA-polymerase to start transcription of a piRNA cluster from non-canonical promoters. Moreover, these proteins prevent such transcripts from splicing and it leads to balance of spliced and unspliced forms in cells.

In opposite to the most piRNA clusters, *flamenco* is considered to be expressed only in somatic ovary tissues *rhi*-independently. Its transcripts are generally alternatively spliced and are processed in Yb-body on the outer mitochondrial membrane. Subsequently such piRNA are used as guide-RNA by PIWI to find corresponding expressed transposons in the nucleus and start their repression. Earlier we have showed that *D. melanogaster* strain, demonstrating flamenco phenotype, also shows lower expression of *rhi* and increased amount of spliced transcripts in comparison with wild type strains.

Methods and Algorithms: We utilized *rhino* gene knockdown system (hybrids of rhino strain and tubulin driver strain) and hybrids of w1118 strain and tubulin driver strain as a control group. We evaluated relative expression of different retrotransposons, spliced and unsliced forms of *flamenco* and *42AB* clusters and various transcripts of *20A* and *38C* clusters in somatic and germline tissues of flies with quantitative PCR.

Results: We detected enhanced expression of several retrotransposons not only in germline but in somatic tissues. Moreover, these flies demonstrated increased amount of spliced transcripts of the *flamenco* and *42AB* clusters in ovaries and in carcass tissues as well.

Conclusion: These facts strongly support our hypothesis about regulation of *flamenco* cluster by *rhi* and significance of *42AB* cluster in regulation of the retrotransposon activity outside the gonads.