A novel piRNA annotation tool (piRAT) unveils new piRNA expression patterns

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Most of the information regarding Piwi-interacting RNAs (piRNAs) expression, biogenesis, and functional roles comes from a limited number of model organisms. In these few models, piRNA expression has been observed to be mostly restricted to germ cells and their surroundings. However, our initial studies in insects revealed piRNA expression in some non-gonadal tissues. These observations led us to explore the expression of piRNAs across different insect lineages and tissues. To achieve this objective, we first had to overcome the challenge of a lack of robust tools for the automated annotation and analysis of piRNAs. For that purpose, we developed a novel piRNA Annotation Tool (piRAT) to annotate piRNAs from both biogenesis pathways using small RNA-seq mapped to a genome. We demonstrated its efficacy in annotating piRNA clusters and identifying ping-pong signatures, thus providing a valuable resource for studying piRNA expression across animals. Furthermore, applying piRAT on small RNA-seq data from somatic and gonadal tissues across insect lineages, we revealed abundant and widespread piRNA expression in non-gonadal tissues in most of the insect lineages studied.