

ABSTRACT

The piRNA pathway is the most recently discovered of the RNA interference pathways. It has been mostly studied in *Drosophila melanogaster* where it was shown to play a key role in silencing transposable elements during germline formation. This pathway relies on the activity of proteins belonging to the Argonaute families that bind small RNA molecules, named piRNAs, which recognize the targets by sequence complementarity. Argonaute proteins are phylogenetically divided into the AGO and PIWI subfamilies. The number of members of each subfamilies is different across organisms, with a notable expansion of PIWIs in various arthropods, including mosquitoes. The hypothesis is that this expansion is associated with functional specialization. For instance, there are experimental evidences suggesting that in mosquitoes of the *Aedes* genus, which are competent vectors for different viruses, proteins of the piRNA pathway are expressed in the soma and have antiviral activity differently than what happens in *D. melanogaster*.

The Asian tiger mosquito *Aedes albopictus* is an invasive species that arrived in Europe in the last decade of the past century and is a menace for public health due to its ability to vector a number of viruses, such as Dengue and Zika. We have limited knowledge of its genome and the way mosquitoes interact with viruses.

Given the role of the piRNA pathway, this study combines bioinformatic and molecular analyses to characterize the piwi genes, validating their structure as annotated in the reference genome and providing a comprehensive picture of their expression throughout the *Ae. albopictus* development.

My results suggest the need for amendments in the current annotation of piwi genes of *Ae. albopictus* and highlights extensive structural variations among individuals. Moreover, expression analyses confirm the central role of the Argonaute proteins in controlling TE movement during germline formation, with exceptions suggesting functional specialization.