Differential piRNA response associated to sex biased TEs in Drosophila species

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Résumé

The piRNA pathway is a conserved mechanism dedicated to Transposable Elements (TEs) silencing in the germline of animal species. Evolutionary rate of the proteins involved in this pathway were shown to be higher than immunity genes, suggesting that strong selection pressure drive their evolution. The abundance of TE in the genome and their activity into the germline are assumed to constrain the piRNA genes evolution.Thus, an important question is to better understand the nature and tempo of the arms race between germline TE activity and the associated host genome response.
In this work, we first compared the transcriptome of D. melanogaster and D. simulans, two sibling species that show contrasting pattern of genomic TE content. We look at the transcriptional activity of TE in both the male and the female germline. Among all the detected TEs, we found that a large fraction is not actively transcribed in both germlines. Considering transcriptionally active TEs, most of them display significant sex differences. Interestingly, in both species, sex-biased TEs present features of recently and highly amplified TEs, suggesting that the genome TE content is linked to the germline-specific TE activity.Comparisons between the two species show that recently amplified TE have a male-biased expression in D. melanogaster, but a female-biased expression in D. simulans.

By sequencing diverse piRNA librariries form ovaries, we show that the sex-biased TEs that have recently expanded are preferentially targeted by secondary piRNA. Conversely, very few ovary piRNA target TEs displaying low copy numbers. Surprisingly, we also found that in testes of both species, the piRNA production is drastically weak. In addition, we observed that most of genes specifically involved in the germline piRNA silencing pathway are highly expressed in ovaries.
These results show that the germline host response using the piRNA pathway is a post-genomic response to TE invasion. TEs displaying sex biaised transcription show features of recent bursts of transpostion and seems to be specific to one sex or the other, depending on the species. Finally, germline piRNA and the associated piRNA genes have similar properties of genes that evolve under sexual selection. Thus, we proposed that sexual selection may also impact genome TE content variations.

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