Host response to an invading TE: extinction vs repression

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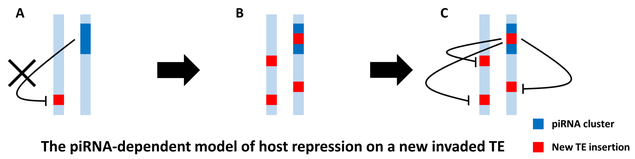
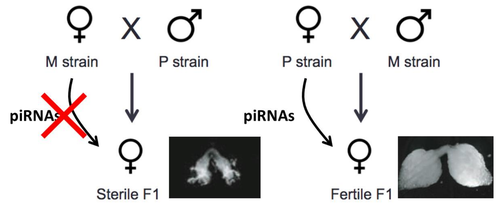
Background

- Transposable elements (TEs) are genomic parasites that burden their host genome with deleterious mutations and incite genome instability.
- To avoid these costs, host genomes control the mobilization of TEs through piRNA-mediated silencing (Bergman et al., 2006).



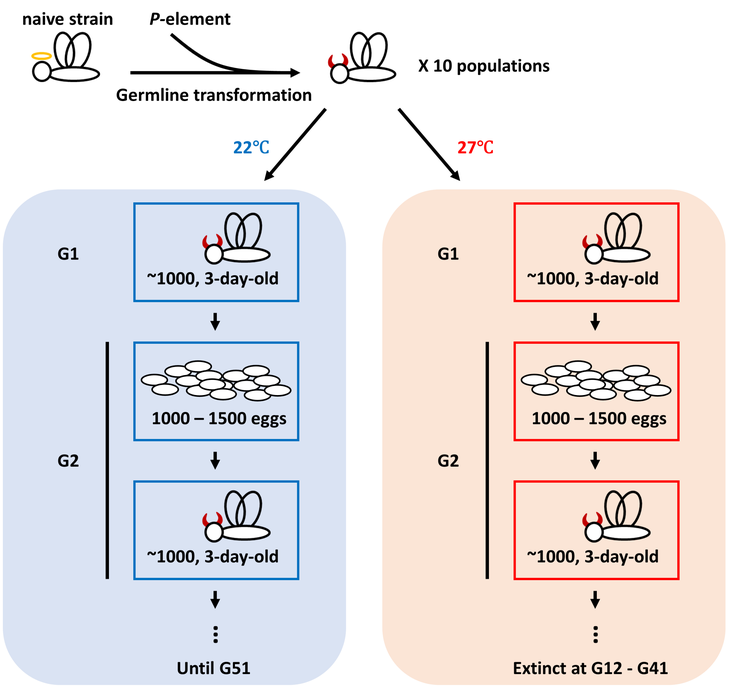
The piRNA-dependent model of host repression on a new invaded TE

- However the mutational and epigenetic processes that give rise to piRNA-mediated silencing when new TEs invade the host remain poorly understood.
- *P*-elements have invaded the genomes of three *Drosophila* species within the last century, providing unique opportunities to study the evolution of piRNA-mediated repression (Kidwell 1983).



Hybrid dysgenesis by *P*-element. Left: hybrid dysgenesis occurs in the crosses between males with *P*-elements (P strain) and females devoid of *P*-elements (M strain). Because the offspring have no maternally deposited piRNAs against *P*-elements, *P*-elements are activated, resulting in gonadal atrophy. Right: the offspring from the reciprocal cross are fertile because *P*-element piRNAs are transmitted from the P-strain mother (Brennecke et al. 2008).

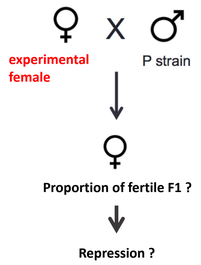
Experiment design



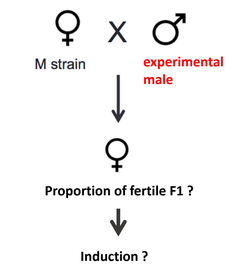
We introduced *P*-elements into a naive *D. melanogaster* strain through 10 independent germline transformations, and chronicled their effects at two different temperatures (22℃, where transposition rate is lower; 27℃, where transposition rate is higher). Successful transformations were confirmed by PCR.

Phenotypic measurements

- Every 5 generations, we measured *P*-element **repression** within each population, by evaluating the ability of individual experimental females to repress hybrid dysgenesis among their F1 offspring females when crossed to P strain males (Harwich).



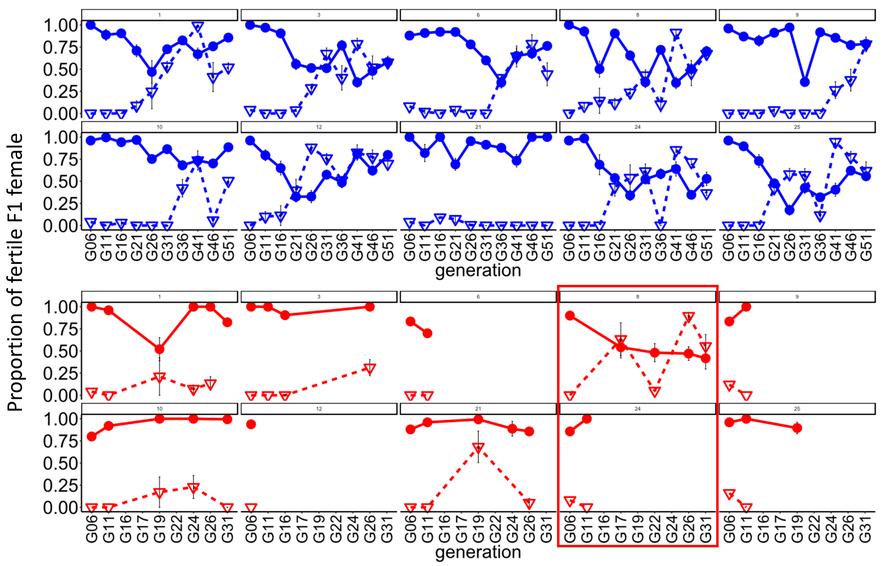
- Every 5 generations, we measured the *P*-element activity (**induction**) within each population, by evaluating the ability for individual experimental males to induce hybrid dysgenesis among F1 offspring females when crossed to M strain females (Canton-S).



- Every generation, 100 adults from each population were frozen for genotyping.
- Every 5 generations, 20 ovaries were harvested from each population and kept for small RNA sequencing.

Results

Most 22℃ populations exhibit increasing *P*-element activity, and also increasing repression

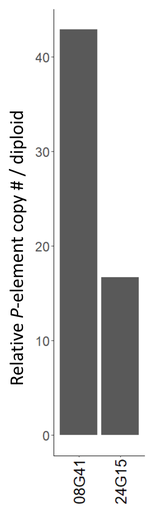


Each panel represents one population from each temperature (22℃ in blue, 27℃ in red). Dashed lines indicate repression crosses (experimental female X Harwich male), higher proportion of fertile F1 female means higher repression. Solid lines indicate induction crosses (experimental male X Canton-S female), higher proportion of fertile F1 female means lower induction. All populations in 27℃ were extinct successively because of the high transposition rate of *P*-element and its associated genomic damage. Two populations from 27℃ used for the following studies are indicated by the red rectangle.

Longer survival of a 27℃ population is likely due to the *P*-element insertion into the piRNA cluster

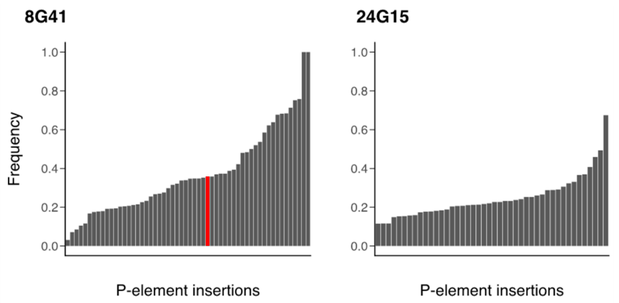
27℃

qPCR



Whole genomic sequencing

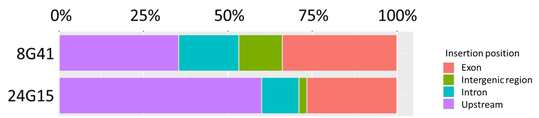
	8G41	24G15
Genomic DNA source	9 females	8 females
Read length	2 x 75 bp	2 x 75 bp
Read number	164 M	177 M
Coverage / individual	20 X	24 X
# of annotated *P*-element	58	44
Estimated copy # / diploid	43.6	21.8
# of *P*-element in piRNA cluster	1	0



qPCR and whole genomic sequencing for *P*-element copy number and insertion were performed on the last generation of two selected populations, one of which survived longer till generation 41 (strain 8), while the other one was extinct quickly at generation 15 (strain 24). The *P*-element insertion into the piRNA cluster is in red.

Unexpected abundant *P*-element insertions into the exons of protein-coding genes

27℃



From the whole genomic sequencing data, we separate the *P*-element insertion position into four categories: exons, intros, intergenic regions and gene regulatory regions (upstream). TE insertions into exons are rare (Zhuang et al. 2014), because of the deleterious effect on gene's function, which might contribute to the early extinction of the 27℃ populations.

Future work

- We are currently analyzing the whole genomic sequencing data from the last generation of the 10 populations from 22℃ to annotate the positions of *P*-element insertions and estimate their population frequency.
- Correspondingly, we will also perform small RNA sequencing on the same 22℃ populations to evaluate their piRNA-mediated repression.
- In addition, we will sequence continuous generations within two 22℃ populations to investigate the evolution process of the host TE regulation.

Acknowledgements

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