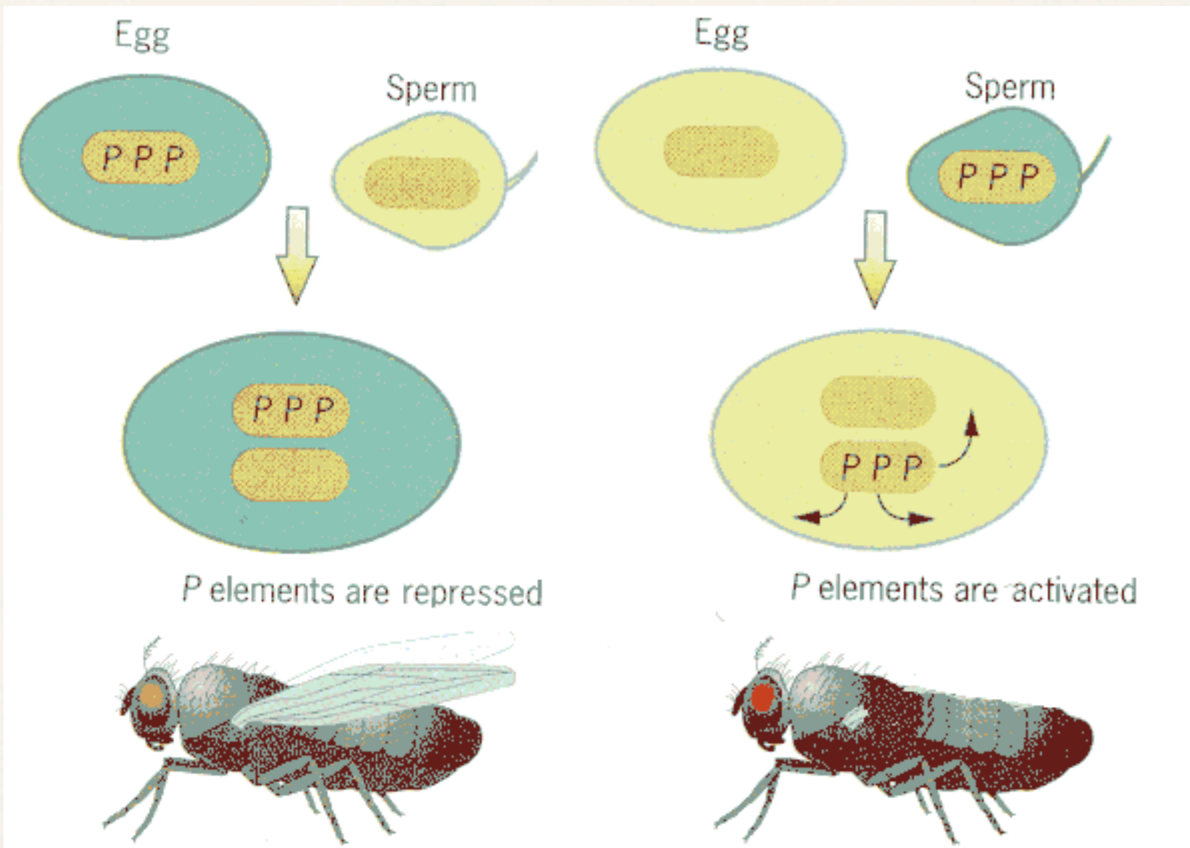
Adaptation to transposon invasion in *Drosophila melanogaster*

Zhiping Weng
UMass Medical School

P-element-mediated hybrid dysgenesis in Drosophila



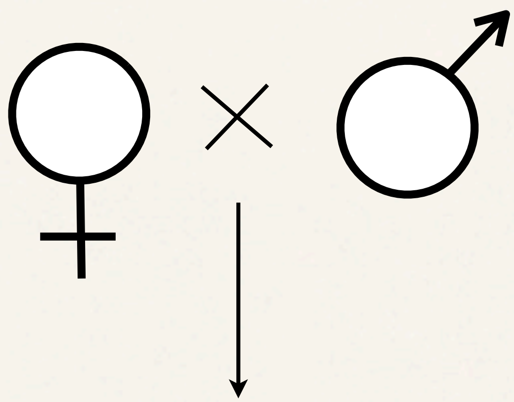
non-dysgenesis
fertile

dysgenesis
sterile

http://www.mun.ca/biology/scarr/P-element_hybrid_dysgenesis.htm

Transposon invasion causes "hybrid dysgenesis"

Mom deposits piRNAs in the egg

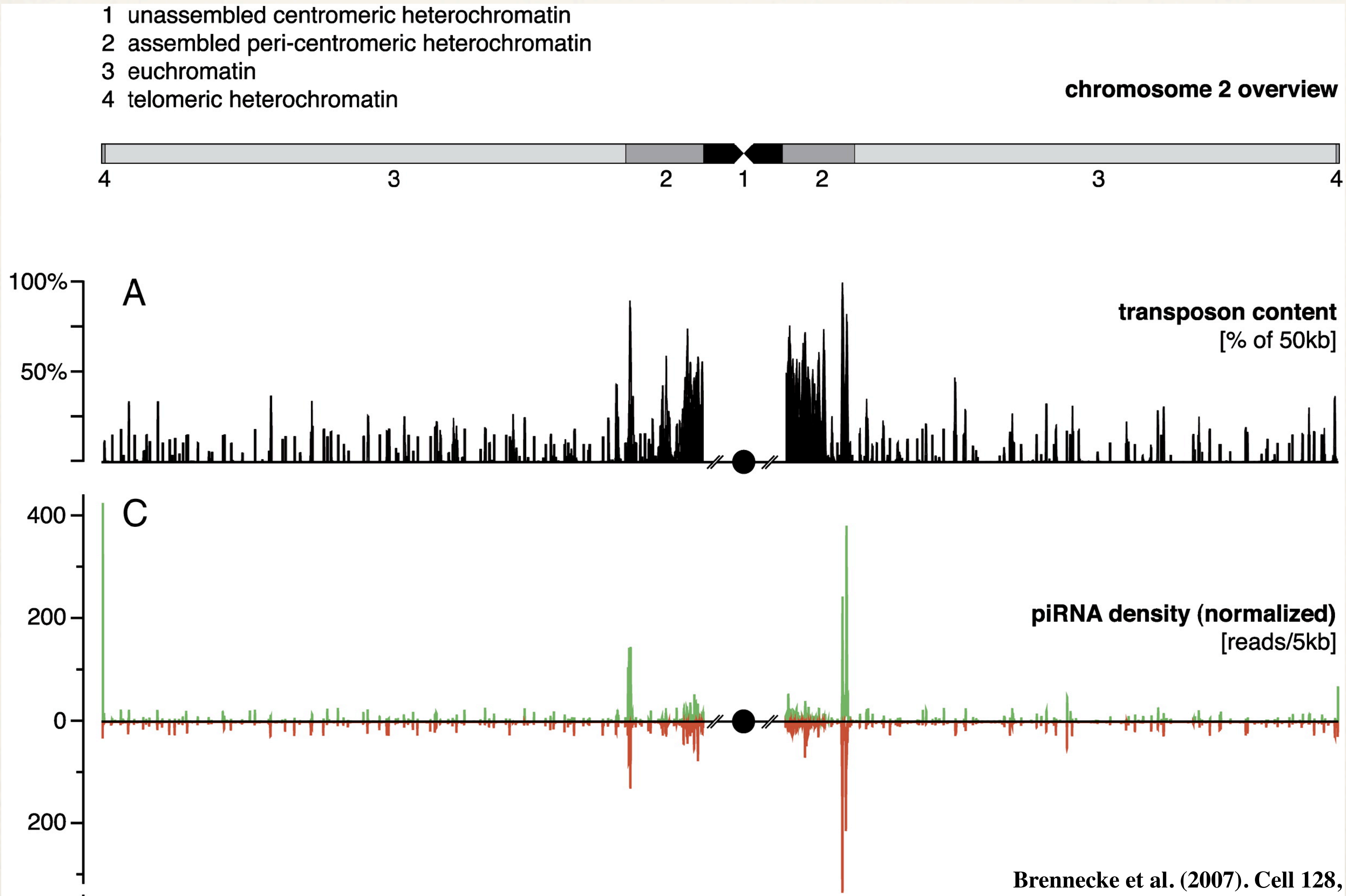


Dad carries a "new" transposon (P-element)

F1 hybrid

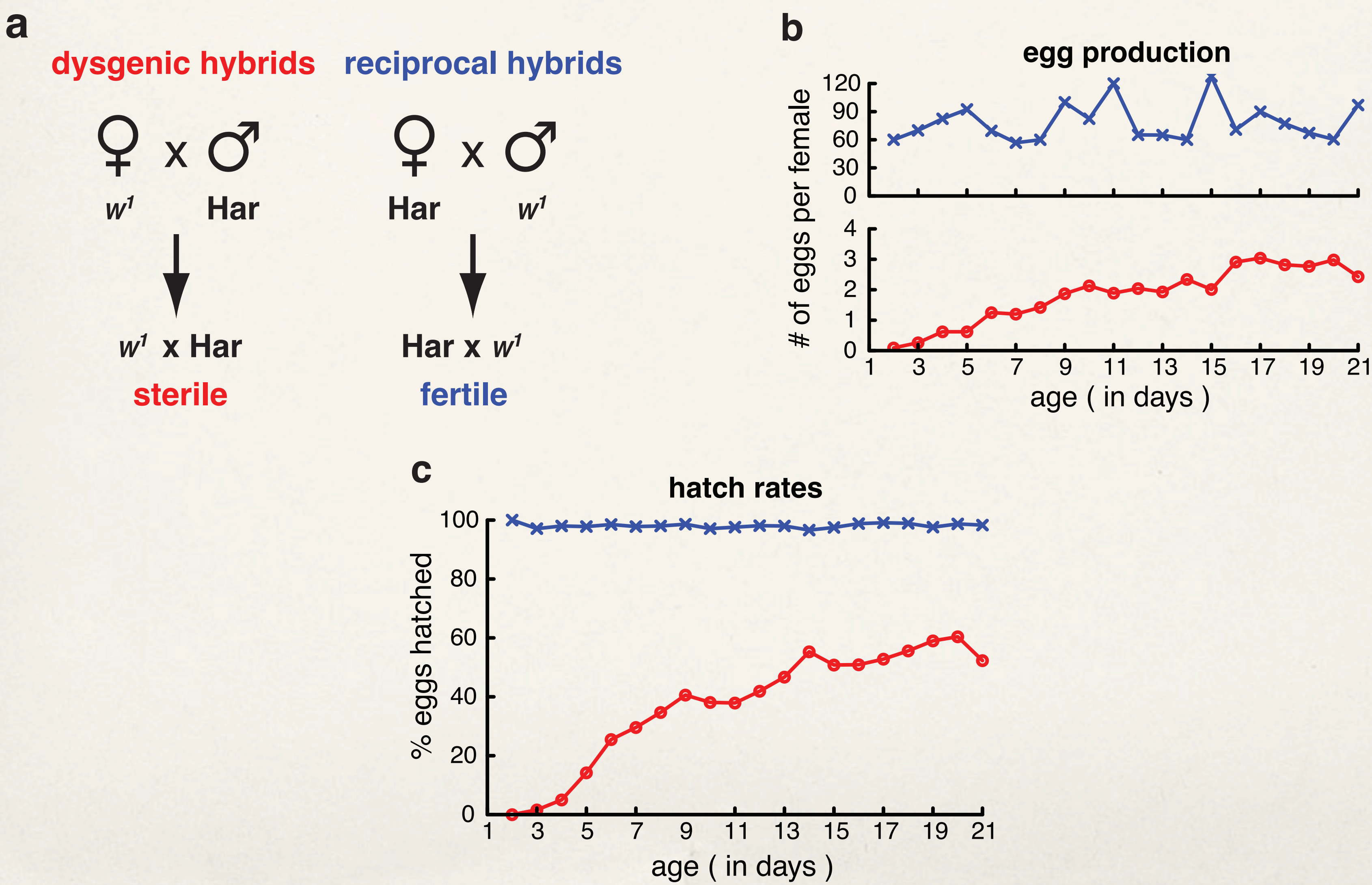
Invading elements escape silencing and lead to genomic instability and hybrid sterility

piRNAs map to transposon-rich heterochromatic clusters

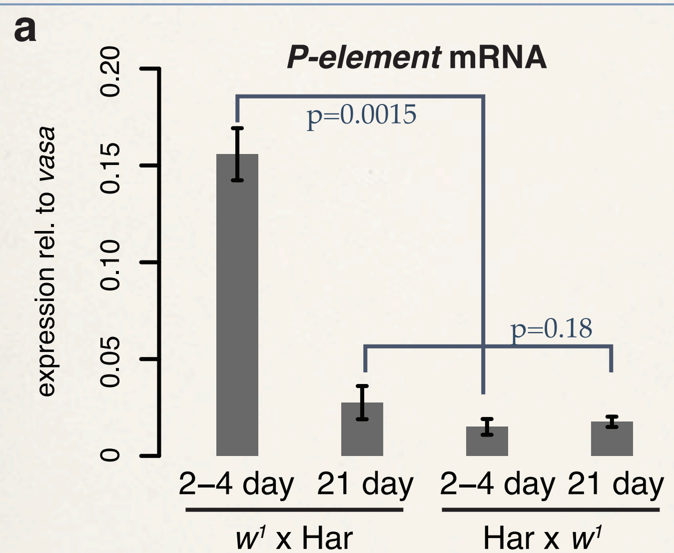


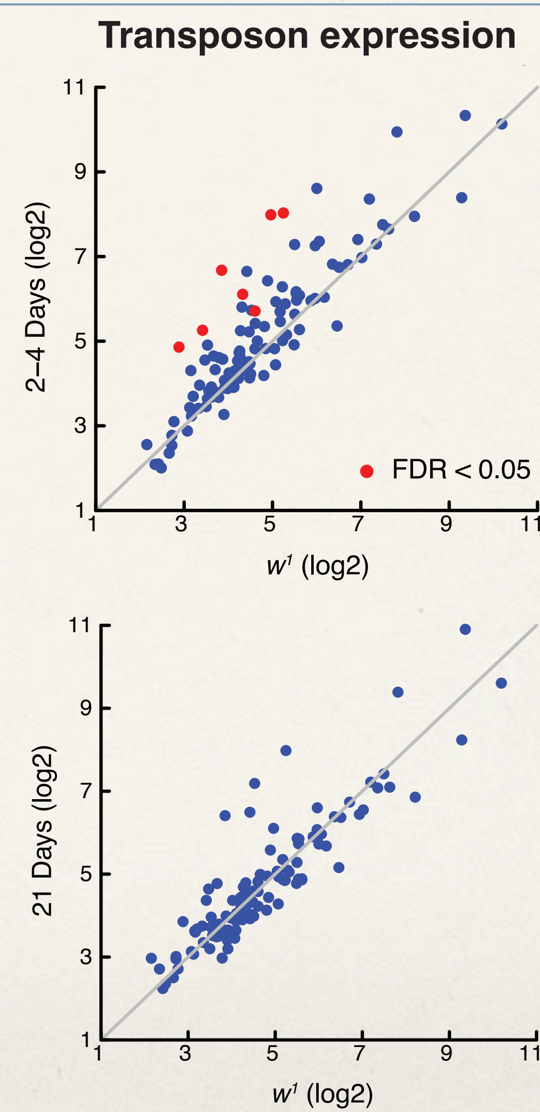
Brennecke et al. (2007). Cell 128, 1089-1103.

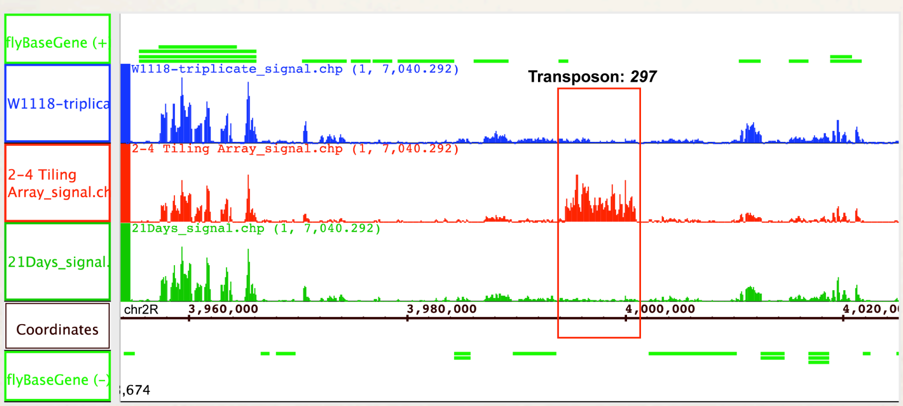
Phenotypic adaptation to P-element invasion



P-element and resident transposon expression

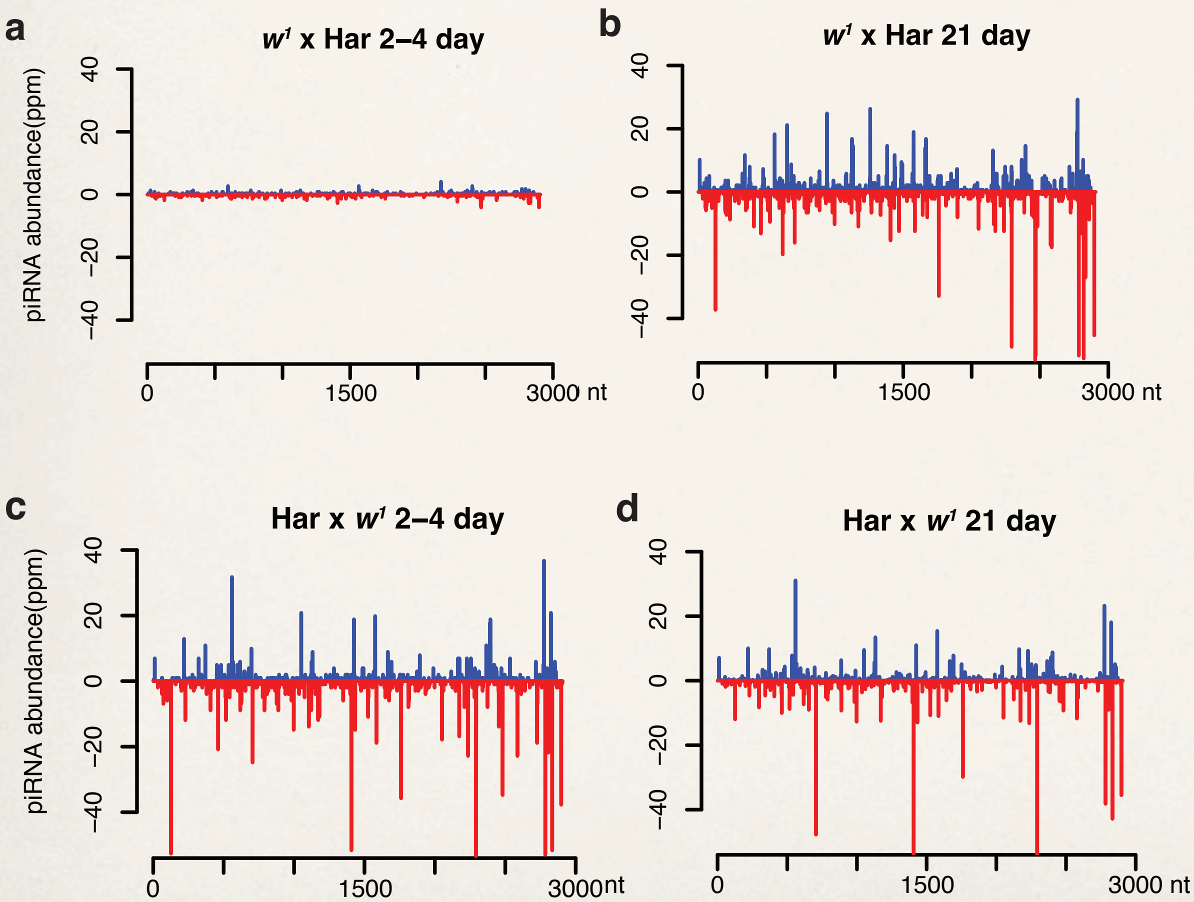




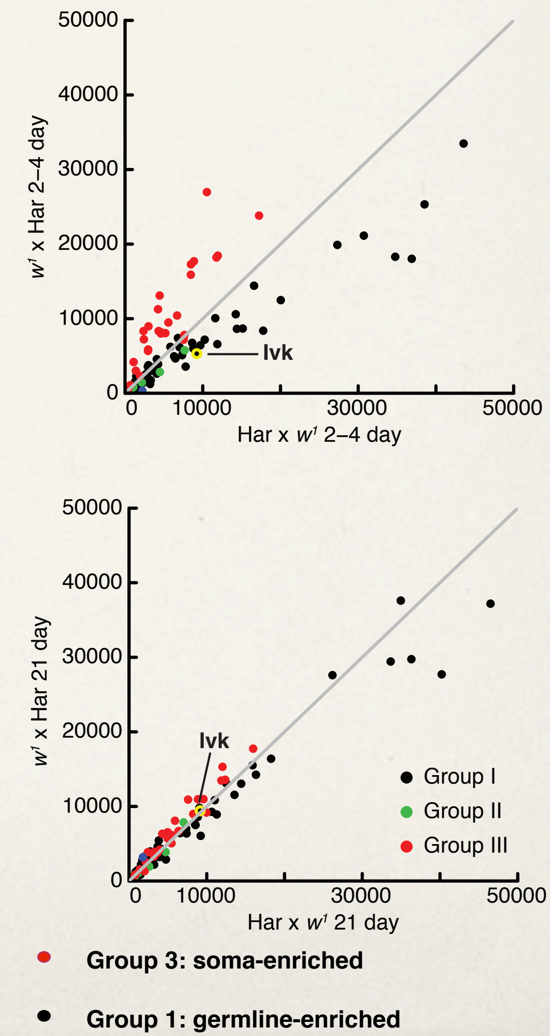


piRNA expression of P-element and resident transposon

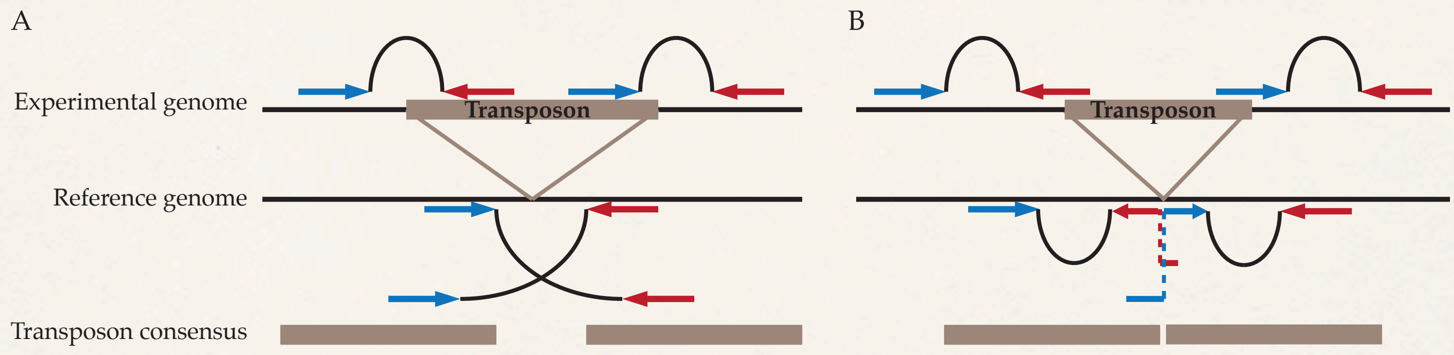
P-element

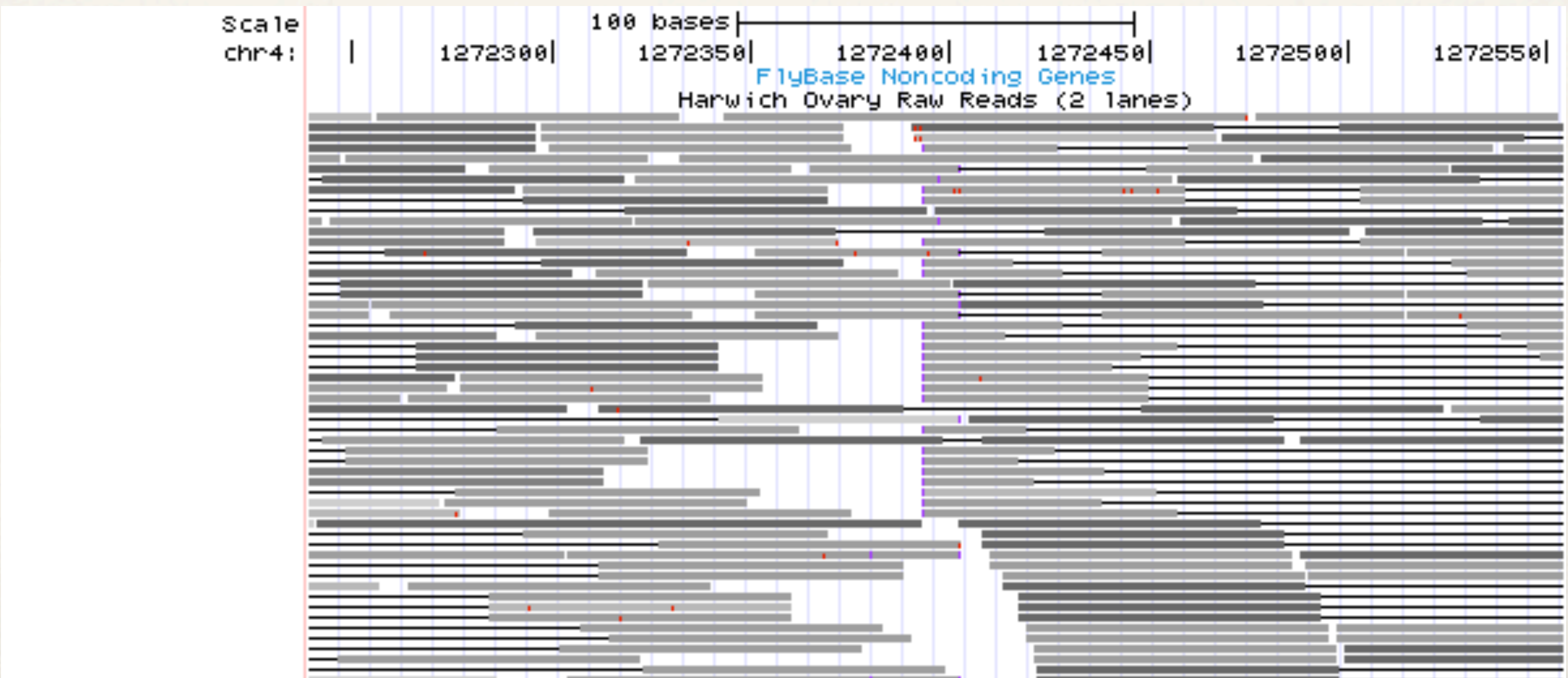


resident transposon



Detection of transposon insertion by Paired-end Genomic Sequencing

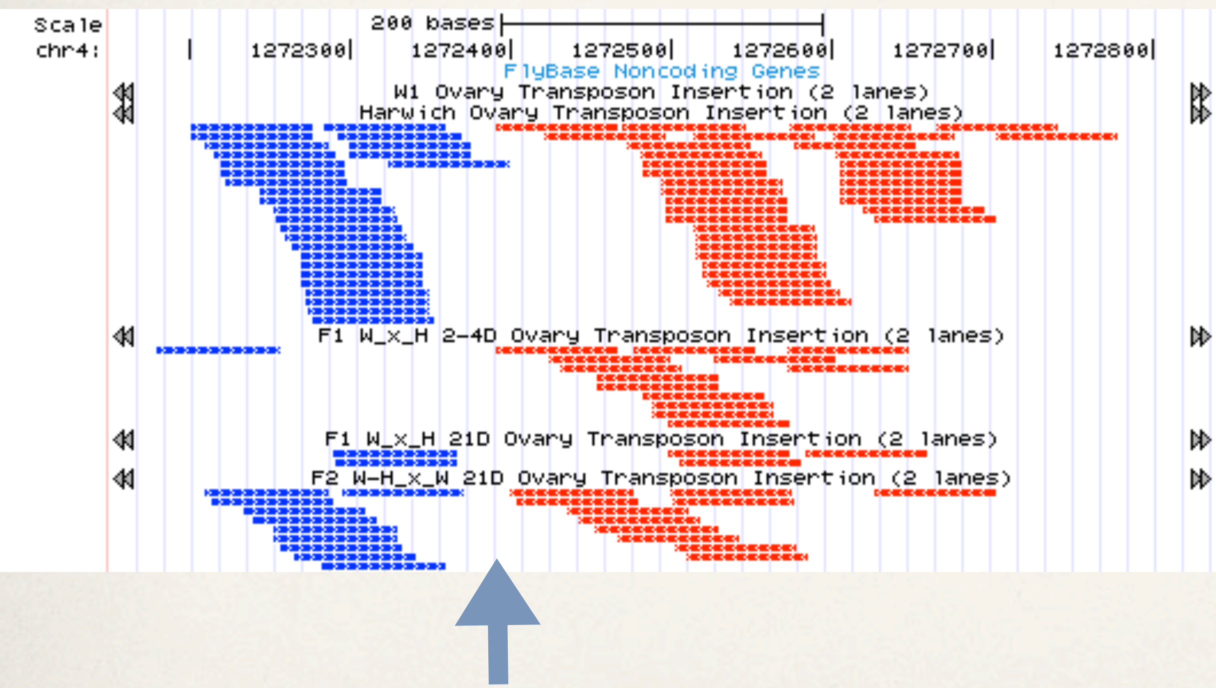


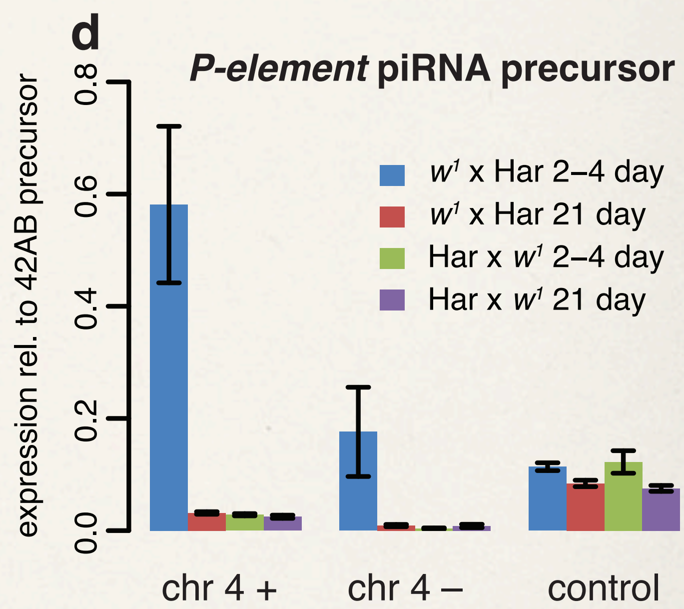


P-element transposition into cluster does not significantly contribute to de novo piRNA production in dysgenic females

- Genomic sequencing
  - F1 2-4 Day, 21 Day *w* x Har dysgenic females
  - F2 21 Days, (*w* x Har) x *w* females
- 814 sites carrying new P-element insertions in at least one of the three progeny populations.
- 14 of these sites mapped to piRNA clusters, but 12 were defined by only single reads and thus represent rare polymorphisms.
- The other 2 sites were identified by multiple reads in 21-day-old dysgenic females, but were not detected in 2-4 day old dysgenic females or in backcrossed F2 progeny.

P-element piRNA precursor abundance at paternal clusters



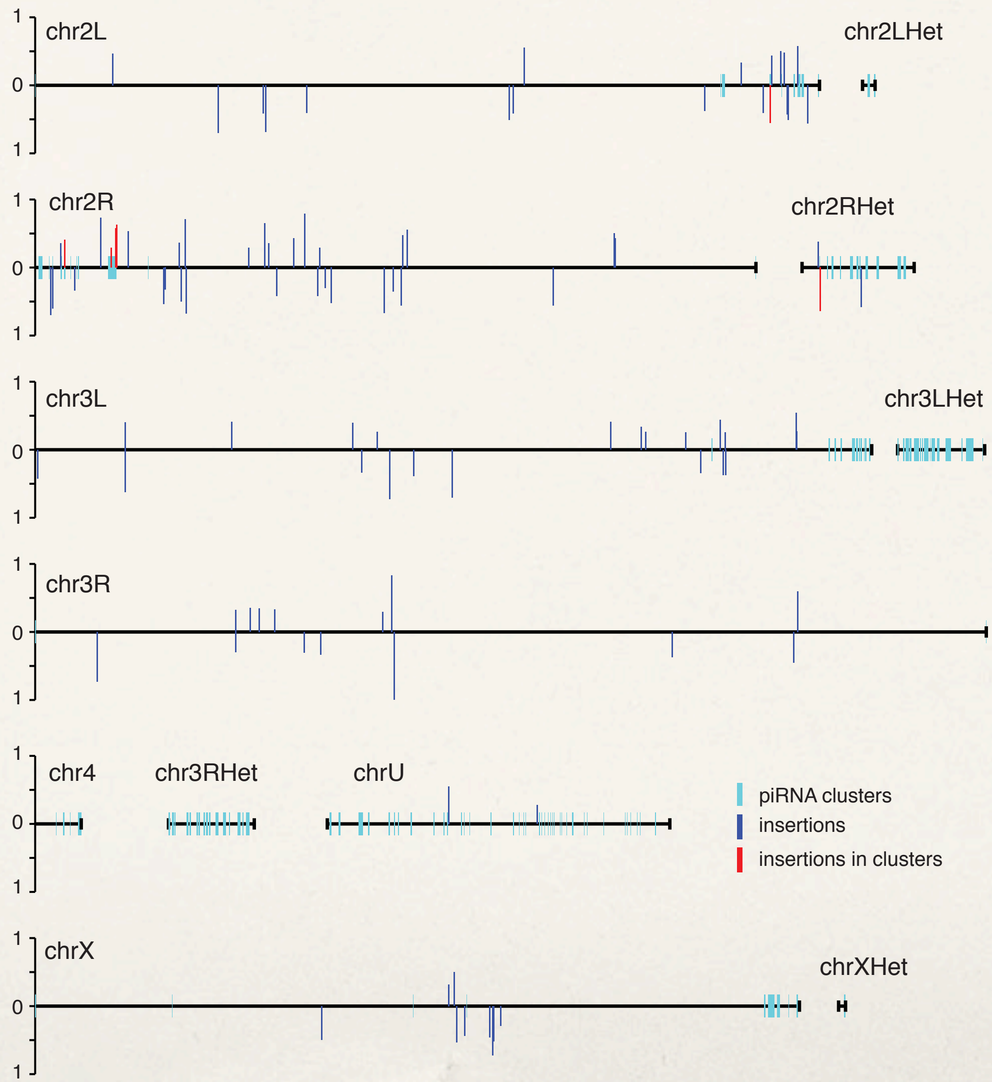


Thus:

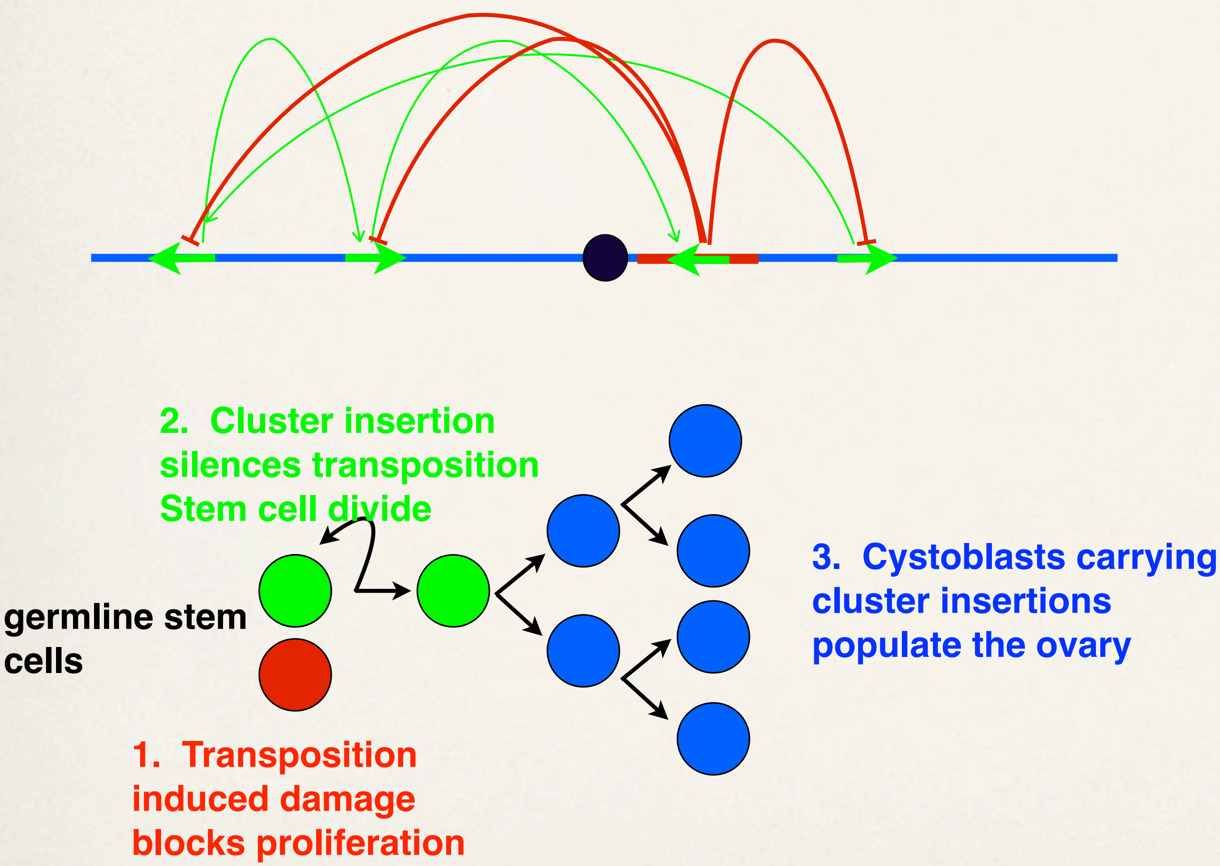
P-element silencing is coupled with de novo production of P-element piRNAs encoded by clusters inherited from fathers.

Resident transposon families mobilized as well

Genome distribution of inherited transposon insertions



Model



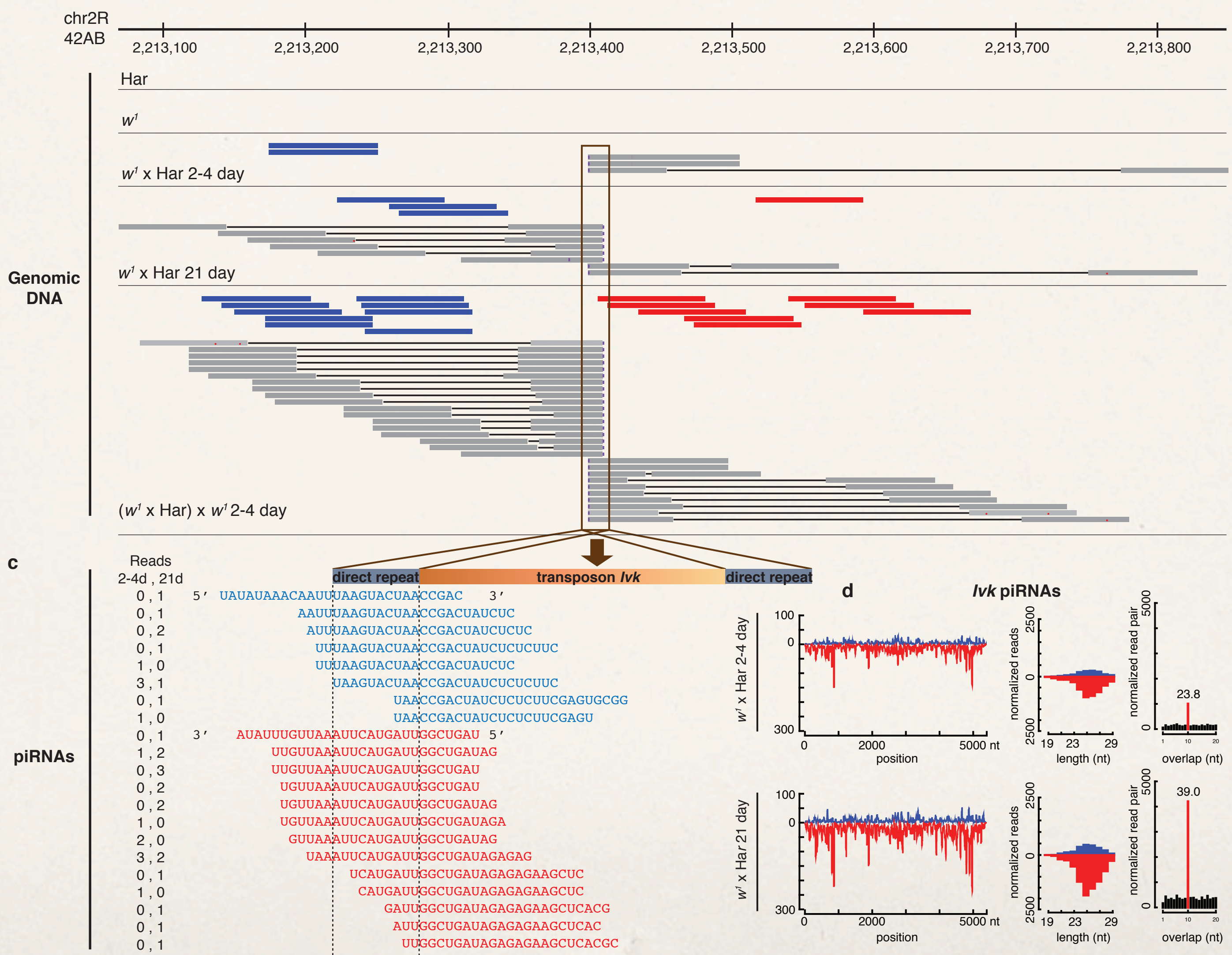
- Transposon insertion into piRNA clusters could provide selective advantage, possibly by enhancing piRNA production and transposon silencing.
- Inherently biased transposition should lead to accumulation of new cluster insertions independent of selective pressure, while selective pressure is required for cluster insertion enrichment through clonal expansion.

Crunch the numbers

Transposon Family	w^1 x Har						$(w^1$ x Har) x w^1		
	2-4 day			21 day			21 day		
	Total reads	Reads in piRNA clusters	% clusters	Total reads	Reads in piRNA clusters	% clusters	Total reads	Reads in piRNA clusters	% clusters
All	2653±31	264±11	9.94±0.40%	4290±18	335±8	7.81±0.18%	867±27	64±6	7.40±0.65%
Inherited cluster insertions									
Bari1	21±2	11±1	53.47±6.05%	37±0	18±0	48.64±0%	1±1	0±0	0±0%
Blood	59±4	6±2	9.99±2.83%	96±2	9±2	9.17±2.23%	10±3	1±1	5.93±7.10%
copia	42±4	9±2	20.44±4.91%	95±3	18±1	18.48±1.25%	9±3	1±1	10.79±11.08%
Ivk	9±2	3±1	32.58±8.85%	18±1	4±0	22.55±2.30%	5±2	1±1	10.47±15.32%
Tabor	25±3	4±2	16.87±7.41%	24±2	4±2	18.25±5.07%	4±2	0±0	0±0%
1731	21±3	11±2	51.72±6.21%	25±3	17±0	68.75±7.09%	2±1	0±1	5.46±17.91%
Total	178±8	44±5	24.72±2.17%	295±6	70±3	23.74±0.88%	31±5	2±1	6.90±4.41%

- The inherited cluster insertions are linked to enhanced transposon silencing.
- Accumulation of piRNA cluster insertions is specific to dysgenic hybrids, where the pressure to increase silencing is strong.

Transposition into a piRNA cluster can lead to de novo piRNA production.



Summary

- The fertility of hybrid females progressively increases as age, indicating the adaptation to P-element invasion takes place in a single generation, within the female germline.
- This is associated with P-element silencing and de novo production of P-element piRNAs that encoded by paternal piRNA clusters.
- Silencing of resident elements correlates with site specific transposon insertions in piRNA clusters.
- Adaptation to transposon invasion is mediated by a combination of epigenetic and genetic mechanisms that enhance silencing and drive changes in chromosome architecture.

Acknowledgments

- **Weng Lab**
  Jie Wang, Jia Xu
- **Bill Theurkauf**
  Jaspreet Khurana
- **Phil Zamore**
  Chengjian Li