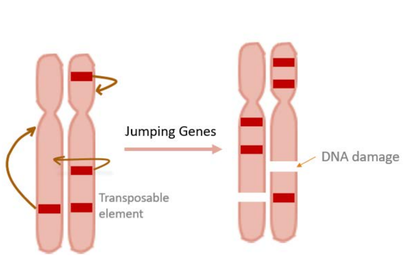
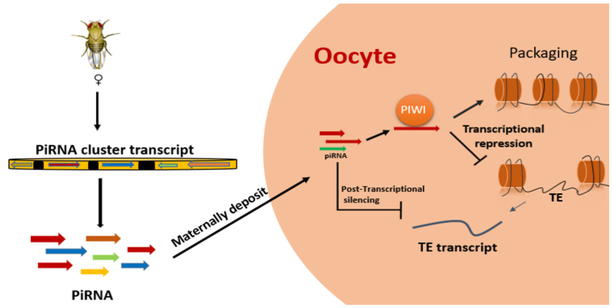
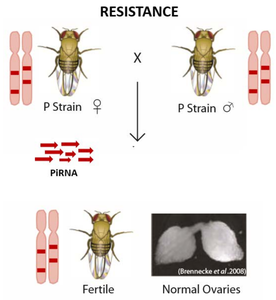
Satellite repeats are associated with host tolerance of an active TE

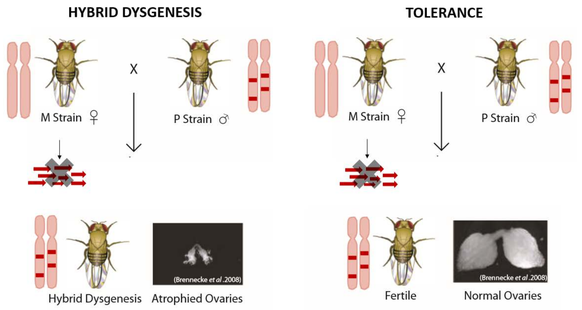
Jyoti Lama & Erin Kelleher
Department of Biology and Biochemistry, University of Houston

P-element activity causes Hybrid dysgenesis

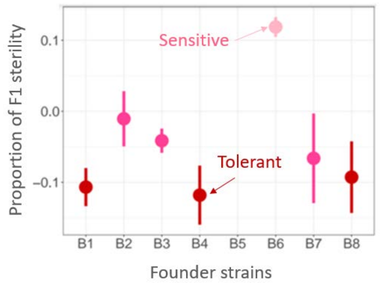




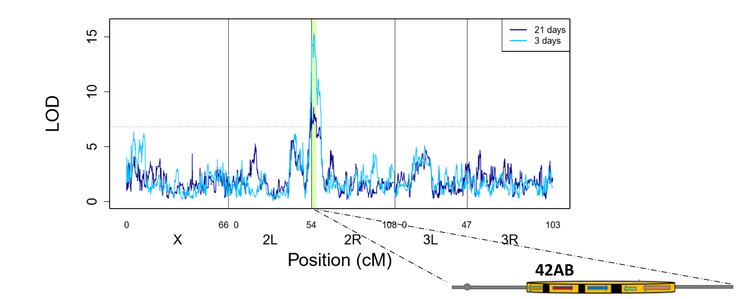




- Some strains were more tolerant producing fewer sterility in offspring
- while some were sensitive producing many sterile offspring.



Genome-Wide Association Study



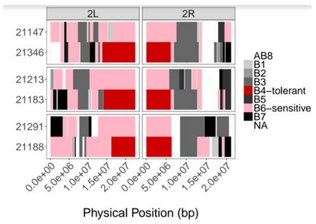
- 42AB encodes piRNAs regulating endogenous TEs but not those regulating *P* elements.

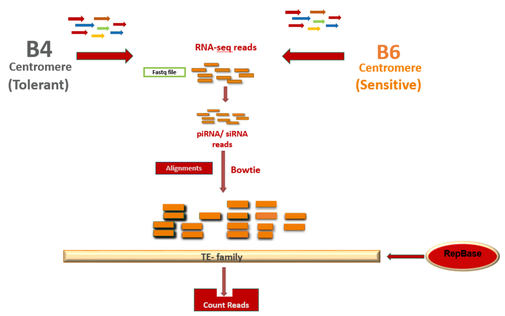
OBJECTIVE

- We aim to find whether the piRNA generated from resistant strains bearing tolerant 42AB alleles differ in their targeting of resident TEs as opposed to the sensitive strains.

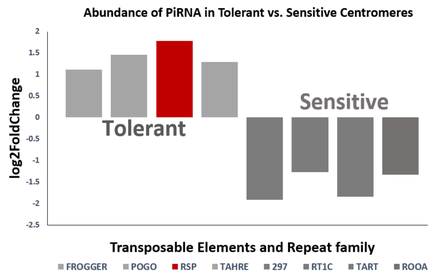
METHODS

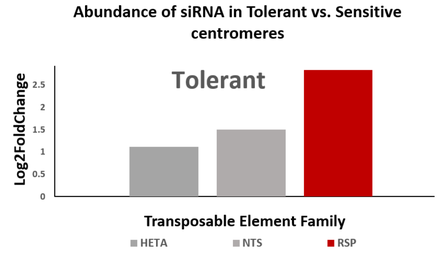
- We performed deep sequencing of piRNAs derived from pairs of founder strains that differed predominantly in the centromere region of second chromosome.



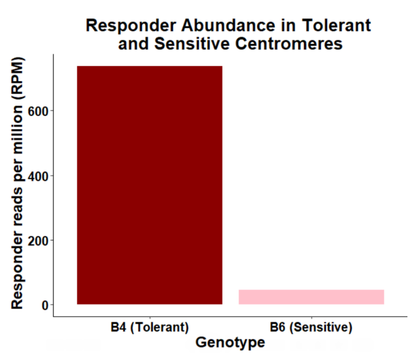


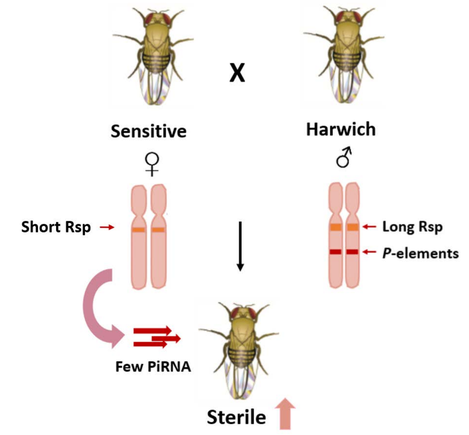
RESULTS





a) piRNA and b) siRNA alignments to Transposable elements and repeats family in tolerant (B4) vs. sensitive (B6).





IMPLICATIONS AND FUTURE DIRECTIONS

- P element mediated high sterility in sensitive strains may be due to incomplete packaging of responder repeats.
- I will mate females with different Rsp copy number to males with different Rsp copy number to test if packaging of Rsp repeats influence *P*-element tolerance.

REFERENCE

- Bao W, Kojima KK, Kohany O. Repbase update, a database of repetitive elements in eukaryotic genomes. Mobile DNA. 2015;6:11. doi: 10.1186/s13100-015-0041-9.
- BRENNECKE J., MALONE C. D., ARAVIN A. A., SACHIDANANDAM R., STARK A., HANNON G. J., 2008 An epigenetic role for maternally inherited piRNAs in transposon silencing. Science 322: 1387–92.
- KHURANA J. S., WANG J., XU J., KOPPETSCH B. S., THOMSON T. C., NOWOSIELSKA A., LI C., ZAMORE P. D., WENG Z., THEURKAUF W. E., 2011 Adaptation to P element transposon invasion in Drosophila melanogaster. Cell 147: 1551–63
- KING E. G., MERKES C. M., MCNEIL C. L., HOOFER S. R., SEN S., BROMAN K. W., LONG A. D., MACDONALD S. J., 2012 Genetic dissection of a model complex trait using the Drosophila Synthetic Population Resource. Genome Res. 22: 1558–66.
- Love, M. I., Huber, W., & Anders, S. (2014). Moderated estimation of fold change and dispersion for RNA-seq data with DESeq2. *Genome Biology*, *15*(12), 550. http://doi.org/10.1186/s13059-014-0550-8

Acknowledgements
We are grateful to Stuart MacDonald for supplying RILs, and to Stuart MacDonald and Libby King for helpful discussion of data analysis. Our research was made possible with funding from the University of Houston Division of Research and NSF DEB# 1457800 to E.S.K.).