

UNIVERSITY of
HOUSTON

COLLEGE of NATURAL SCIENCES & MATHEMATICS

BRUNO AND P-ELEMENT TRANSPOSITION:
POSITIVE REGULATOR OR CELLULAR RESPONDER?

Lorissa V. Saiz BS; BA, Erin S. Kelleher PhD



Lorissa Saiz



facebook.com/lsaizresearch



@98eagll

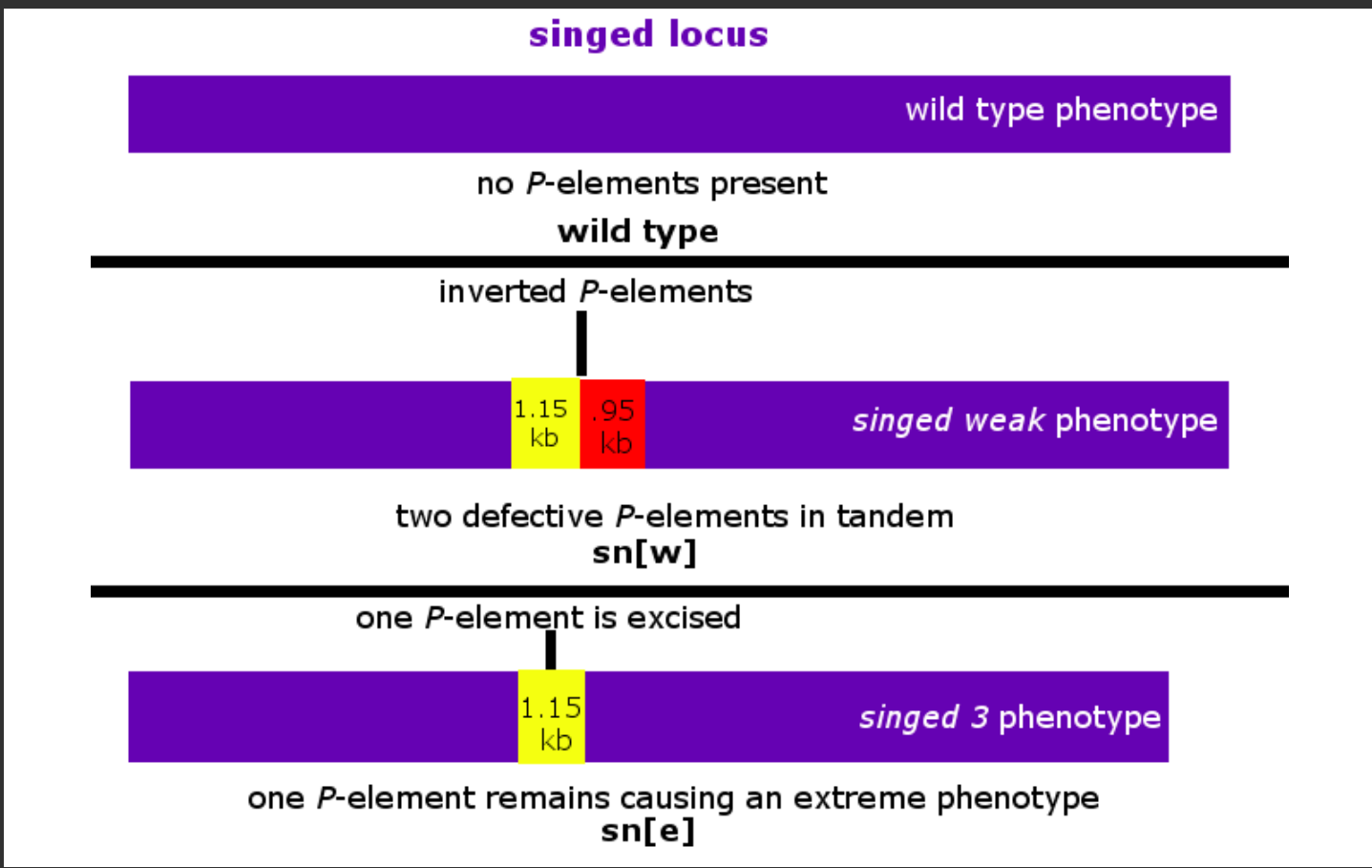
Introduction

Transposable elements (TEs) are obligate genetic parasites that spread throughout genomes and guarantee their transmission to offspring by replicating in germline cells. TE's are abundant in the genomes of every organism, so understanding ways organisms tolerate or repress them is imperative.

The P-element causes ovarian atrophy in female flies. It has been proven that maternally inherited piRNAs have an important role in transposition repression since they are antisense to TEs, and the absence of these piRNAs in dysgenic crosses allow us to study mechanisms of tolerance.

We isolated a gene, *bruno*, as a possible source of natural variation in P-element tolerance. *bruno* is a protein coding gene and has no known function in TE regulation.

Materials and Methods



Fertility assays led to the hypothesis that *bruno* is a source of natural variation in P-element tolerance or resistance. Based on preliminary data from this experiment, we expect that *bruno* is a tolerance factor. (Figures 1, 2 and 3)

By performing RNA extraction on *Drosophila* ovaries, cDNA synthesis and qPCR amplification we can observe P-element expression relative to *rpl32*. (Figure 3)

By crossing flies with specific genotypes, we can determine rates of P-element excision and whether *bruno* confers tolerance or resistance to P-element activity. If excision rates are higher or similar, it is likely that *bruno* is conferring tolerance. If they are lower it is likely *bruno* is conferring resistance. (Figure 4)

Results

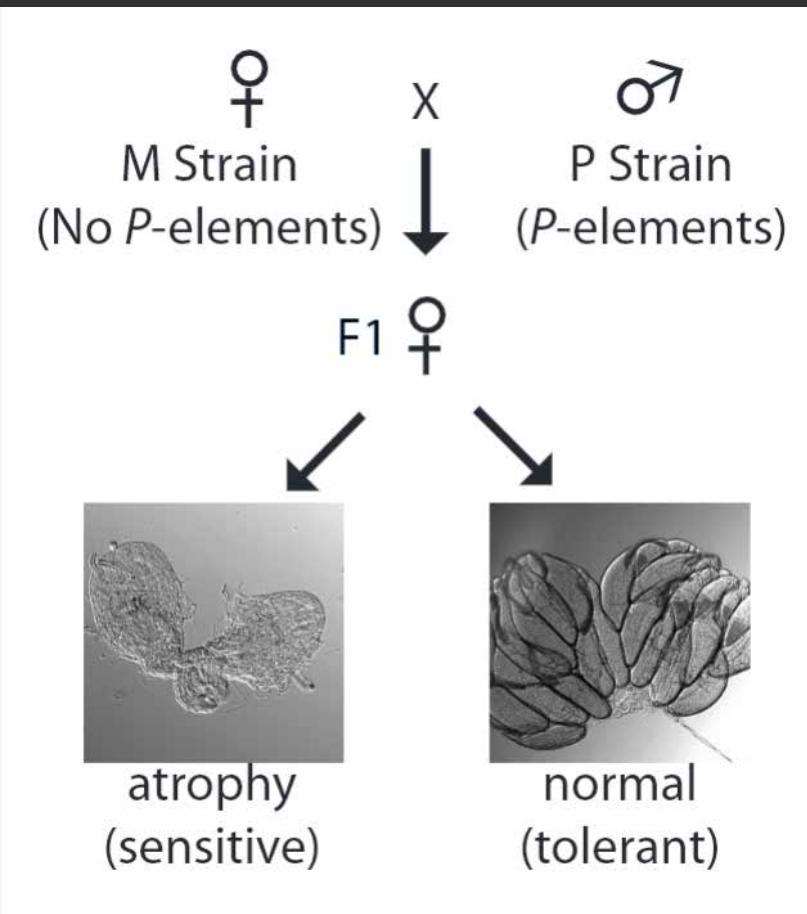


Figure 1: A dysgenic cross between a naive maternal strain and a P-element containing paternal strain results in offspring with atrophied ovaries in sensitive strains and normal ovaries in tolerant strains.

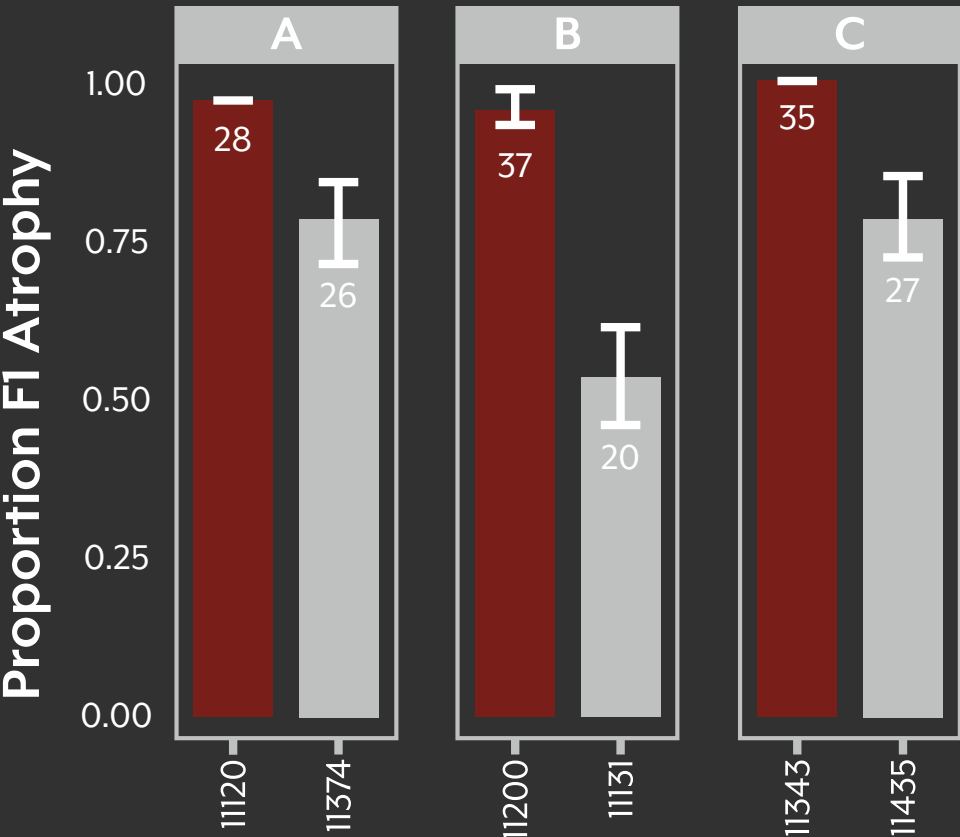


Figure 2: Proportion of ovarian atrophy in F1 offspring is much lower in tolerant strains than in sensitive strains.

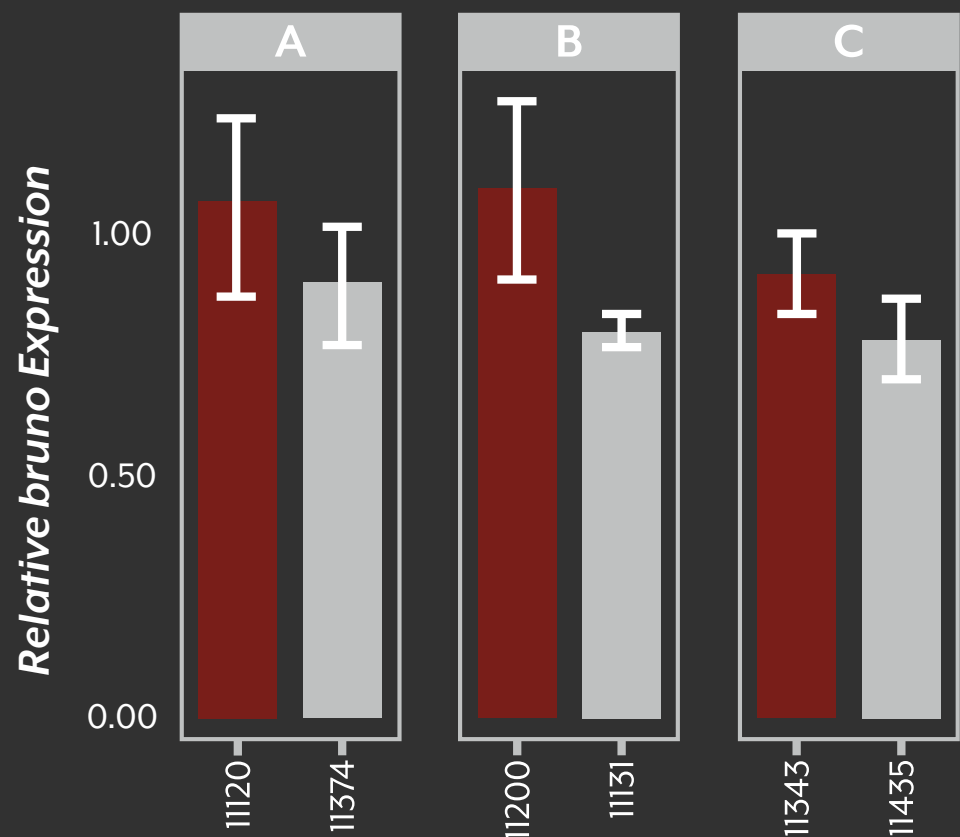


Figure 3: Sensitive and tolerant *bruno* alleles differ significantly in *bruno* expression.

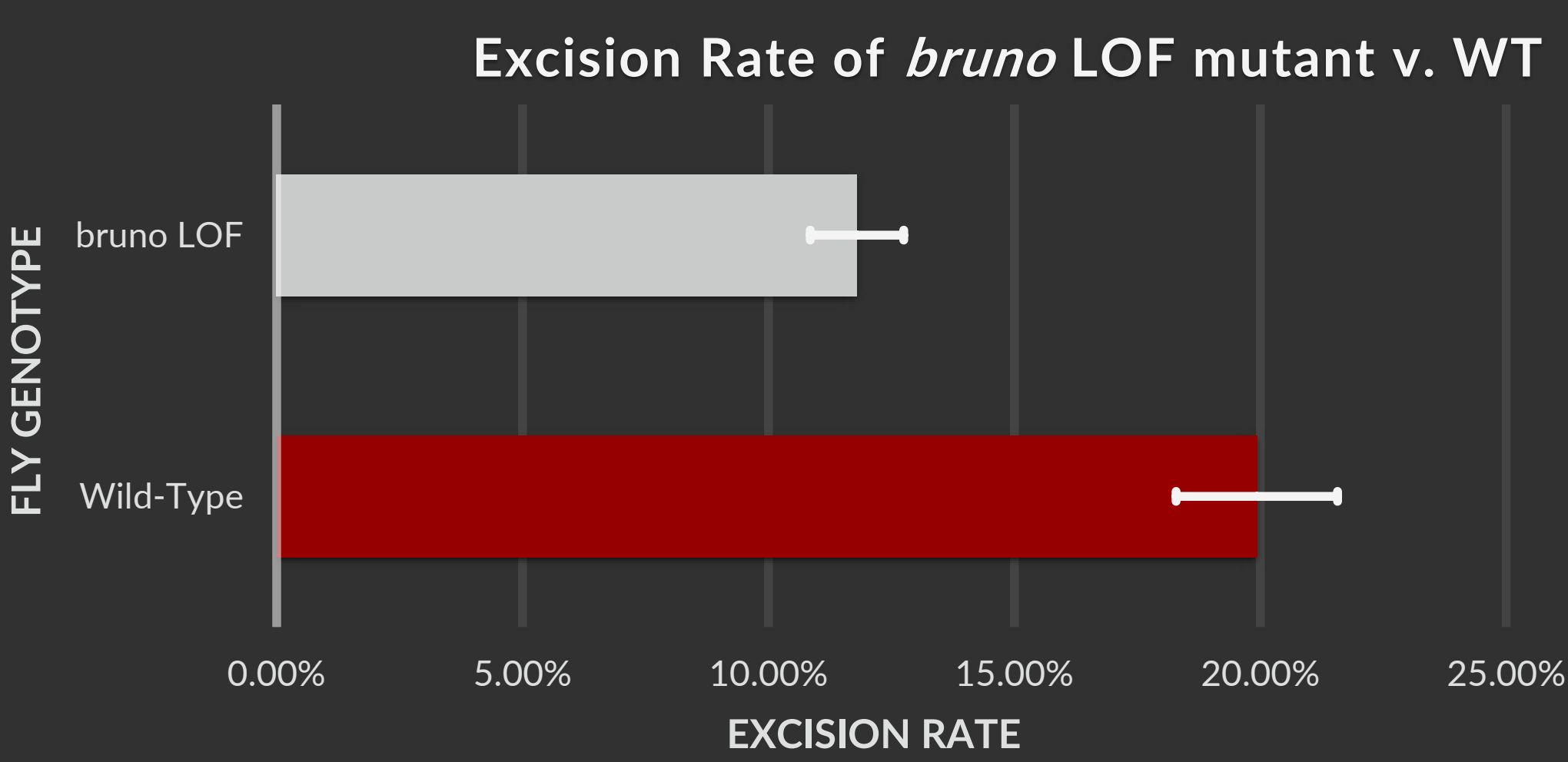


Figure 4: Excision rate in *bruno* LOF mutants [aretQB] is much lower than excision rate in WT

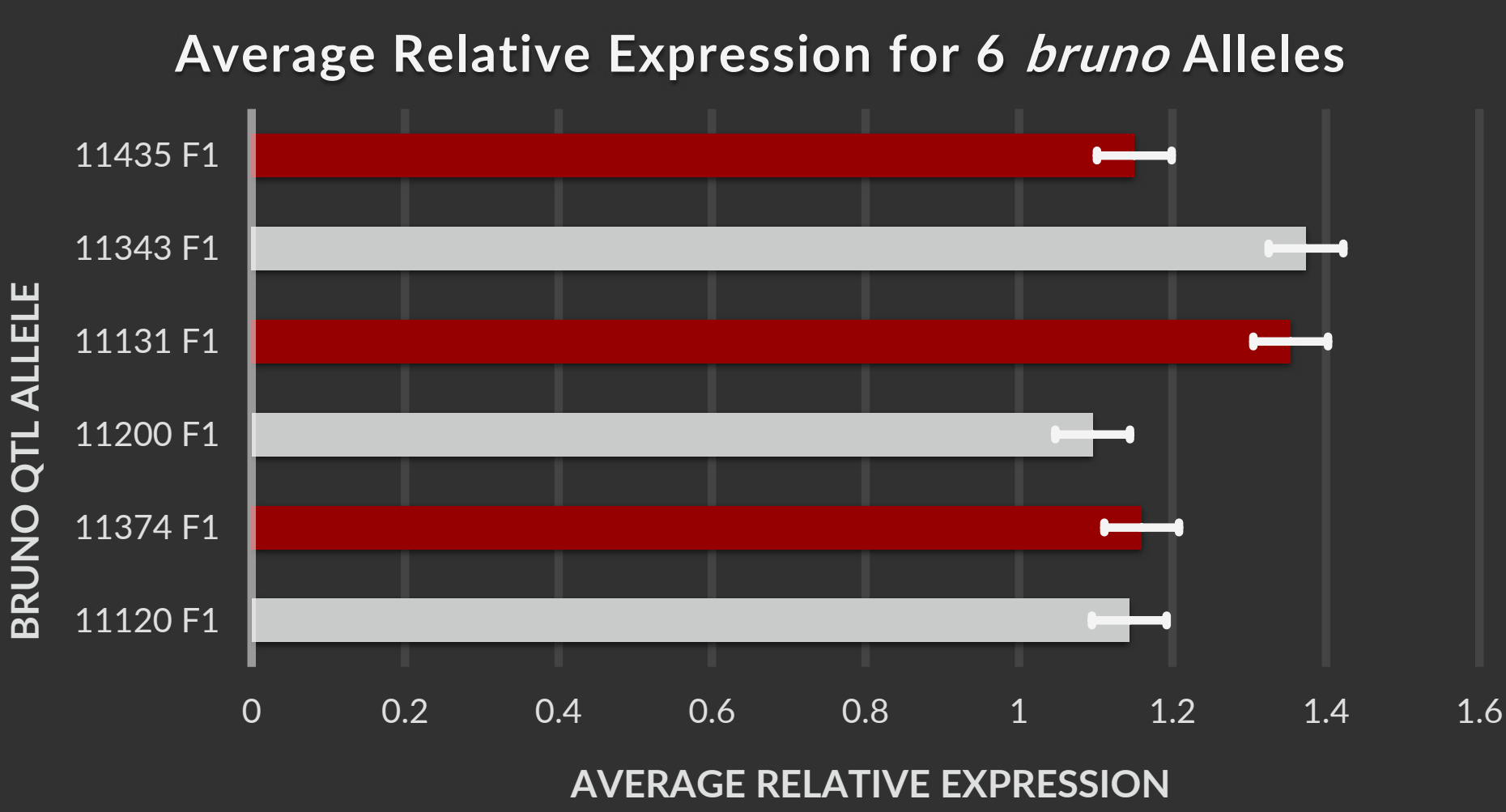


Figure 5: P-element expression relative to *rpl32* is not significantly different.

Conclusion

Through qPCR, we found that in the 2 naturally occurring alleles from 3 different genetic backgrounds(Kelleher et al 2018), *bruno* function does NOT play a role in P-element expression. P-element expression between *bruno* sensitive and tolerant pairs was not significantly different. These results strongly suggest that *bruno* is acting as a P-element tolerance factor.

In lab generated *bruno* mutants (aretQB), we found that the P-element excision rates were surprisingly much lower than wild-type excision rates. This suggests that *bruno* might be an upstream regulator of P-element activity.

Next...

Run qPCR expression assay on dysgenic *bruno* (aretRM and aretQB) offspring to determine the difference in P-element expression between the mutants and the wild type.

Run excision assays on the 2 naturally occurring alleles from 3 different genetic backgrounds alleles to determine if P-element excision rates differ between sensitive and tolerant allele pairs.

References

Kelleher, E. 2016, "Reexamining the P-Element Invasion of *Drosophila melanogaster* Through the Lens of piRNA Silencing", *Genetics*, p.1513-1531.

Kelleher, E., Jaweria, j. Akoma, U., Ortega, L., Tang, W.,2018, "QTL mapping of natural variation reveals that the developmental regulator *bruno* reduces tolerance to P-element transposition in the *Drosophila* female Germline.", *PLOS Biology*

Parisi, Michael J., et al. "The Arrest Gene Is Required for Germline Cyst Formation During *Drosophila* Oogenesis." *Genesis*, vol. 29, no. 4, John Wiley & Sons, Inc., Apr. 2001, pp. 196-209

Acknowledgements

NSF Division of Environmental Biology #1457800 to E.S.K. Funded Project

Special thanks to Jyoti Lama, Dr. Shuo Zhang, and Brandon Mistretta for training me and quality assessing samples, Rosa Cornejo for her amazing poster design, Zack Wilke, Lisa Nguyen and Ashley Argueta-Bonilla for assisting with experiment setup and data collection, and most of all Erin Kelleher for her brilliant mentorship and endless patience.