

BACKGROUND

Meiotic drive violates the fundamental law of segregation, changing allele inheritance from 50% to 100% of the time. An extreme sex-ratio meiotic drive (SR) trait is an X-linked selfish genetic element (SGE) which causes the carrier males to produce mostly female offspring (Figure. 2). The SR trait has been identified in two sexually dimorphic stalk-eyed fly species, *Teleopsis whitei* and *Teleopsis dalmanni*¹⁰ (Figure. 4). Recent research suggests that despite *T. whitei*'s and *T. dalmanni*'s close evolutionary relationship, the mechanism of the SR trait might occur differently¹⁰ and that there are fewer genomic differences between standard (ST) and SR *T. whitei* males (Figure 3).

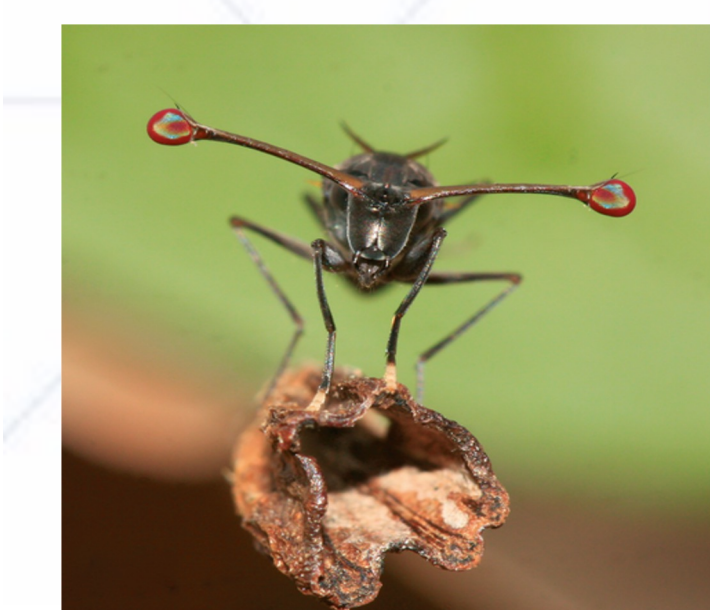


Figure 1. A male *Teleopsis* illustrating eyestalk ornament.⁴

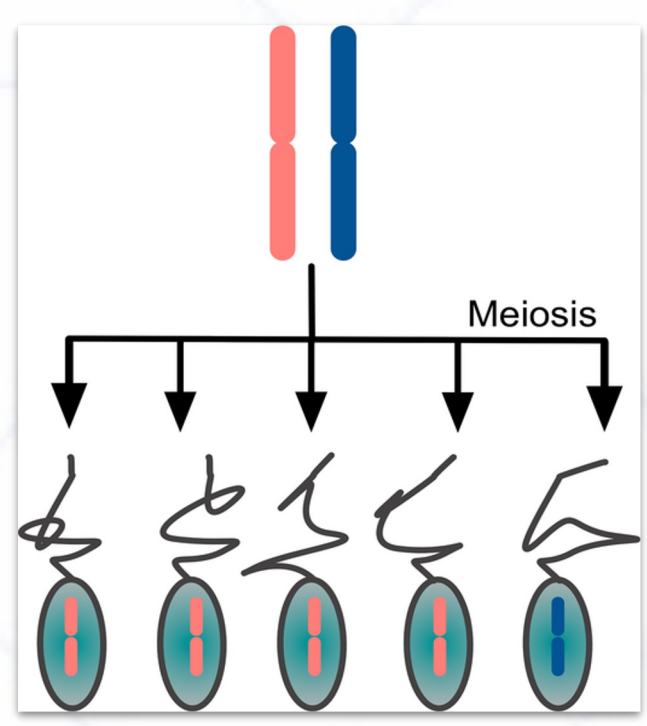


Figure 2. Segregation distorters (here shown in red) get transmitted to >50% of the gametes.¹

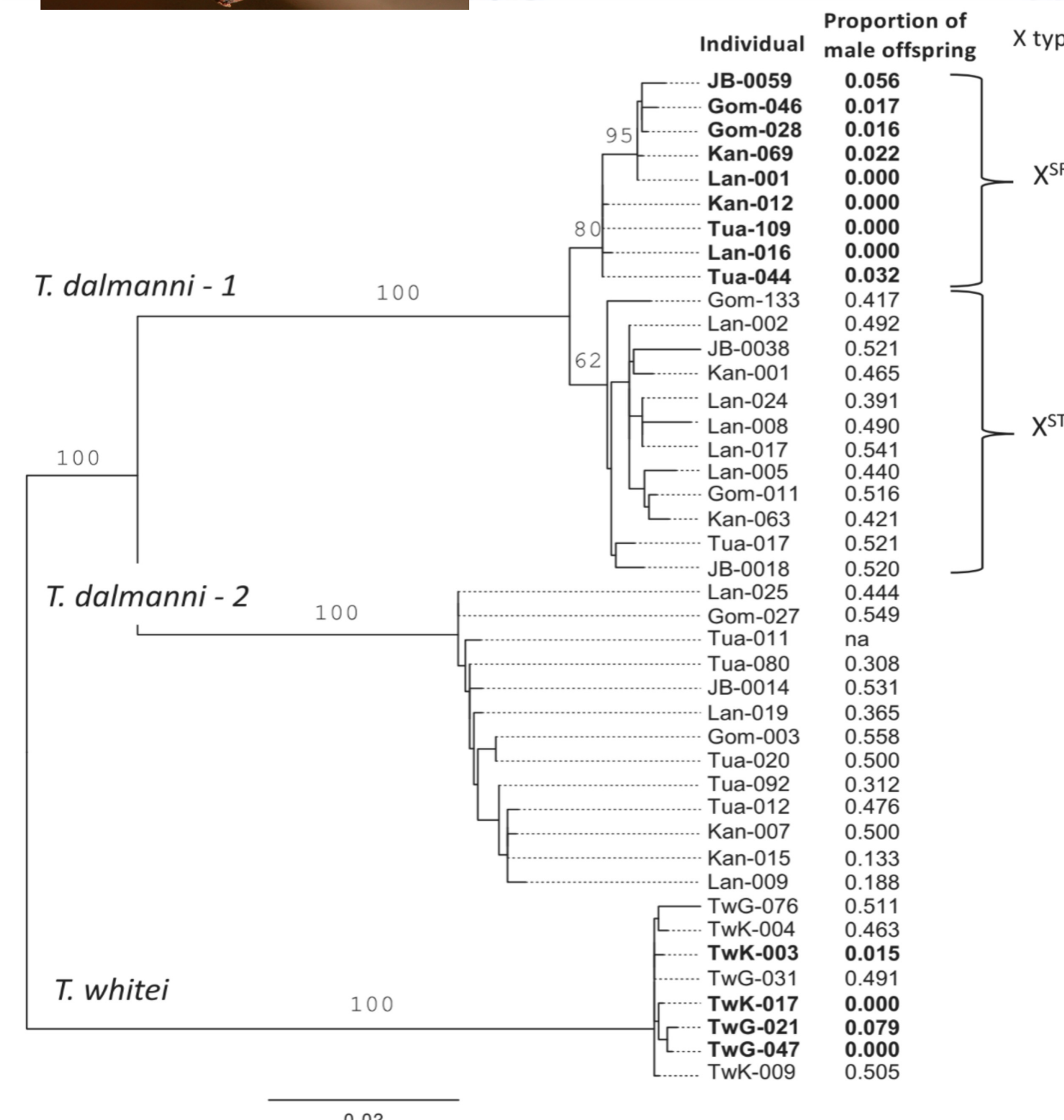


Figure 3. Phylogenetic relation and presence of SR in males of *T. dalmanni* 1, *T. dalmanni* 2, and *T. whitei*.¹⁰

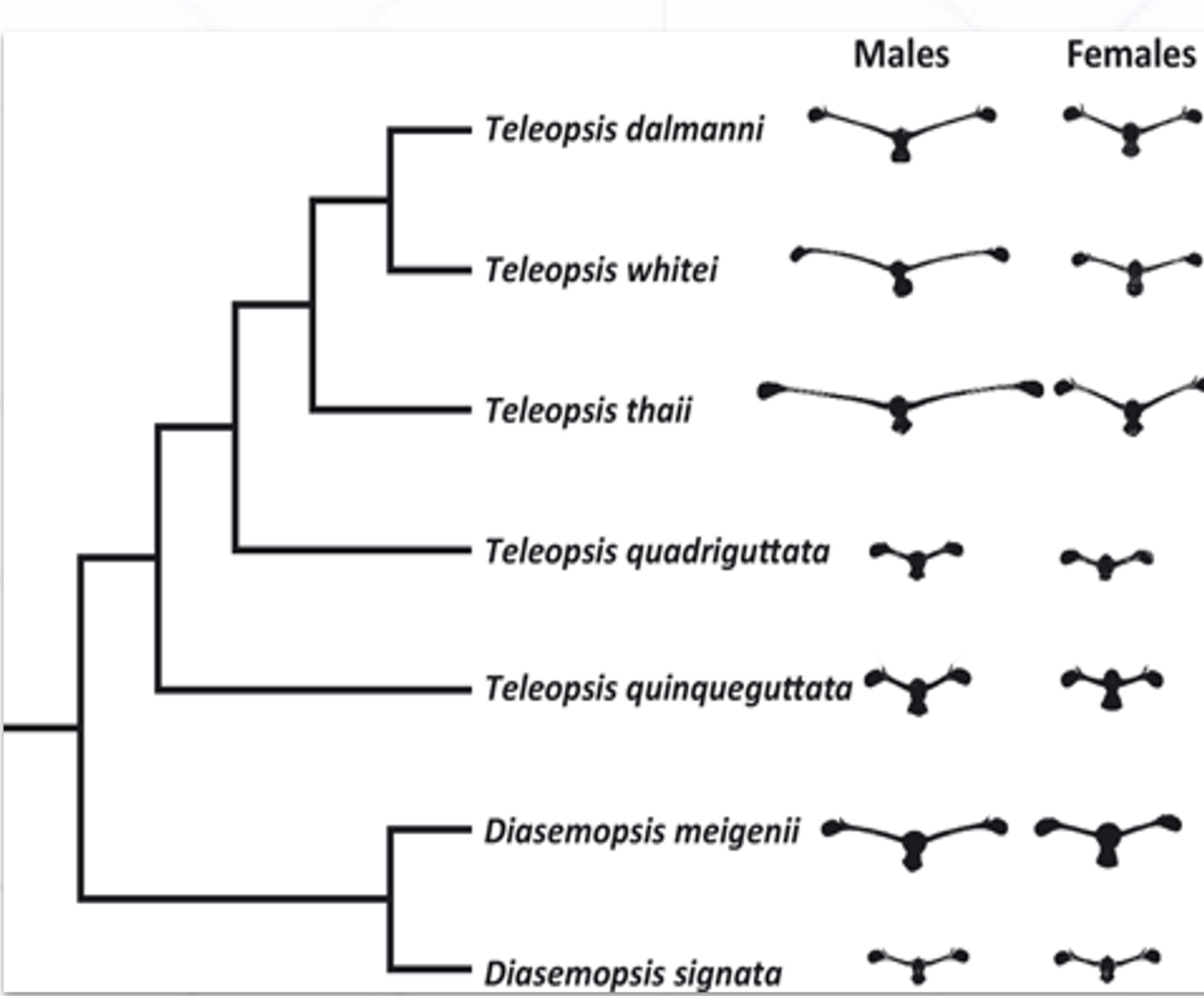


Figure 4. Phylogenetic relation of *Teleopsis* males and females that display sexual dimorphic eyestalk trait. Tree is a composite phylogeny adapted from Baker & Wilkinson (2001) and Földvári *et al.* (2007).³

REFERENCES

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GOALS

To analyze *T. whitei* whole genome sequence and RNA-seq data and determine what gene(s) and mutations may be responsible for meiotic drive.

Main Questions:

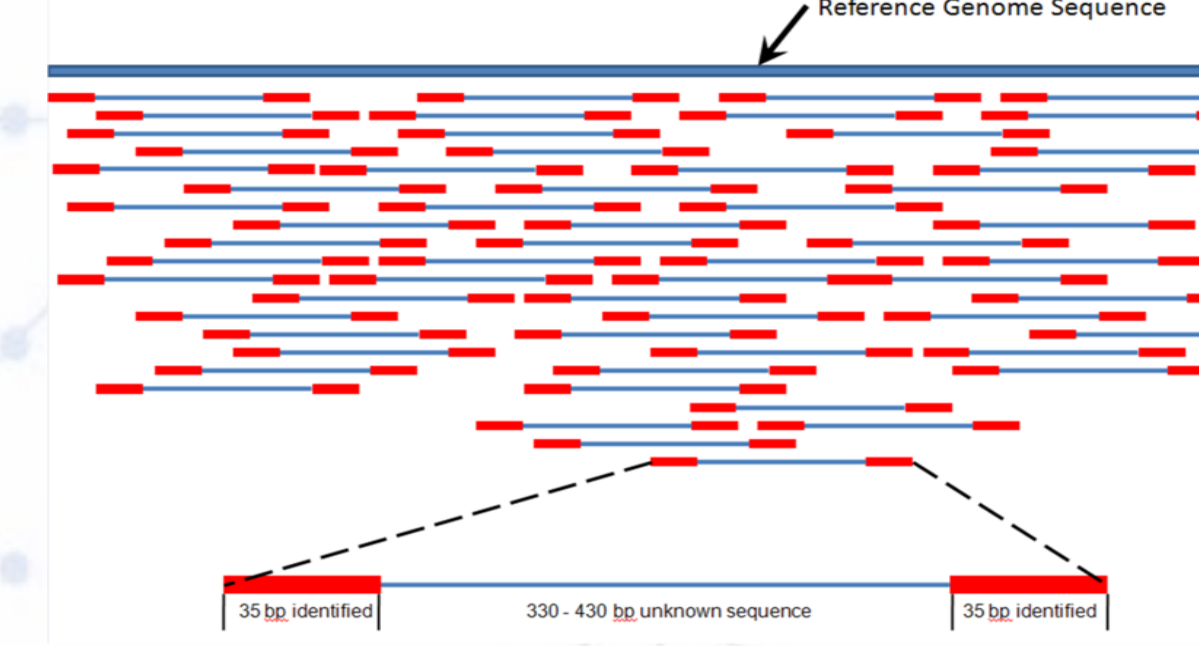
1. Do the genes that cause meiotic drive in *T. dalmanni* also cause meiotic drive in *T. whitei*?
2. What other genes or mutations are involved in meiotic drive in *T. whitei*?

METHODS

Data Collection:

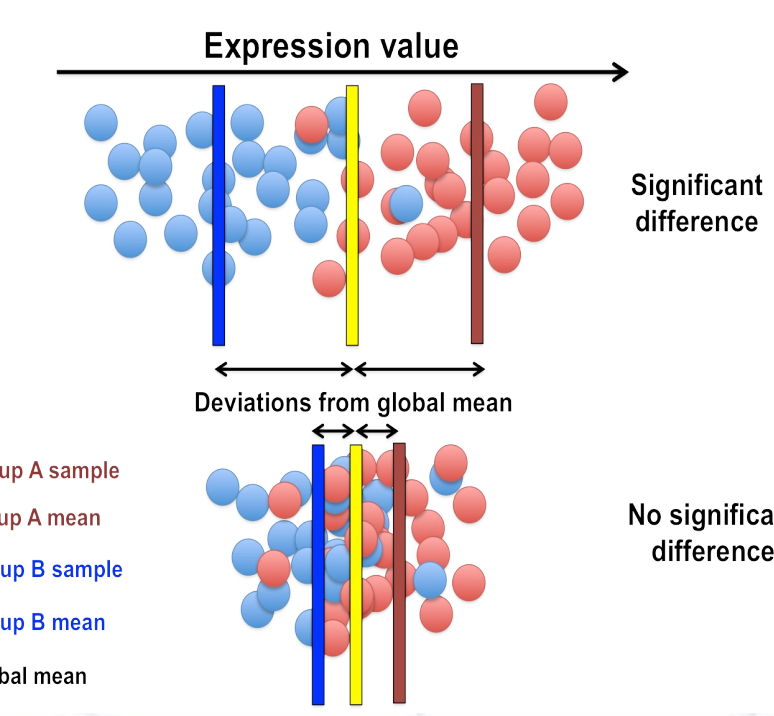
1. *T. dalmanni* and *T. whitei* males were captured in the field in Malaysia
2. Males were classified as SR or ST based on offspring sex ratio¹⁰
3. Sequencing performed by Illumina HiSeq method (4 RNA and 20 DNA data sets sequenced)

RNA⁵ & DNA⁶ Alignment:
Bioinformatic software to align¹¹ and sort² the reads to a reference genome



RNA and DNA sequencing reads. Aligning our reads with a reference genome will allow us to sort and identify which genes are similar and different. (https://biocorecr.github.io/RNAseq_course_2019/alignment.html)

Quantification & Visualization:
Count the number of reads and visualize the alignment against a reference genome⁸



Statistically analyze the DNA and RNA reads to identify any changes in expression or coverage levels between SR and ST *T. whitei* males. (https://biocorecr.github.io/CRG_Bioinformatics_for_Biol_Ogists/differential_gene_expression.html)

Statistical Analysis:
Differential Expression (DE) and Differential Coverage (DC) DESeq⁹ in R

Data Interpretation:

1. Comparison to *T. dalmanni* data
2. FlyBase⁷

RESULTS

Table 1. Genetic Differentiation in *T. whitei* and *T. dalmanni*

| | <i>T. whitei</i> (no. of genes) | <i>T. dalmanni</i> (no. of genes) |
|----|------------------------------------|--------------------------------------|
| DE | 16 | 596 |
| DC | 0 | 120 |

Table 2. Top 10 Adjusted p-values in DC genes in *T. whitei*

| FBgn ID | padj |
|-----------------------|-------------|
| 1.FBgn0085382.1.path2 | 0.257711204 |
| 2.FBgn0053523.5.path2 | 0.257711204 |
| 3.FBgn0035799.1.path1 | 0.301382439 |
| 4.FBgn0033836.1.path2 | 0.301382439 |
| 5.TwORF306.path1 | 0.344620657 |
| 6.FBgn0053966.1.path1 | 0.344620657 |
| 7.FBgn0029962.1.path2 | 0.370040896 |
| 8.FBgn0051118.1.path2 | 0.370040896 |
| 9.FBgn0040069.1.path2 | 0.370040896 |
| 10.TwORF320.path2 | 0.373273022 |

Table 3. Annotation of the Significant DE Genes in *T. whitei*

| FBgn ID | Arm Location in Drosophila | Drosophila Gene Name | Function |
|-----------------|----------------------------|----------------------------------|--|
| 1. FBgn0029848 | X | 1. Biotinidase | 1. hydrolase activity & biotinylation |
| 2. FBgn0001208 | 3L | 2. Henna | 2. iron ion binding & tyrosine biosynthetic process |
| 3. FBgn0265052 | 2R | 3. Sulfotrans-ferase 3 | 3. sulfotransferase activity |
| 4. FBgn0038938 | 3R | 4. NA | 4. transmembrane transporter activity |
| 5. FBgn0027556 | X | 5. NA | 5. potassium channel regulator activity |
| 6. FBgn0086909 | 2L | 6. NA | 6. hydroxylysine kinase activity |
| 7. FBgn0035978 | 3L | 7. UDP-glucose pyrophosphorylase | 7. UDP-glucose metabolism |
| 8. FBgn0263352 | 3L | 8. Upstream of N-ras | 8. translator repressor activity |
| 9. FBgn0040827 | 3L | 9. NA | 9. NA |
| 10. FBgn0036551 | 3L | 10. NA | 10. inositol metabolic process |
| 11. FBgn0039789 | 3R | 11. NA | 11. sulfate transport |
| 12. FBgn0030013 | X | 12. Phospho-lipase A2 group III | 12. phospholipid metabolic process |
| 13. FBgn0030593 | X | 13. NA | 13. ecdysteroid metabolic process |
| 14. FBgn0031974 | 2L | 14. NA | 14. N-acetyltransferase activity & histone acetylation |
| 15. FBgn0030482 | X | 15. NA | 15. branched-chain-amino-acid transaminase activity |
| 16. FBgn0052656 | X | 16. Musin 11A | 16. extracellular matrix structure & chitin binding |

DISCUSSION

- The comparison of SR and ST *T. whitei* males revealed 16 RNA genes that were significantly differentially expressed. None of which are differentially expressed in *T. dalmanni*.
- No significant differences in DNA differential coverage were identified.
- Our results suggest that there is less genetic differentiation among the chromosomes with meiotic drive. And the differences observed in expression between *T. whitei* and *T. dalmanni* indicate that different molecular mechanisms are likely at play to cause Meiotic Drive.
- Future analyses will include additional comparisons of *T. whitei* genomic data to the *T. dalmanni* data.
- In addition, we will look for single nucleotide sequence differences between SR and ST males in *T. whitei*.
- Through these analyses we aim to determine whether the SR trait in *T. whitei* occurs by a different mechanism, and whether the data suggests that SR has independently evolved in *T. whitei*.