

Cooperation of Selfish Genetic Elements in Stalk-Eyed Flies

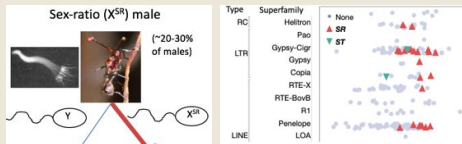
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Abstract

SGEs are selfish genetic elements that increase the likelihood of their own transmission regardless of the host's best interest. Transposable elements (TEs) and meiotic drivers are both types of SGEs. SGEs subsequently result in genetic conflict as they disrupt functional elements in the genome. We are working to better understand the cooperation of selfish genetic elements in Stalk-Eyed flies. Transposable elements are counteracted by small non-coding RNA molecules called piRNA. These RNA molecules work by reducing the expression of TEs by degrading TE RNA transcripts. Prior work in stalk-eyed flies has shown that TEs are expressed at a higher rate in male carriers of meiotic drive (SR males). We are comparing the expression of piRNA in SR and wild-type males using small RNA sequencing analysis software (proTRAC, PILFER) designed for this type of data. If meiotic drive and TEs cooperate, we would expect to see increased expression of piRNAs targeting TEs in SR males.

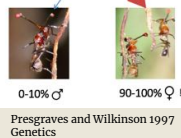
Introduction

- Our goal is to understand how the expression of small RNAs that regulate TEs (piRNAs) may change due to the presence of meiotic drive
- piRNAs produce RNAi which degrade the expression of TEs



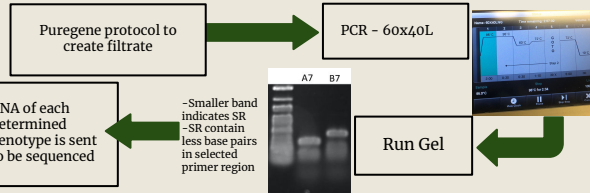
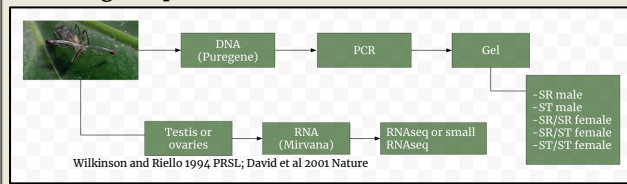
Work by Dr. Reinhardt et al. displayed that several TE families are overexpressed in SR males.

Work by Eric Lai and colleagues. Found that when RNAi pathway is repressed sex ratio is exhibited and there is an excess of females in the population. When RNAi is not mutated there is a 50:50 male to female ratio. Displays decrease expression of piRNA increases meiotic drive.



Methods

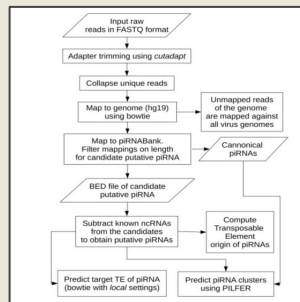
Collecting samples:



Bioinformatics:

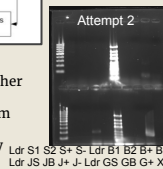
- Pilfer
- ProTRAC

Softwares compare piRNA sequence reads to the stalk eyed fly genome. The softwares detect, visualize and analyze piRNA clusters (Ray, Rishav et al.)

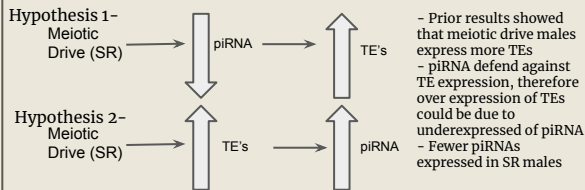


Gel Attempts-

- First attempt - with control DNA (not shown)
- First attempt did not display bands -> problem in either PCR or DNA extraction
- Second attempt with manufactured master mix -> see if the problem was in PCR
- DNA ladder is present however fly DNA did not display bands indicating problem in DNA extraction



Results



Bioinformatics:

Fastq piRNA reads:

```
[reshlab@7b122 shared]$ head R5B257-345.trimmed.fastq
@M551536.167.IV3.LBMC4F.1.11181.19411.1843.1.N;B:TTAGCCAT+AGAGACA
TCTGTCGACATCATATGCTTGAGGCTGTA
+
AAAAAEEEEEEEEEEEEEEEEEEEEEEEE
@M551536.167.IV3.LBMC4F.1.11181.18201.1843.1.N;B:TTAGCCAT+AGAGACA
TCTGTCGACATCATATGCTTGAGGCTGTA
+
AAAAAEEEEEEEEEEEEEEEEEEEEEEEE
```

Fasta (fa) of the fly genome (beginning of Chromosome 1):

```
chr1.fa chr1.1 chr1.2 chr1.3 chr1.4 chr1.5 chr1.6 chr1.7 chr1.8 chr1.9 chr1.10 chr1.11 chr1.12 chr1.13 chr1.14 chr1.15 chr1.16 chr1.17 chr1.18 chr1.19 chr1.20 chr1.21 chr1.22 chr1.23 chr1.24 chr1.25 chr1.26 chr1.27 chr1.28 chr1.29 chr1.30 chr1.31 chr1.32 chr1.33 chr1.34 chr1.35 chr1.36 chr1.37 chr1.38 chr1.39 chr1.40 chr1.41 chr1.42 chr1.43 chr1.44 chr1.45 chr1.46 chr1.47 chr1.48 chr1.49 chr1.50 chr1.51 chr1.52 chr1.53 chr1.54 chr1.55 chr1.56 chr1.57 chr1.58 chr1.59 chr1.60 chr1.61 chr1.62 chr1.63 chr1.64 chr1.65 chr1.66 chr1.67 chr1.68 chr1.69 chr1.70 chr1.71 chr1.72 chr1.73 chr1.74 chr1.75 chr1.76 chr1.77 chr1.78 chr1.79 chr1.80 chr1.81 chr1.82 chr1.83 chr1.84 chr1.85 chr1.86 chr1.87 chr1.88 chr1.89 chr1.90 chr1.91 chr1.92 chr1.93 chr1.94 chr1.95 chr1.96 chr1.97 chr1.98 chr1.99 chr1.100 chr1.101 chr1.102 chr1.103 chr1.104 chr1.105 chr1.106 chr1.107 chr1.108 chr1.109 chr1.110 chr1.111 chr1.112 chr1.113 chr1.114 chr1.115 chr1.116 chr1.117 chr1.118 chr1.119 chr1.120 chr1.121 chr1.122 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