

# Investigating the Function of Putative Sperm Length Genes Using Mutants

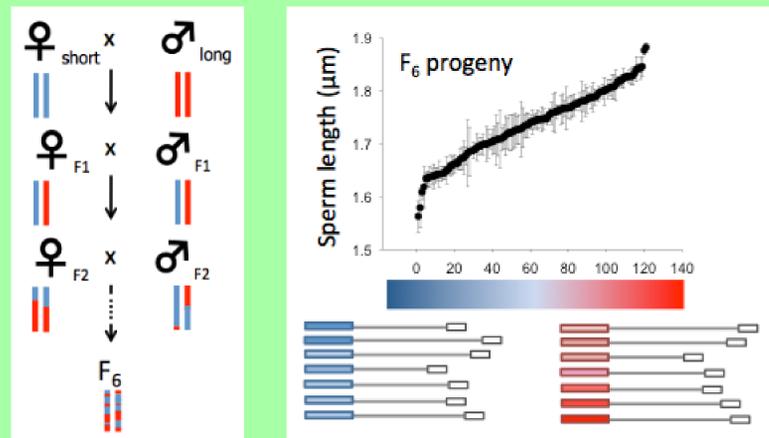
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## Introduction

- The fruit fly is a model organism because of its small size, simple diet, short life cycle, and genes comparable to that of humans. <sup>1</sup>
- In *Drosophila melanogaster*, males with long sperm are more likely to have more offspring after mating with polygamous females as compared to males with shorter sperm. <sup>2</sup>
- Sperm length coevolves with the length of the seminal receptacle (SR), a female sperm storage organ. <sup>2</sup>
- To understand the genetic basis of sperm length, sperm length was assessed in putative sperm length gene mutants.
- We look at genes Tenectin and Serrano, which are expressed post-meiotically during sperm elongation and morphogenesis.

## Methods

### RAD QTL Mapping



(Mollie Manier. Unpublished Data.)

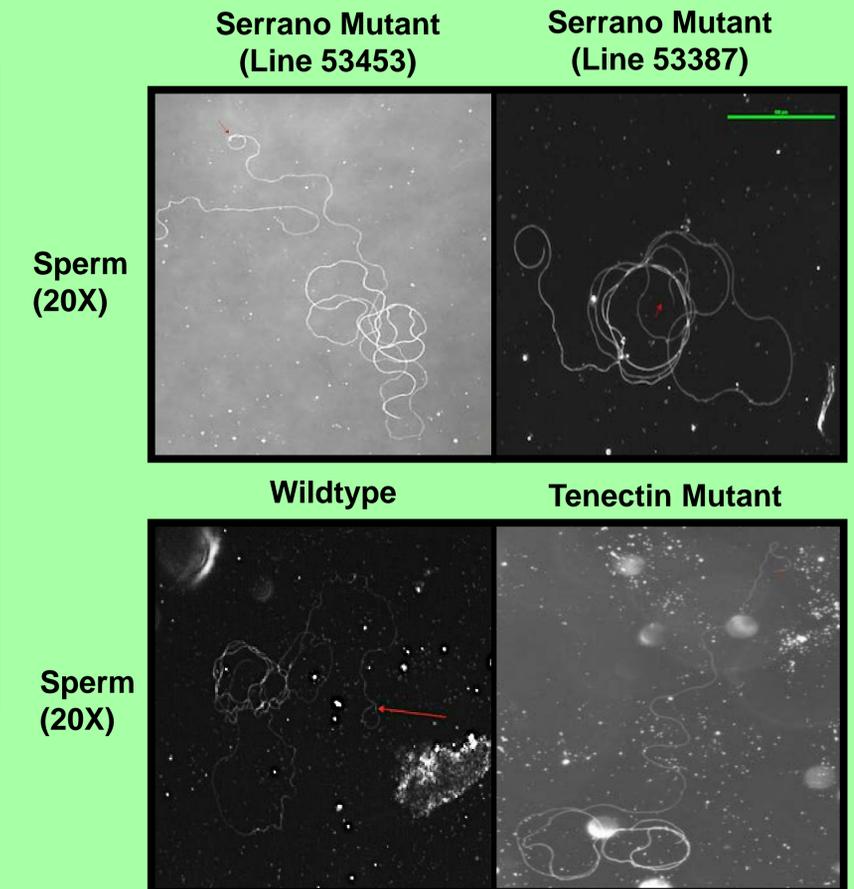
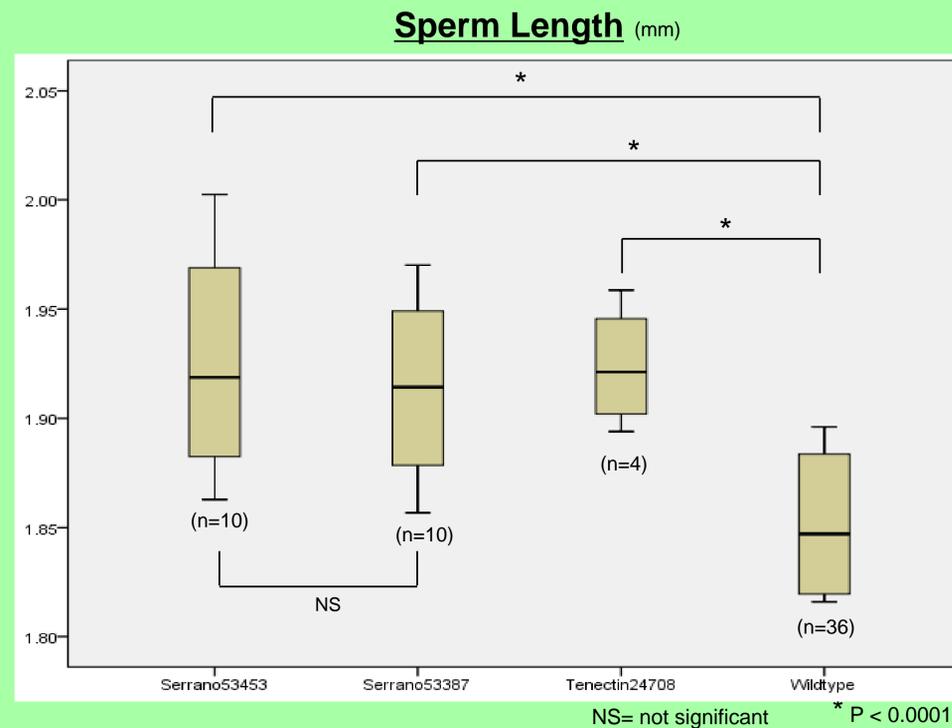
↓ SNPs  
↓ Genes  
↓ Gene function in sperm length

Serrano had 7 SNPs and Tenectin had 3 SNPs.

### Sperm Length

- Mutant lines obtained from the Bloomington Stock Center. <sup>3</sup>
- 10-day old virgin males from each line dissected.
- Sperm collected from one seminal vesicle.
- Sperm were stained, observed and measured.
- Analyzed the longest four measurements from each male.
- The average sperm length of the males was calculated to determine an average length for each line.
- A t-test was used to compare two mutant lines of the same gene.
- A t-test was used to compare the mutants to wildtype.
- Published wildtype data served as reference for analysis. <sup>4</sup>

## Results



\* Arrow indicates sperm head. Scale represents 100 µm.

### Statistical Analysis

#### Serrano Mutant (54354) vs. Serrano Mutant (53387)

P-value = 0.780853       $\alpha = 0.05$   
 $P < \alpha$ , do not reject null hypothesis stating that there is no difference between the sperm lengths of the two data sets.

#### Serrano Mutants vs. Wildtype

P-value = 2.30436E-10       $\alpha = 0.05$   
 $P < \alpha$ , reject null hypothesis stating that there is no difference between the sperm lengths of the two data sets.

#### Tenectin Mutant vs. Wildtype

P-value = 4.47838E-07       $\alpha = 0.05$   
 $P < \alpha$ , reject null hypothesis stating that there is no difference between the sperm lengths of the two data sets.

### Conclusion

Statistical analysis shows that lines 53453 and 53387 are not statistically different from each other. Since the two lines have similar sperm lengths, both lines for Serrano are phenotypically comparable. Two independent knockout mutants resulted in a similar outcome. According to the t-test, the sperm lengths of the three mutant lines are significantly greater than that of wildtype. Based on the results, both genes appear to be involved in negative regulation of sperm length, which relates to known information that Tenectin and Serrano are involved in morphogenesis and development.

## Future Directions

- Increasing sample size to obtain stronger confidence about the conclusions made.
- Phenotyping other putative sperm length gene mutants as was conducted to determine their role in sperm length.
- Analyzing the SR lengths of the same mutant lines to see if they are significantly different from that of wildtypes and if there is coevolution with the length of sperm.

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## References

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