

Characterizing Candidate Genes for Sperm and Seminal Receptacle Length in *Drosophila melanogaster*

Reem Al Shabeeb | Dr. Mollie Manier | Department of Biological Sciences, The George Washington University

Background

- The genetics of spermatogenesis has been well-studied for 20 years, but little is known about genetics of variation in sperm length.
- Sperm length is important in sperm competition, which occurs when females mate with multiple males and can evolve rapidly and contribute to new species formation via reproductive isolation¹.
- Sperm length coevolves with the length of the seminal receptacle (SR), a female sperm storage organ².
- Fruit fly is a model organism because of its small size, large family size, short life cycle, genetic manipulation methods and genes homologous to humans.
- In this research two genes were investigated: *crossveinless c* (*cv-c*) and *tenebrion* (*tnc*).

Methods

- Mutant lines were obtained from the Bloomington Stock Center³, Bloomington, Indiana.
- Each mutant line was crossed with its original genetic background to generate a genetically similar control.
- Virgin males were dissected at 5 days old, and virgin females were frozen at 5 days old and dissected at a later time.
- Seminal vesicles from males were dissected into 1X phosphate buffered saline (PBS), and sperm were spread on a slide, dried, fixed and stained, imaged on a Nikon upright microscope, and measured using ImageJ software.
- SR's were dissected into PBS, secured under a coverslip with clay on the corners to achieve optimal compression, imaged and measured as above.
- A t-test was used to compare the mutant lines to the control.

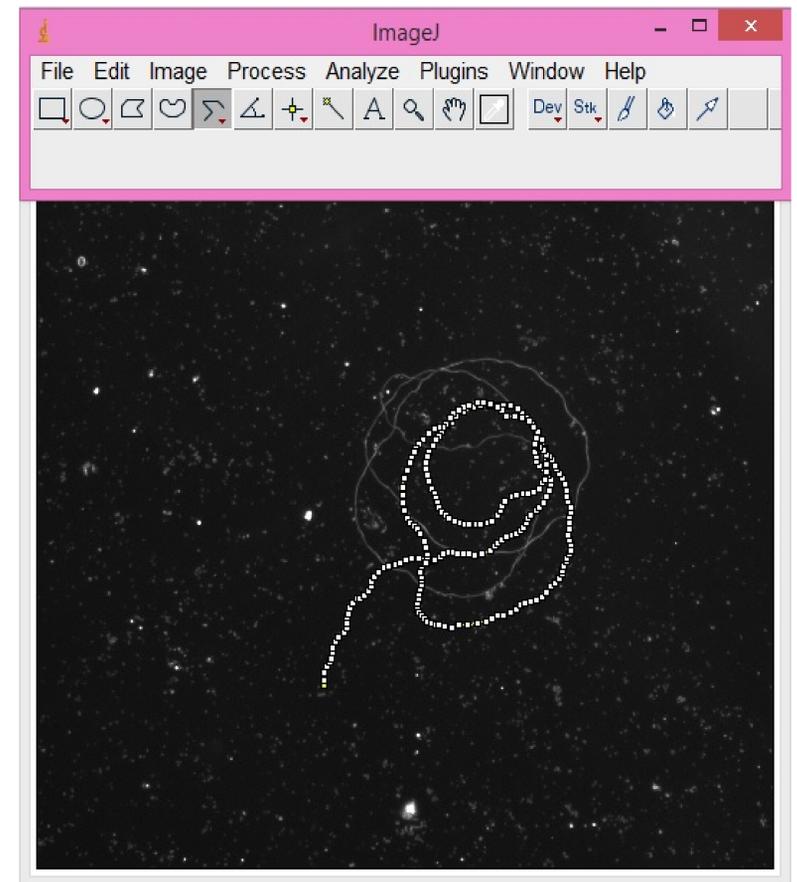


Fig. 4. Wild-type sperm being measured using ImageJ (darkfield, 400X magnification).

Results

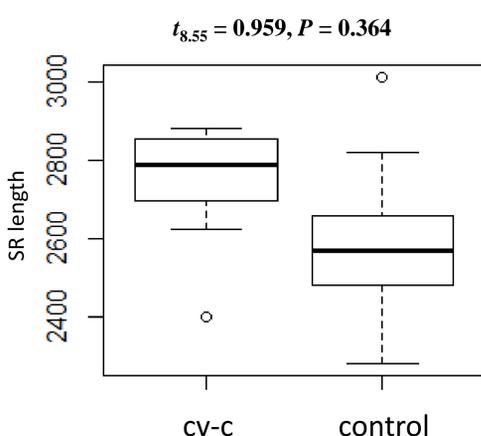


Fig. 1. SR lengths of *cv-c* mutants are not significantly longer than control wild-type.

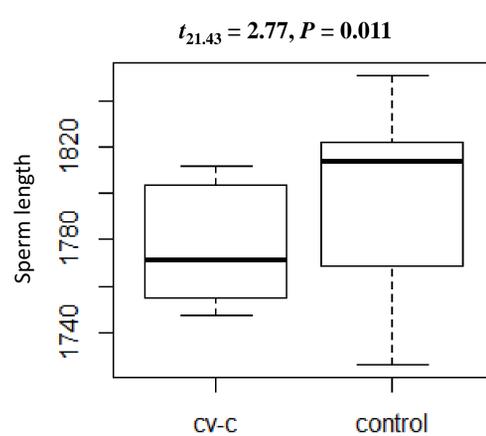


Fig. 2. Sperm lengths of *cv-c* mutants are not significantly different from control wild-type.

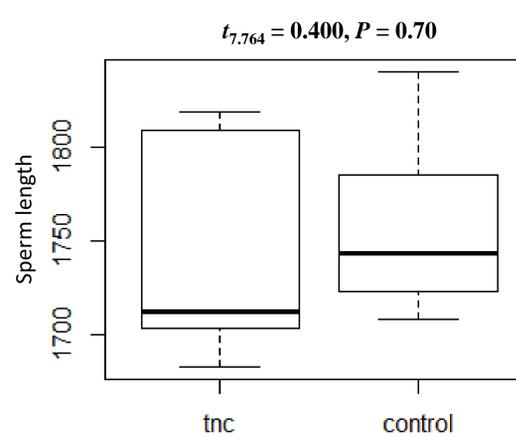


Fig. 3. Sperm lengths of *tnc* mutants are not significantly different from control wild-type.

- There was no change in sperm length in both mutant lines. This result could mean that either these genes do not play a role in sperm length, or a functionally gene or set of genes is taking over the role of the knocked out gene. Alternatively, the knockout may not have been effective in *tnc*; future efforts will validate this using qPCR.
- However, longer SR's were observed in *crossveinless c*. This result suggests that this gene plays a role in negatively regulating SR length and may have pleiotropic effects on sperm length.
- Pleiotropy acting on *crossveinless c* to control both sperm length and SR length is a possible mechanism for coevolution of these two traits across the *Drosophila* phylogeny.

Future Directions

Future studies will investigate:

- The roles of these genes during spermatogenesis.
- The role of more genes using mutant lines.

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Works Cited

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2. Miller, G.T., S. Pitnick. 2002. Sperm-female coevolution in *Drosophila*. *Science* 298:1230-1233.
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4. <http://imagej.nih.gov/ij/>