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Investigating the genotypic-phenotypic relationship between the gene *small optic lobes (sol)* and sperm length

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Introduction

Sperm length variation plays a major role in post-copulatory sexual selection and can cause rapid evolutionary diversification within species. Despite its significance, the underlying genetic mechanisms for sperm length are not well understood. *Drosophila* have the most varied sperm lengths ranging from 0.32mm to 5,800mm long,[1] making the fruit fly an ideal organism to study sperm length. Preliminary research in the Manier Lab used RAD QTL mapping to identify nearly 300 candidate genes associated with sperm length variation. This study investigates the effect of silencing one of the candidate genes, *small optic lobes (sol),* on the sperm length in *D. melanogaster*.

Methods

1. The GAL4/UAS system was used for the RNAi knockdown of the gene *sol* in *D. melanogaster* testes during early spermatogenesis.

2. Mature sperm from adult males were dissected from the testes, stained with DAPI, imaged, and measured using *ImageJ*.[2]

3. Measurements were analyzed to determine the genotypic-phenotypic relationship between *sol* and sperm length.

Results

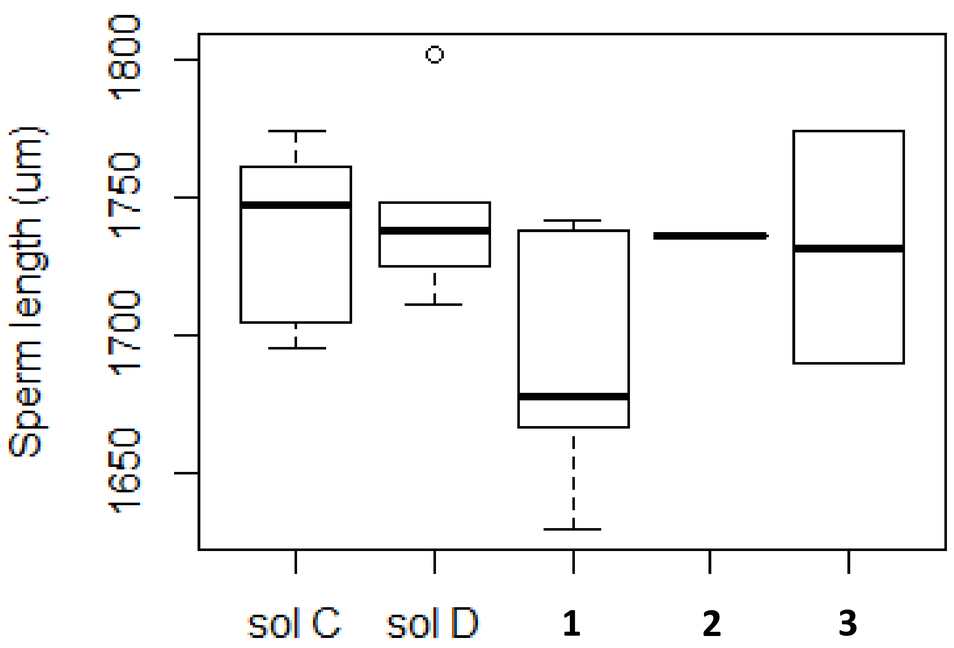

Fig 1. Sperm length of two mutant families (*sol* C and *sol* D) and three control families (1, 2, and 3). The *sol* families are not statistically different from the control families. $F_{4,17} = 1.649$, $P = 0.208$

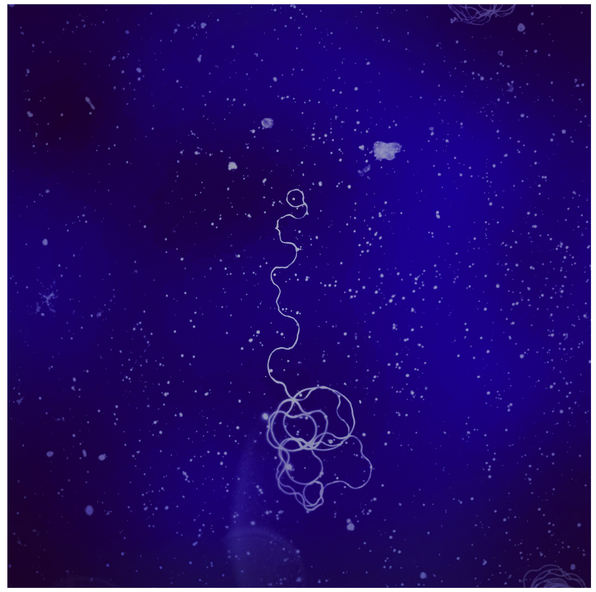

Fig 2. *D. melanogaster* sperm (darkfield, 200x magnification)

Discussion

The results suggest that the candidate gene *sol* does not direct the development of sperm length. This effect may not be apparent if a functionally redundant gene is taking over the role of *sol* in spermatogenesis or if the *sol* knockdown was not fully effective.

Future Work

Future efforts will examine the effect of the *sol* knockdown on gene expression using qPCR and test a more effective knockdown driver. Other candidate genes will be investigated using the RNAi knockdown system. This information will be important for understanding the underlying genetic mechanisms of spermatogenesis as well as for future studies of reproductive evolution.

Acknowledgements

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References

[1] Pitnick et al. 1999. Evolution of multiple kinds of female sperm storage organs in *Drosophila*. Evolution 53:1804-1822.

[2] Schneider, C. A.; Rasband, W.S. & Eliceiri, K.W. (2012), “NIH Image to ImageJ: 25 years of image analysis”, Nature methods 9(7): 672-675