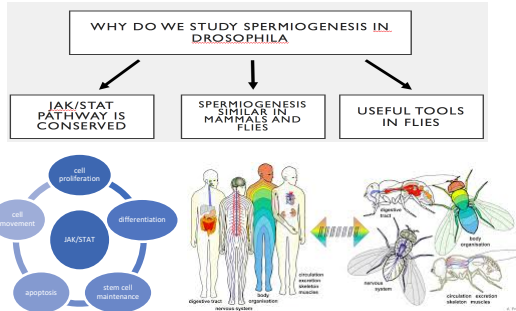


# Use of HPC to analyze changes in gene expression during fruit fly spermiogenesis

Sepideh Dadkhah, Douglas Harrison, Jeremiah J Smith  
Department Of Biology, University of Kentucky, Lexington, KY 40506

## Introduction

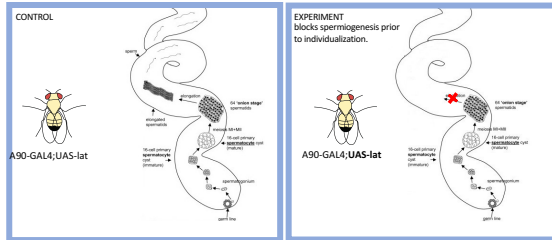


In the fruit fly, *Drosophila melanogaster*, JAK/STAT signaling during spermiogenesis is known to play a crucial role in the maintenance of stem cells of the testis. Recent studies in our lab have shown that activation of the JAK/STAT pathway in somatic cyst cells is also required for the later stages of spermiogenesis like individualization.

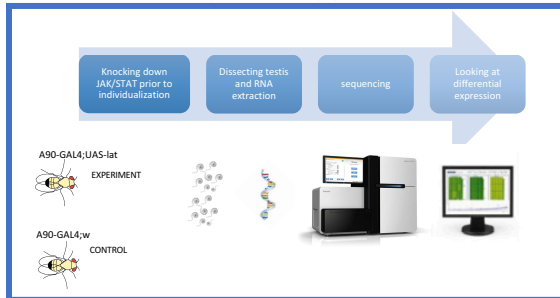
The main goal of this project is to characterize the events downstream of JAK/STAT signaling in spermiogenesis and more specifically to determine the mechanism by which JAK/STAT activation regulates individualization, a later stage in spermiogenesis where 64 individual spermatids are formed from a 64-interconnected spermatid bundle.

This study has compared transcriptional profiles of testes in which JAK/STAT signaling has been genetically arrested prior to individualization to testes from wild type flies using RNA-seq methods.

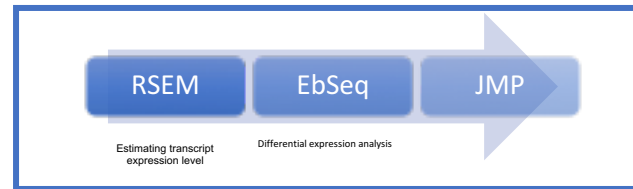
## Experiment and control set up



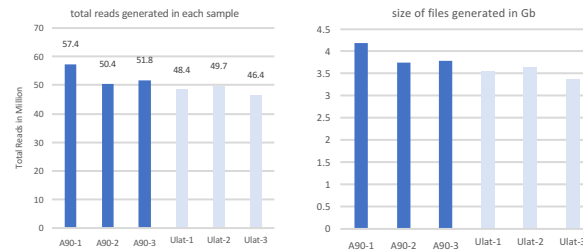
## Experimental pipeline



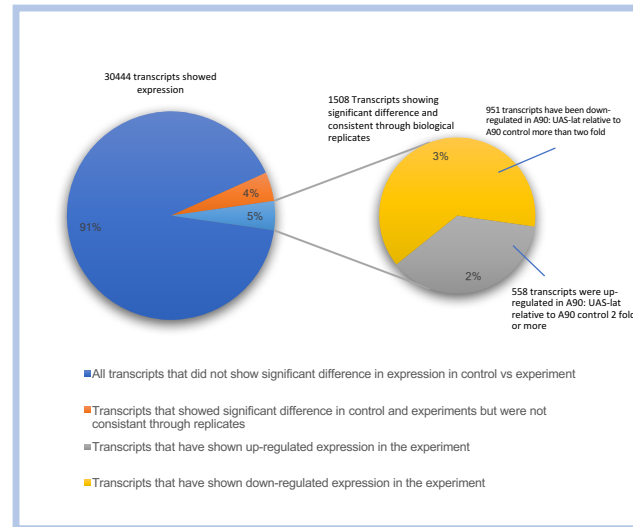
## Bioinformatic pipeline



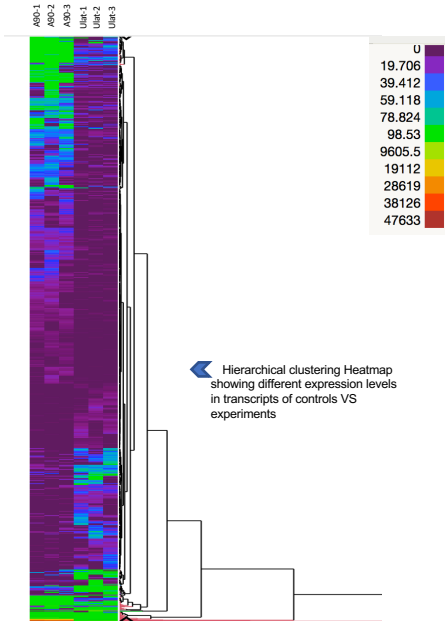
### Raw data statistics



## Expression profile



## Differential expression analysis



## Use of HPC

Because of the high data volume of Next-generation sequencing experiments, analyses are time-consuming and high-performance computing clusters like the DLX provide great advantages for such research.

In this specific project using the software mentioned on a remote HPC has greatly helped by using parallelization strategies to achieve faster runtimes of the analysis and providing more storage and computing power than available on other platforms.

Transcriptional profiling of the testis after changes in the JAK/STAT pathway has made this experiment the first in its kind of RNAseq transcriptional profiling experiments in flies.

## Future Directions

- Comparison of transcriptional profiling of this study with transcriptional profile studies done with other fertility mutants.
- Confirm transcript expression using qPCR.
- Analyzing expression of specific transcripts that are known to be binding sites for STAT.
- Functionally analyze candidates that are target for individualization during spermiogenesis

## Citation

Arbouzova, N.I., and Zeitler, M.P. (2006). JAK/STAT signalling in *Drosophila*: insights into conserved regulatory and cellular functions. *Development* 133, 2605-2616.

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Amoyel, M., and Bach, E.A. (2012). Functions of the *Drosophila* JAK/STAT pathway: Lessons from stem cells. *JAK/STAT* 1, 176-183.

Fabian, L., and Brill, J.A. (2012). *Drosophila* spermiogenesis: Big things come from little packages. *Spermatogenesis* 2, 107-212.

Fuhrer, M.T. (1993). *Spermatogenesis. In The Development of Drosophila melanogaster*. M. Bate, and A. Martinez-Arias, eds. (Cold Spring Harbor, NY: Cold Spring Harbor Laboratory Press).

Wang, L. (2014). The JAK/STAT pathway is reutilized in *Drosophila* spermatogenesis. PhD Thesis. (Lexington, KY: University of Kentucky).

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- **Research Category:** Bio-informatics, NGS, Development, Spermiogenesis, JAK/STAT Pathway
- **Description of research:** This study has compared transcriptional profiles of testes in which JAK/STAT signaling has been genetically arrested prior to individualization during spermiogenesis to testes from wild type flies using RNA-seq methods.
- The main goal of this project is to characterize the events downstream of JAK/STAT signaling in spermiogenesis and more specifically to determine the mechanism by which JAK/STAT activation regulates individualization, a later stage in spermiogenesis where 64 individual spermatids are formed from a 64-interconnected spermatid bundle.

