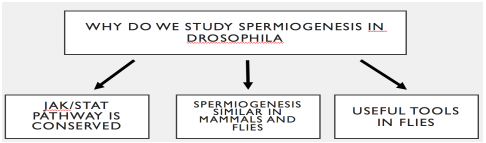
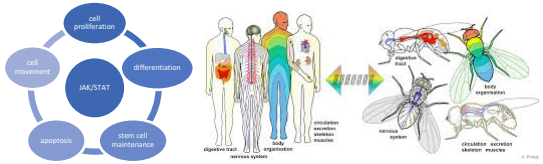
Use of HPC to analyze changes in gene expression during fruit fly spermiogenesis

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

Introduction



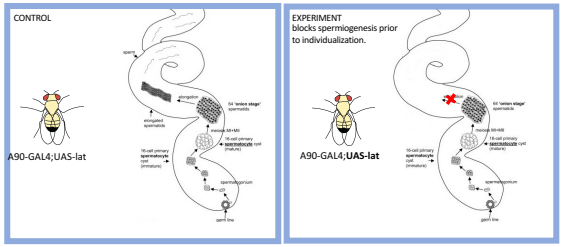


In the fruit fly, *Drosophila melanogaster*, JAK/STAT signaling during spermiogenesis is known to play a crucial role in the maintenance of stem cells of the testis. Recent studies in our lab have shown that activation of the JAK/STAT pathway in somatic cyst cells is also required for the later stages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

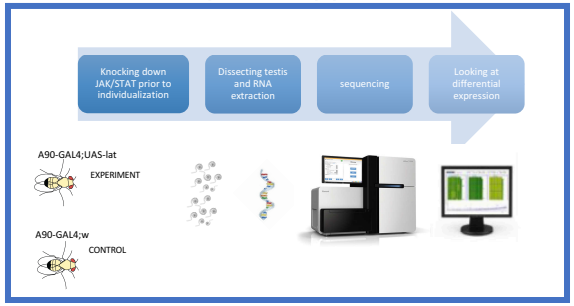
The main goal of this project is to characterize the events downstream of JAK/STAT signaling in spermiogenesis and more specifically to determine the mechanism by which JAK/STAT activation regulates individualization, a later stage in spermiogenesis where 64 individual spermatids are formed from a 64-interconnected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

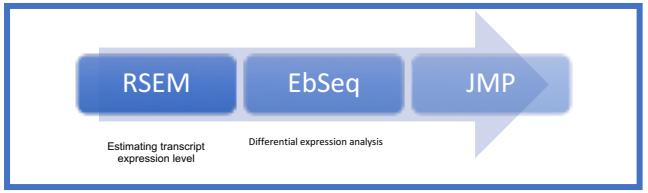
Experiment and control set up



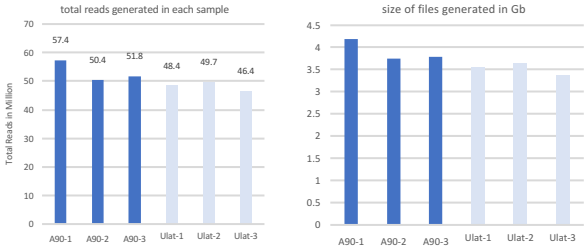
Experimental pipeline



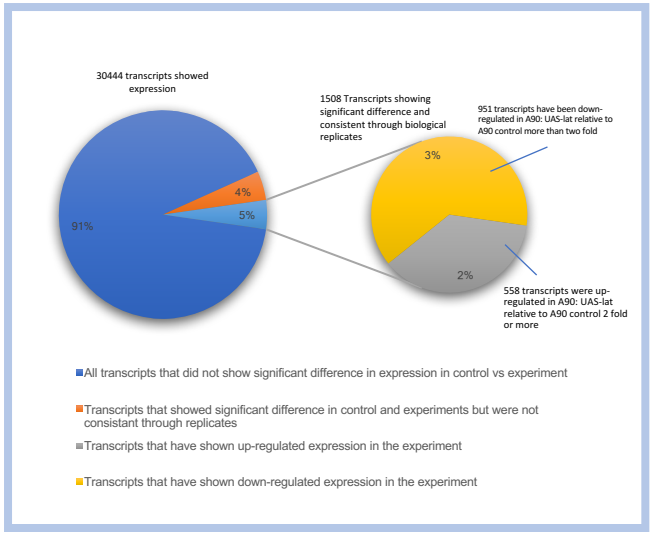
Bioinformatic pipeline



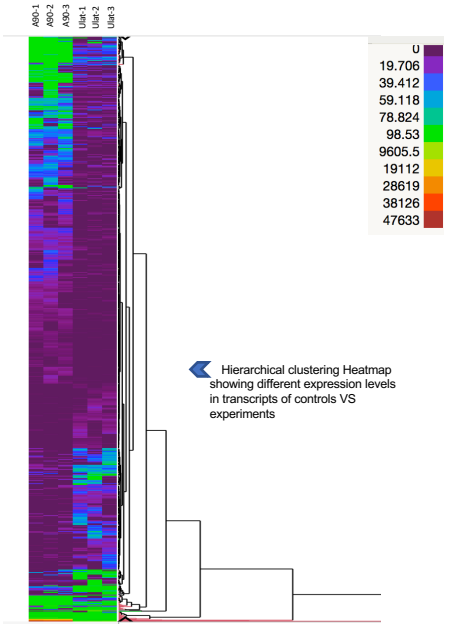
Raw data statistics



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 then 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 Zeidler, M.P. (2006). JAK/STAT signalling in *Drosophila*: insights into conserved regulatory and cellular functions. Development *133*, 2605-2616
Harrison, D.A. (2012). The JAK/STAT pathway. Cold Spring Harbor perspectives in biology *4*, a011205
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Fabian, L., and Brill, J.A. (2012). Drosophila spermiogenesis: Big things come from little packages. Spermatogenesis *2*, 197-212
Fuller, 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)
8-Tang, 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.