Cellular heterogeneity underlying poly-functional fat body tissue in Drosophila melanogaster

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Introduction

Fat body tissue is a multi-functional tissue. In *Drosophila melanogaster*, fat body tissue is involved in including

- reproduction,

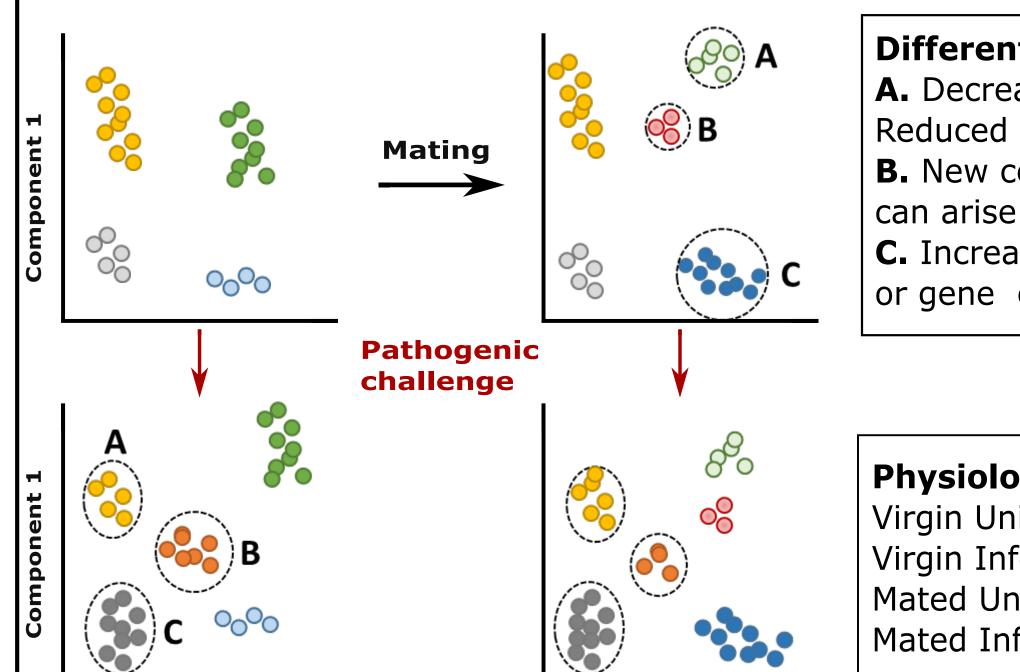
Component 2

- immunity, and
- nutrient metabolism

However, we do not understand how polyfunctionality of the fat body tissue is maintained.

Hypothesis

Physiological conditions have differential impact on distinct subpopulations.



Different scenarios:

- A. Decreased cell number/ Reduced gene expression **B.** New cell populations can arise
- C. Increased cell number or gene expression

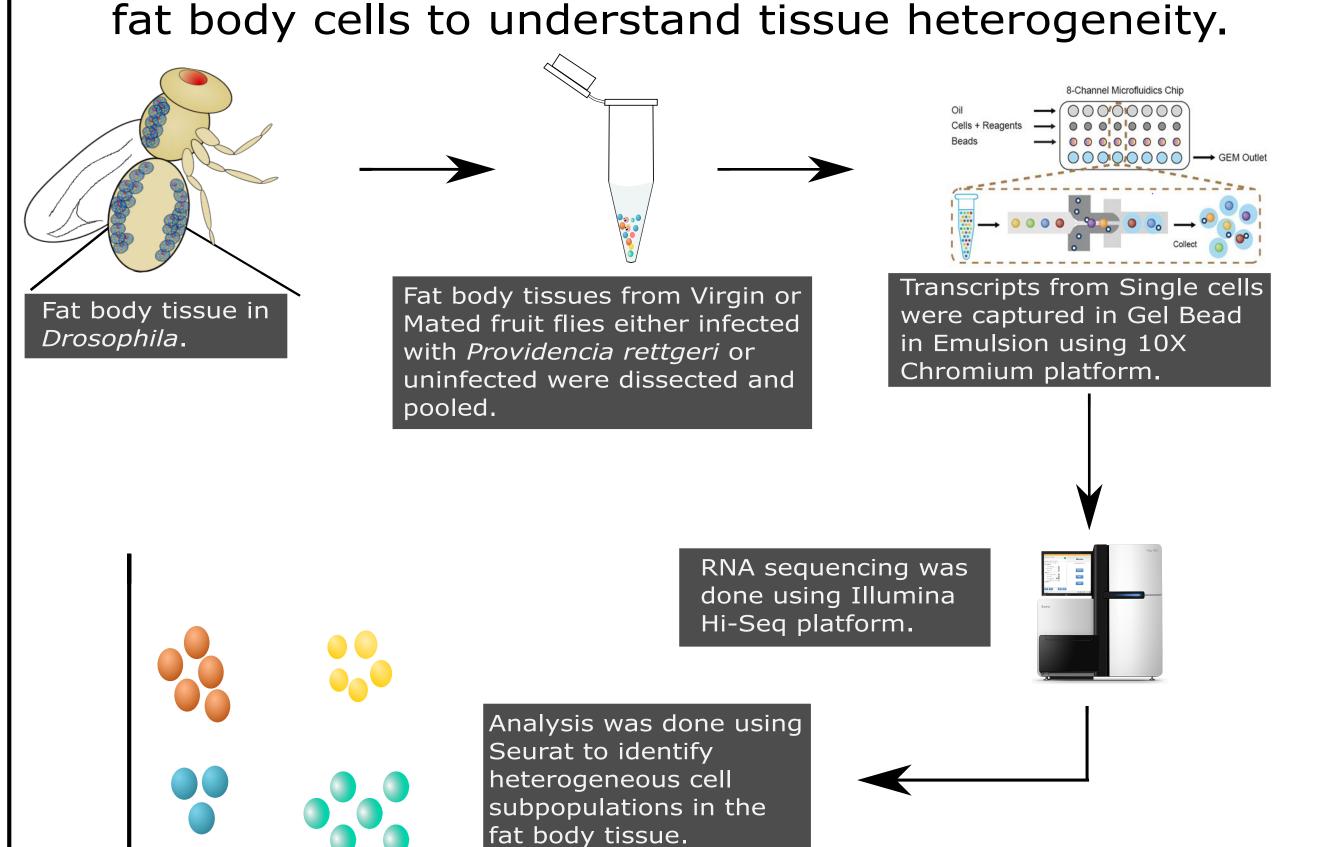
Physiological conditions:

Virgin Uninfected (VU) Virgin Infected (VI) Mated Uninfected (MU) Mated Infected (MI)

Experimental Approach

Component 2

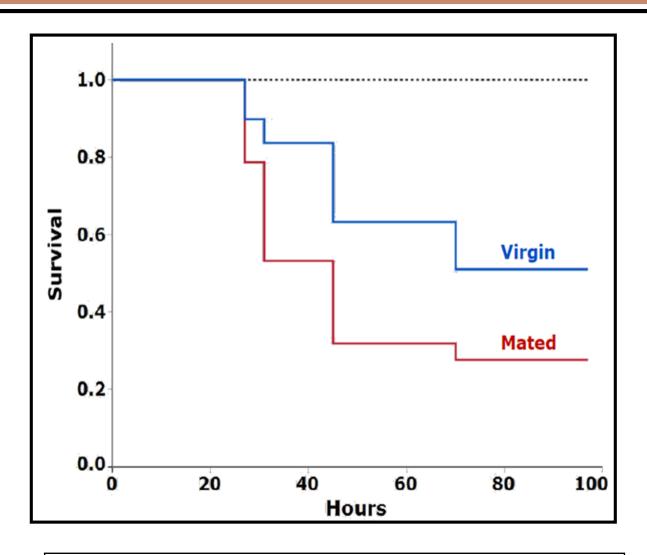
We used single-cell RNA sequencing on fat body cells to understand tissue heterogeneity.

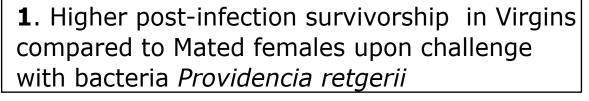


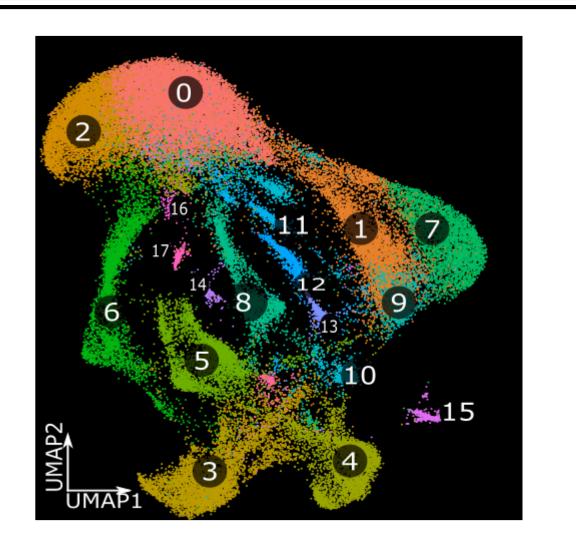
Conclusions

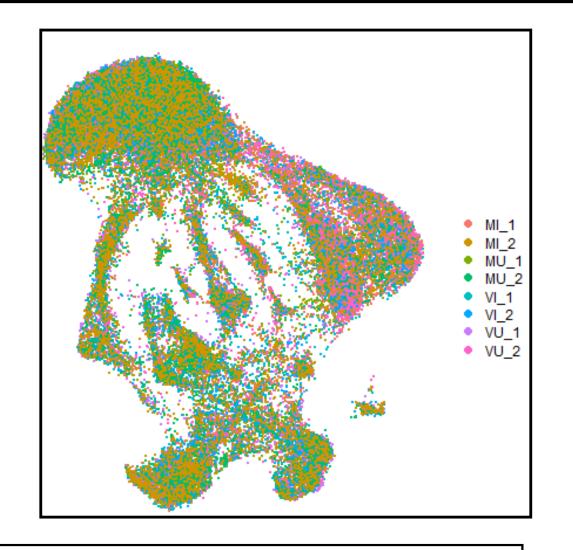
- (1) Drosophila fat body tissue consists of heterogeneous subpopulations
- (2)No new subpopulations arise under different physiological conditions
- (3)Gene expression changes upon infection are cluster-specific
- (4) Insulin signalling may have a role in lower immunity in mated females
- (5)Trade-offs may be mediated via higher expression of Yp1 and vitelline membrane proteins

Results









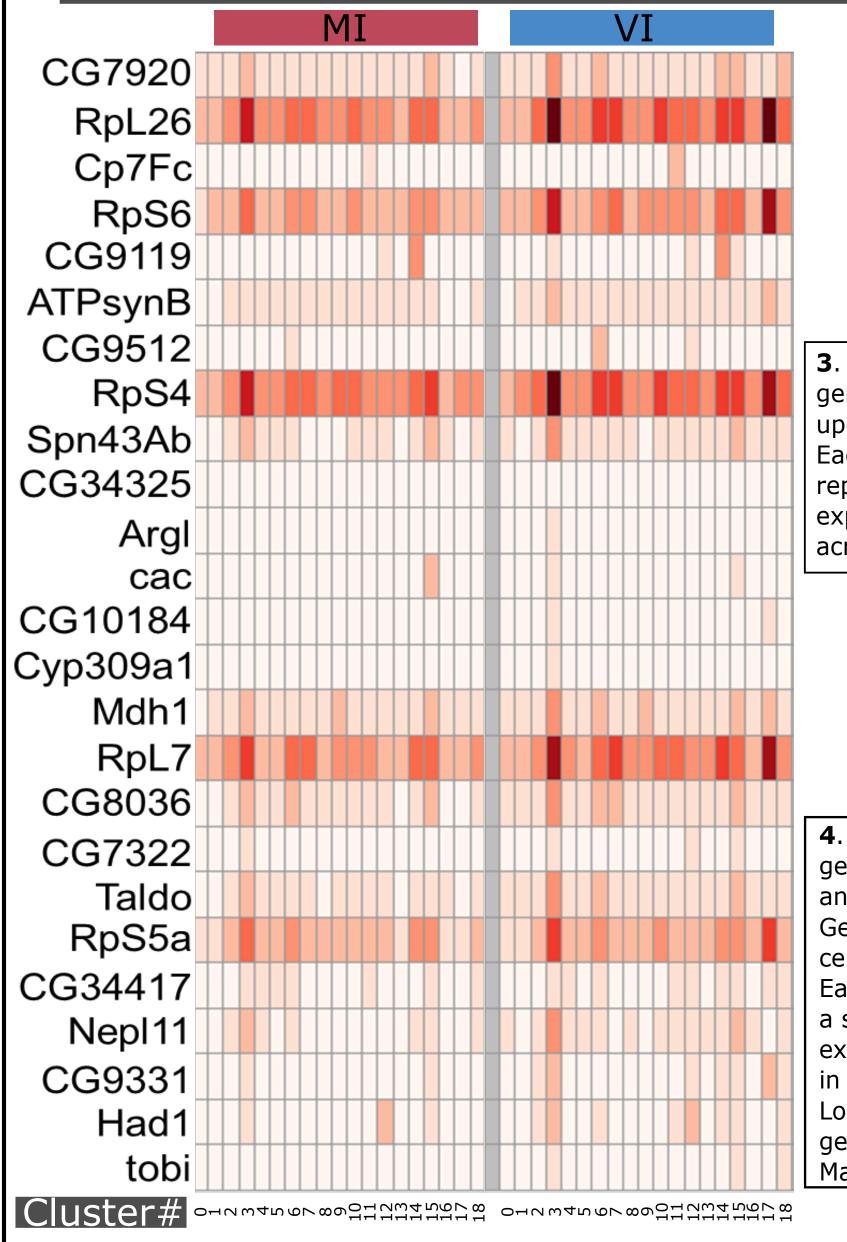
2a&2b. Heterogeneity in the fat body tissue of female *D.melanogaster*. Plots show 2-D projection of Single-cell data integrated over four different treatments: VU, VI, MU and MI. Each dot represents a single cell. Different numbers indicate distinct clusters present in the tissue. 2b shows cells colored by different treatments.

Differential response to Infection of Virgin & Mated

Gene Expression

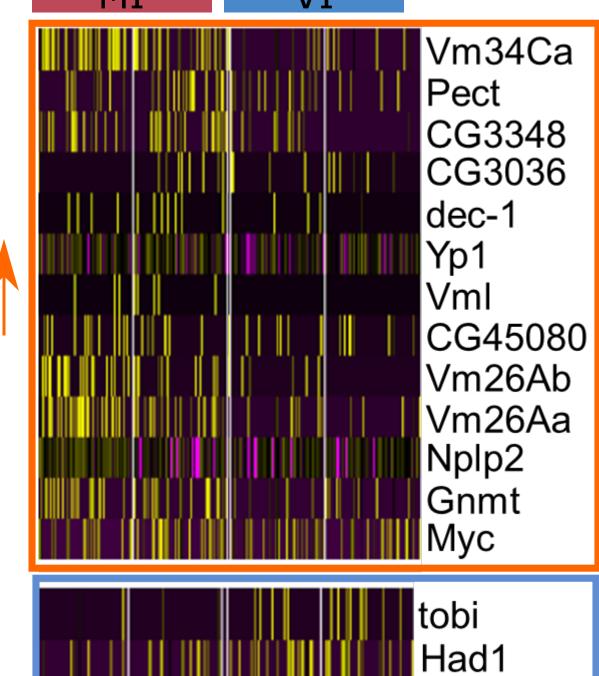
Upregulated

Downregulated

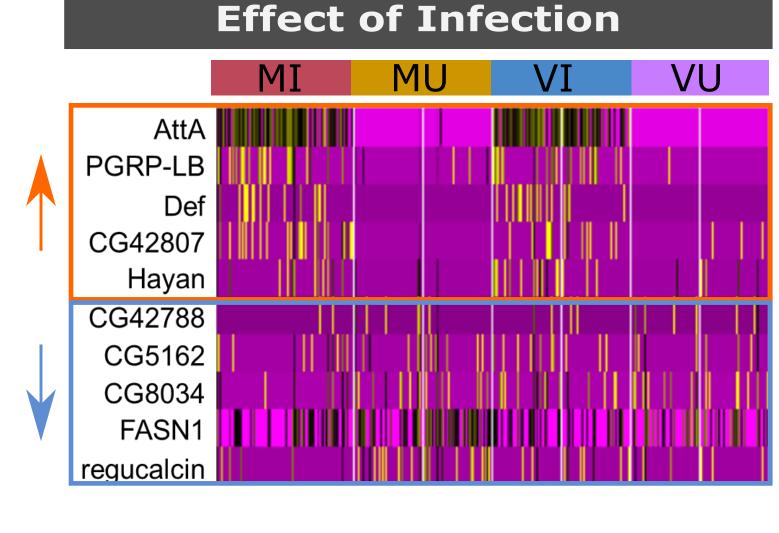


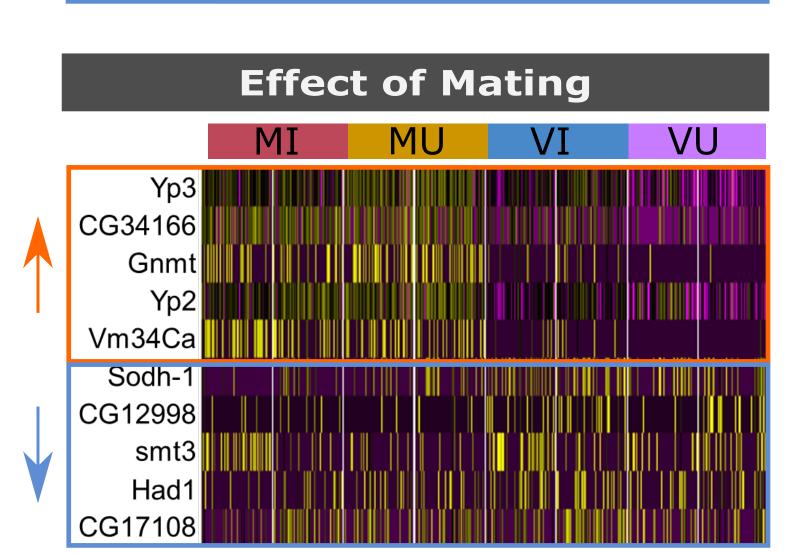
3. Cluster-specific expression of genes which are downregulated upon infection in mated females. Each column in the heatmap represents a distinct cluster. Gene expression plotted is averaged across cells within a cluster.

4. Differentially expressed genes between infected mated and virgin females. Gene expression for a single cell is plotted in the heatmap. Each line represents expression of a single cell. Upper panel shows expression of genes upregulated in Mated-Infected. Lower panel shows expression of genes downregulated in Mated-Infected.



RpL7 Cyp309a1 CG34325 CG9512 CG9119 Cp7Fc RpL26



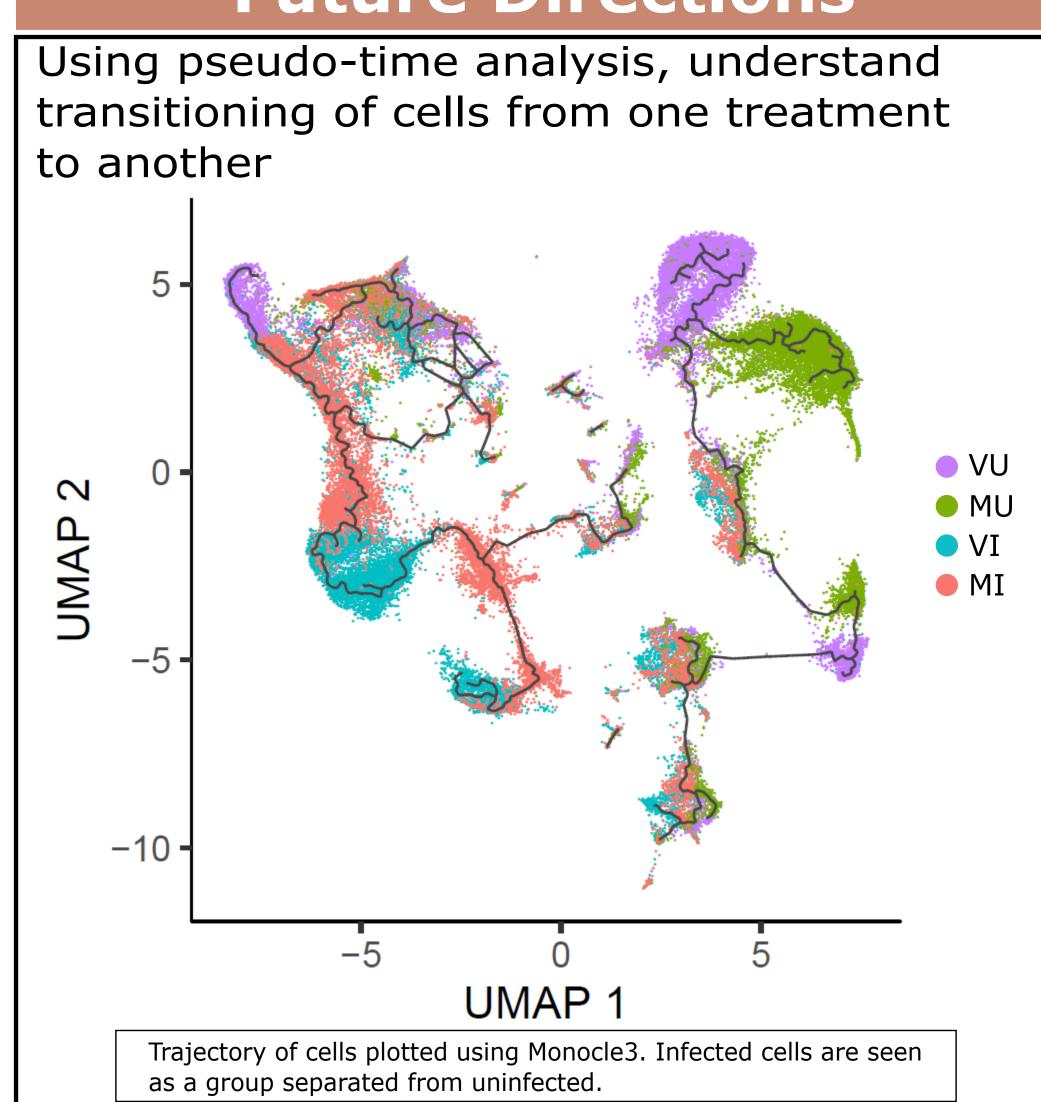


References

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Future Directions



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