

# Mining Transcriptomics Data

## Genes up-regulated in mosquito tissues during Wolbachia infection

### Learning objectives

- Review the types of expression searches in VEuPathDB
- Run a direct comparison search in a microarray dataset

### Introduction

*Wolbachia pipiensis* is a maternally inherited intracellular bacterium that is found in a wide range of arthropod species. It induces diverse reproductive abnormalities in its hosts. The virulent *Wolbachia* strain wMelPop has been introduced into the Dengue virus mosquito vector, *Aedes aegypti*, as a strategy to reduce disease transmission by shortening mosquito lifespan.

wMelPop grows to high densities particularly in the brain but also in the somatic tissues of its mosquito host. In this exercise, the goal is to find *Aedes aegypti* genes that are up-regulated in both head and muscle during infection with Wolbachia. Additionally, we want to determine possible functions shared by these genes.

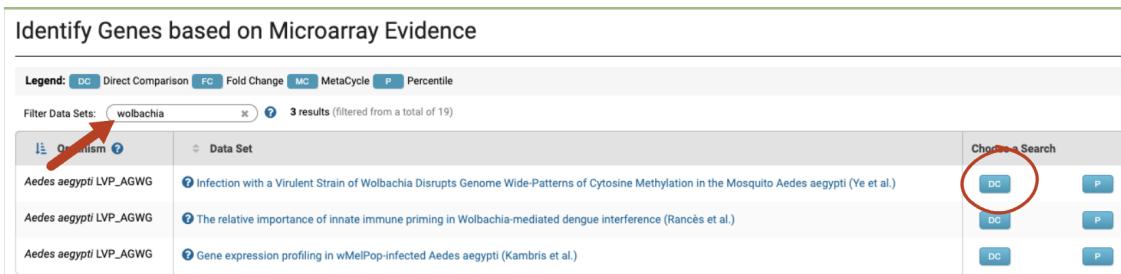
The VEuPathDB VectorBase has data and informatics resources for vectors of human pathogens, including *Aedes*, *Anopheles*, *Culex*, *Glossina*, *Ixodes*, etc. VectorBase has a microarray data set that compares Wolbachia infected and uninfected mosquito head and muscle.

1. Navigate to [VectorBase.org](https://www.vectorbase.org)<sup>1</sup>

2. From the sidebar or header, search for “microarray” and click on Microarray Evidence



3. Identify the appropriate dataset titled 'Infection with a Virulent Strain of Wolbachia Disrupts Genome Wide-Patterns of Cytosine Methylation in the Mosquito Aedes aegypti (Ye et al.)' For this experiment, choose the Direct Comparison search.



| Organism               | Data Set  | Choose a Search                      |
|------------------------|---|--------------------------------------|
| Aedes aegypti LVP_AGWG | ⑦ Infection with a Virulent Strain of Wolbachia Disrupts Genome Wide-Patterns of Cytosine Methylation in the Mosquito Aedes aegypti (Ye et al.) | <input checked="" type="button"/> DC |
| Aedes aegypti LVP_AGWG | ⑦ The relative importance of innate immune priming in Wolbachia-mediated dengue interference (Rancès et al.)                                    | <input type="button"/> DC            |
| Aedes aegypti LVP_AGWG | ⑦ Gene expression profiling in wMelPop-infected Aedes aegypti (Kambris et al.)  | <input type="button"/> DC            |

4. Configure the search to return genes that are up-regulated 2-fold in infected head vs. uninfected. **How many genes did you get?**



Identify Genes based on A. aegypti LVP\_AGWG Infection with a Virulent Strain of Wolbachia Disrupts Genome Wide-Patterns of Cytosine Methylation in the Mosquito Aedes aegypti Microarray (direct comparison)

Configure Search Learn More View Data Sets Used

Reset values to default

Experiment

Infection with a Virulent Strain of Wolbachia Disrupts Genome Wide-Patterns of Cytosine Methylation in the Mosquito Aedes aegypti

Direction

Up-regulated

Comparison

head infected v head uninfected

Fold difference >=

2.0

Protein Coding Only:

protein coding

Up-regulation in Wolbachia-infected Aedes \*

Wolbachia infection in head an... 695 Genes

Add a step

Step 1

Get Answer

<sup>1</sup> Note that this exercise uses VectorBase.org as an example database, but the same functionality is available on all VEuPathDB resources where this type of data is present.

5. Add a step to your search strategy to intersect with genes up-regulated in muscle
- Intersect your search result with another search that returns genes up-regulated 2 fold in infected muscle vs. uninfected. Your combined result will be genes that are up-regulated in both head and muscle in response to Wolbachia infection.
  - How many genes did you get that are upregulated in both head and muscle in response to Wolbachia infection?

Up-regulation in Wolbachia-infected Aedes \*

Step 1: Wolbachia infection in head an... 695 Genes

Step 2: Wolbachia infection in head an... 827 Genes

Wolbachia infection in head an... 394 Genes

**Add a step**

Up-regulation in Wolbachia-infected Aedes \*

Step 1: Wolbachia infection in head an... 695 Genes

Step 2: Wolbachia infection in head an... 827 Genes

Wolbachia infection in head an... 394 Genes

**Add a step**

Add a step to your search strategy

Choose how to combine with other Genes: 1 INTERSECT 2

Choose which Genes to combine. From...: A new search

Transform into related records

Use Genomic Colocation to combine with other features

Direct Comparison Percentile

Configure Search Learn More View Data Sets Used

Reset values to default

Experiment: Infection with a Virulent Strain of Wolbachia Disrupts Genome-Wide Patterns of Cytosine Methylation in the Mosquito Aedes aegypti

Direction: Up-regulated

Comparison: head infected v head uninfected, muscle infected v muscle uninfected

Fold difference >= 2.0

Protein Coding Only: protein coding

Run Step

6. Explore the molecular functions of the up-regulated genes. Determine enriched Molecular Function Gene Ontology (GO) terms for the upregulated genes. Make sure you are viewing the combined result (the Step 2 result will be highlighted in yellow) and click Analyze Result to open the Enrichment Tool.

What gene functions are shared by the combined result? What biological role can you envision for these mosquito genes during the *Wolbachia* infection?

Up-regulation in *Wolbachia*-infected *Aedes* \*

Wolbachia infection in head an... 827 Genes

Wolbachia infection in head an... 695 Genes Step 1

394 Genes Step 2

+ Add a step

394 Genes (355 ortholog groups)

Organism Filter select all | clear all | expand all | collapse all Hide zero counts Reference only

Search organisms... Arthropoda 394 Mollusca 0

Gene Results Genome View New Analysis X

Analyze your Gene results with a tool below.

Gene Ontology Enrichment Metabolic Pathway Enrichment Word Enrichment

Gene Ontology Enrichment

Find Gene Ontology terms that are enriched in your gene result. [Read More](#)

Parameters

Organism: *Aedes aegypti: LVP\_AWWS* Ontology: Molecular Function Evidence: Computed, Curated Limit to GO Slim terms: No P-Value cutoff: 0.05

Analysis Results:

| GO ID      | GO Term                            | Genes in the bkgd with this term | Genes in your result with this term | Percent of bkgd genes in your result | Fold enrichment | Odds ratio | P-value  | Benjamini | Bonferroni |
|------------|------------------------------------|----------------------------------|-------------------------------------|--------------------------------------|-----------------|------------|----------|-----------|------------|
| GO:0003824 | catalytic activity                 | 3624                             | 162                                 | 4.5                                  | 1.62            | 2.38       | 9.32e-14 | 1.57e-11  | 3.32e-11   |
| GO:0008233 | peptidase activity                 | 647                              | 54                                  | 8.3                                  | 3.03            | 3.69       | 1.38e-13 | 1.57e-11  | 4.93e-11   |
| GO:0016787 | hydrolase activity                 | 1527                             | 91                                  | 6.0                                  | 2.16            | 2.76       | 1.47e-13 | 1.57e-11  | 5.24e-11   |
| GO:0004175 | endopeptidase activity             | 473                              | 45                                  | 9.5                                  | 3.45            | 4.17       | 2.08e-13 | 1.57e-11  | 7.42e-11   |
| GO:0004252 | serine-type endopeptidase activity | 346                              | 38                                  | 11.0                                 | 3.98            | 4.83       | 2.21e-13 | 1.57e-11  | 7.87e-11   |
| GO:0008236 | serine-type peptidase              | 372                              | 39                                  | 10.5                                 | 3.80            | 4.59       | 4.66e-13 | 2.37e-11  | 1.66e-10   |