



The search question

Wolbachia pipientis 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.

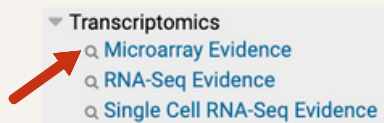


What platform is best suited for this question?



This knowledgebase has data and informatics resources for vectors of human pathogens, including *Aedes*, *Anopheles*, *Culex*, *Glossina*, *Ixodes*, etc.

What search is best suited for this question?



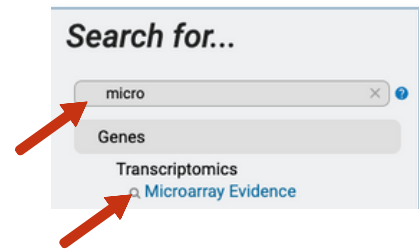
VectorBase has a **microarray** data set that compared *Wolbachia* infected and uninfected mosquito head and muscle. The **Direct Comparison** search for this dataset returns genes whose expression varies between samples in pairwise comparisons.

What is a possible search strategy that will answer this question?

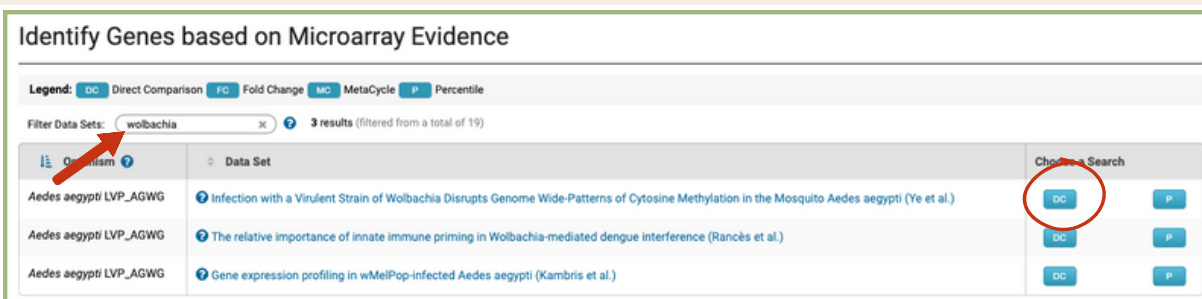
Use the Microarray Evidence data and the Direct Comparison search in two steps- (1) identify genes that are up-regulated in **infected vs. uninfected head** samples, (2) intersect with another search that returns genes up-regulated in **infected vs uninfected muscle** samples.

1. Navigate to the appropriate search

- Navigate to VectorBase.org
- From the sidebar or header, search for "microarray" and click on **Microarray Evidence**

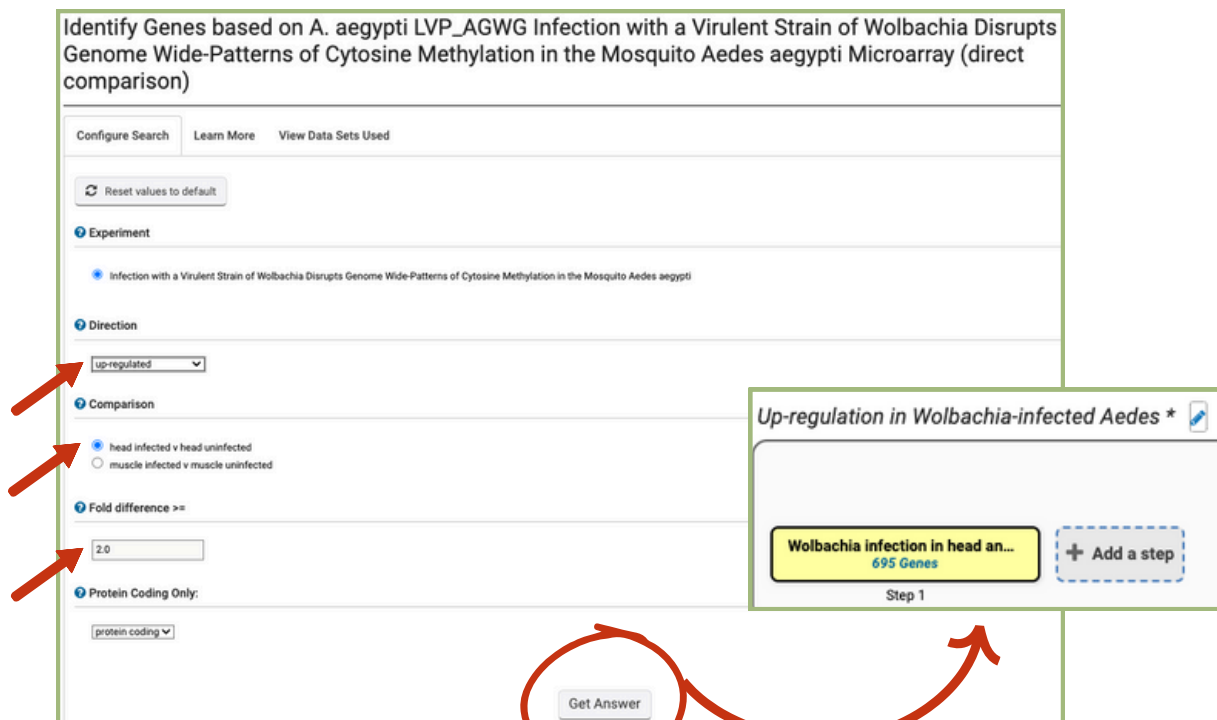


2. Choose appropriate experiments & parameters within the search



- Choose the **Direct Comparison** search for the dataset titled 'Infection with a Virulent Strain of Wolbachia Disrupts Genome Wide-Patterns of Cytosine Methylation in the Mosquito *Aedes aegypti* (Ye et al.)'
- Configure the search to returns genes that are up-regulated 2 fold in infected head vs. uninfected.

How many genes did you get?



3. Add a step to your search strategy to intersect with genes up-regulated in muscle

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

Wolbachia infection in head an...
695 Genes

Step 1

+ Add a step

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.

Add a step to your search strategy

Combine with other Genes

1 Choose how to combine with other Genes

1 INTERSECT 2

2 Choose which Genes to combine. From...

A new search

microd

Transcriptomics

Microarray Evidence

How many genes did you get that are upregulated in both head and muscle in response to *Wolbachia* infection?

Add a step to your search strategy

Direct Comparison

Configure Search

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

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

Wolbachia infection in head an...
695 Genes

Step 1

Wolbachia infection in head an...
827 Genes

Step 2

394 Genes

4. 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 yellow) and click Analyze Result to open the Enrichment Tool.

Up-regulation in Wolbachia-infected Aedes *

Wolbachia infection in head an... 827 Genes

Wolbachia infection in head an... 695 Genes

Step 1

Step 2

394 Genes (355 ortholog groups)

Gene Results Genome View New Analysis

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_AGWG

Ontology: Molecular Function

Evidence: Computed, Curated

Limit to GO Slim terms: No

P-Value cutoff: 0.05 (0 - 1)

Submit

Analysis Results:

77 rows

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

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

