

Case studies: Combining orthology and expression data

Diving into the *Drosophila* immune response

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Drosophila orthology

- Get orthology data for 36 species of *Drosophila* + 4 mosquitoes (outgroup)

Drosophila orthology

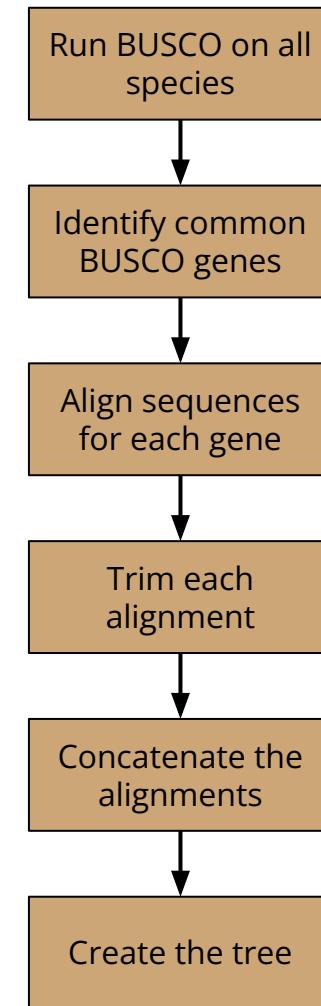
- Get orthology data for 36 species of *Drosophila* + 4 mosquitoes (outgroup)
- Apply the OMA methodology
- Requires phylogenetic tree to guide the determination of orthology relationships
⇒ How do we get this tree?

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BUSCOphile

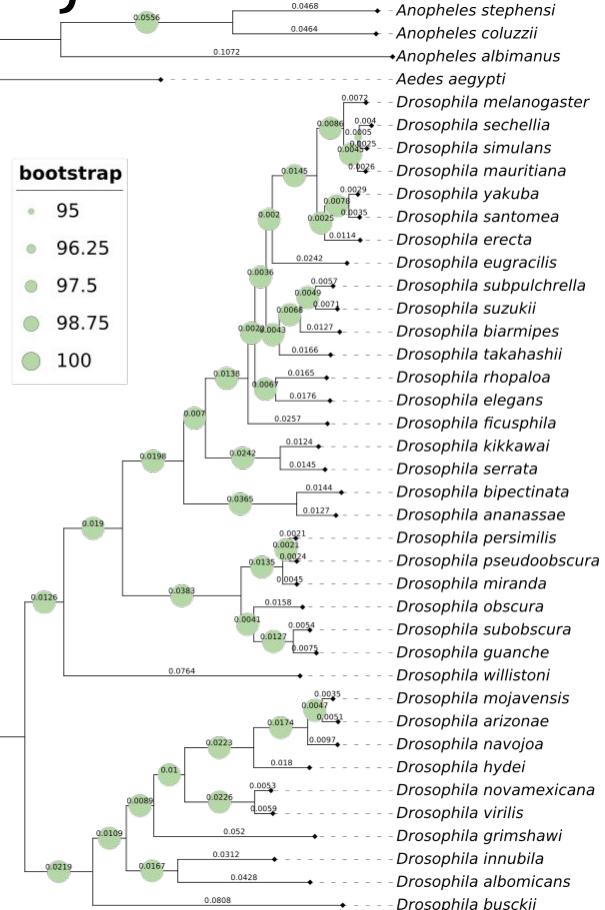
- Snakemake workflow relying on BUSCO
- 2892 common genes
- Sequence alignment: MUSCLE
- Alignment trimming: trimAI
- Tree creation: IQ-TREE



Drosophila phylogeny

Tree scale: 0.1 ← 0.2743 →

- Almost half of them at **chromosome level**
- All have **good genome completeness**
 - BUSCO scores: > 90% complete, < 5% fragmented, < 5% missing
- All (except *D. melanogaster*) are annotated by the NCBI eukaryotic annotation pipeline
 - Datasets are coherent and standardised



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DrosOMA



SIB Dros^{oma}

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Dros^{oma} orthologous matrix
browser

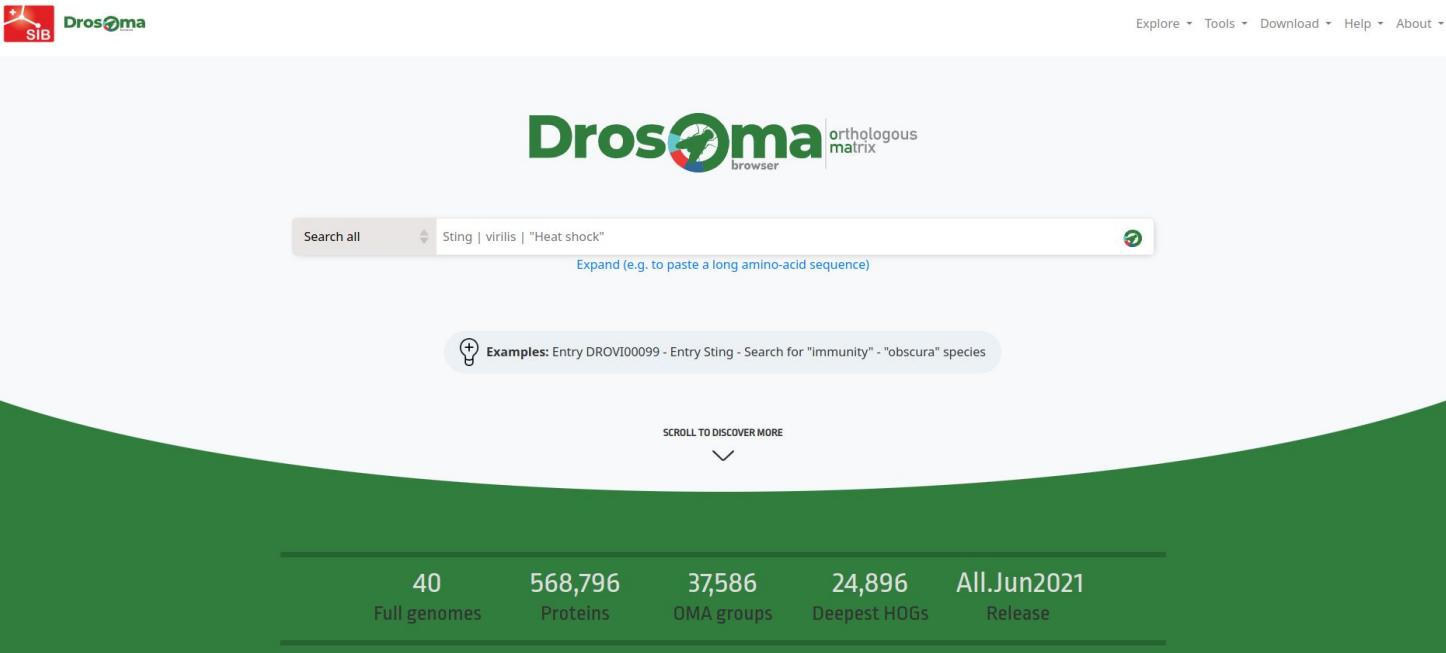
Search all ▾ Sting | virilis | "Heat shock"

Expand (e.g. to paste a long amino-acid sequence)

Examples: Entry DROVI00099 - Entry Sting - Search for "immunity" - "obscura" species

SCROLL TO DISCOVER MORE

40 Full genomes 568,796 Proteins 37,586 OMA groups 24,896 Deepest HOGs All.Jun2021 Release



<https://drosoma.dcsr.unil.ch/>

Thiébaut A, Altenhoff AM, Campli G et al. DrosOMA: the Drosophila Orthologous Matrix browser. F1000Research 2023, 12:936

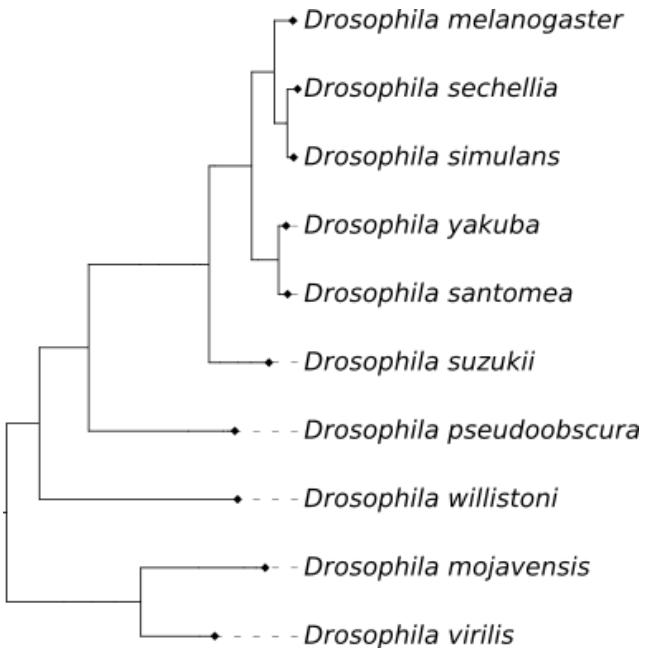
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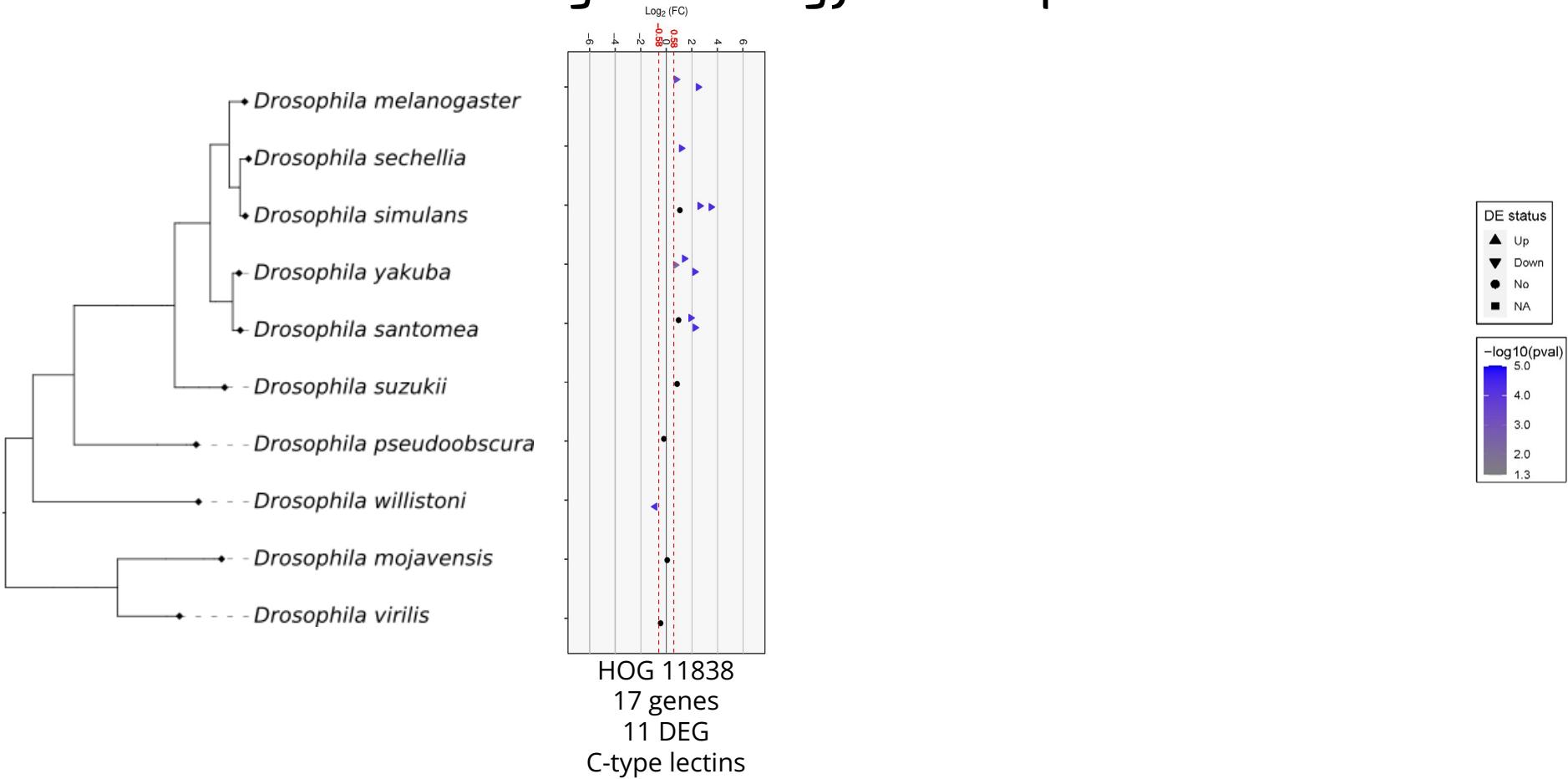
Expression data of *Drosophila* immune response

- RNA-seq experiments done by Jean-Luc Imler's team @IBMC, Strasbourg
- 10 *Drosophila* species:
 - *D. melanogaster*
 - *D. mojavensis*
 - *D. pseudoobscura*
 - *D. santomea*
 - *D. sechellia*
 - *D. simulans*
 - *D. suzukii*
 - *D. virilis*
 - *D. willistoni*
 - *D. yakuba*
- Injection of 2,3-cGAMP vs Tris
 - 2,3-cGAMP = compound mimicking viral infection
- Sequencing, trimming, mapping... ⇒ Differential expression analyses
 - <https://gitlab.com/aathbt/rnaseq-analysis-workflow>

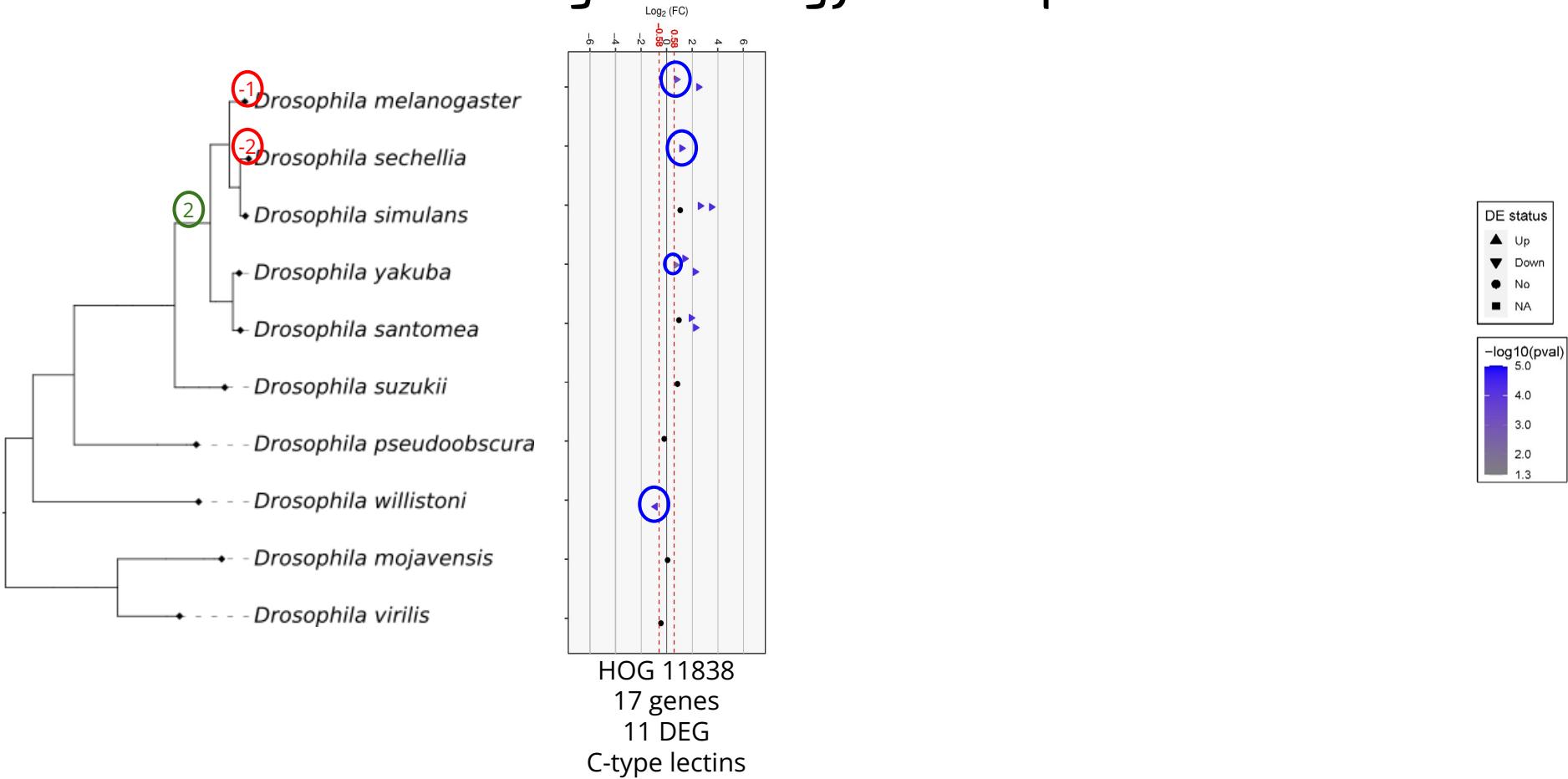
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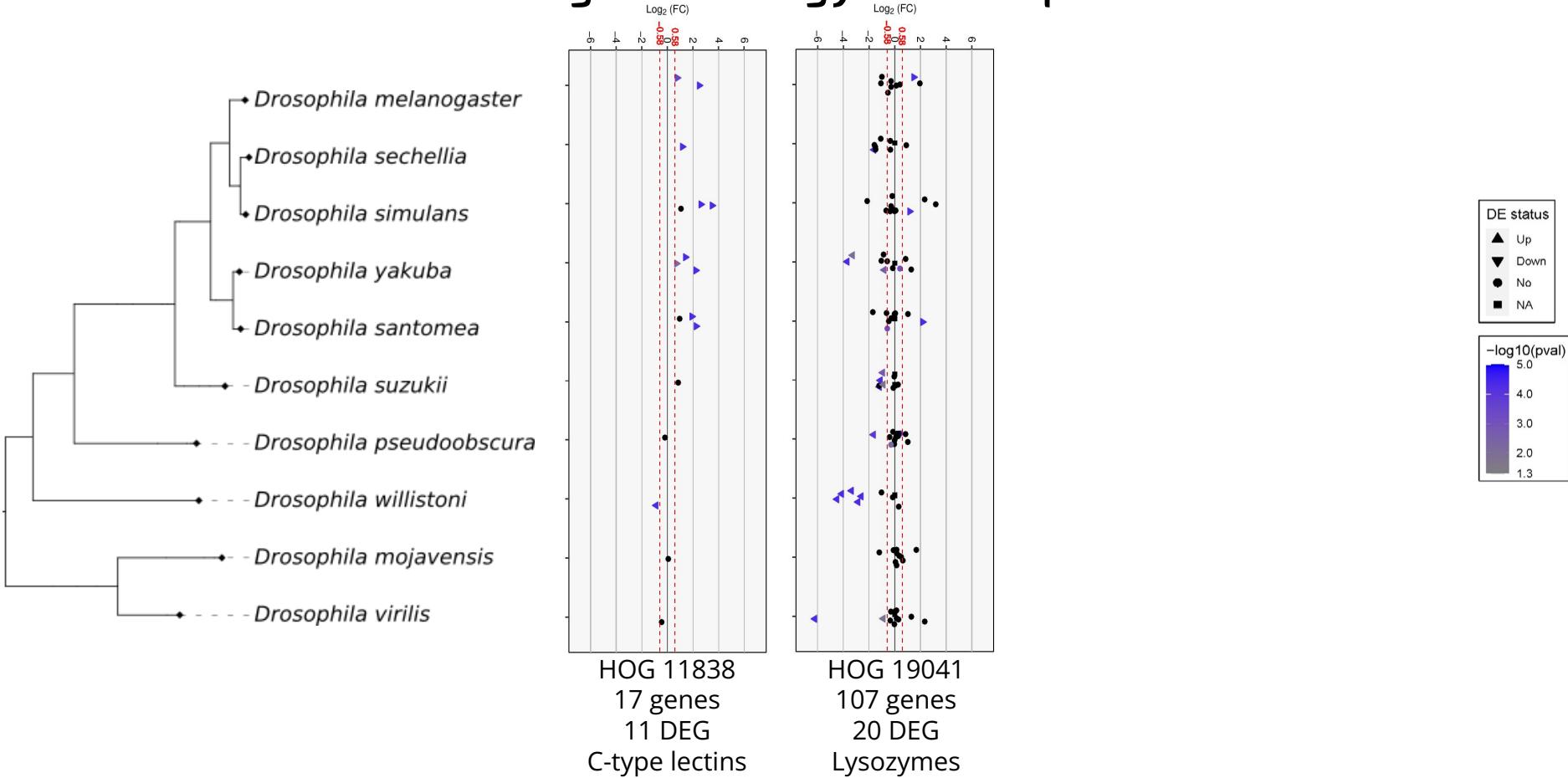
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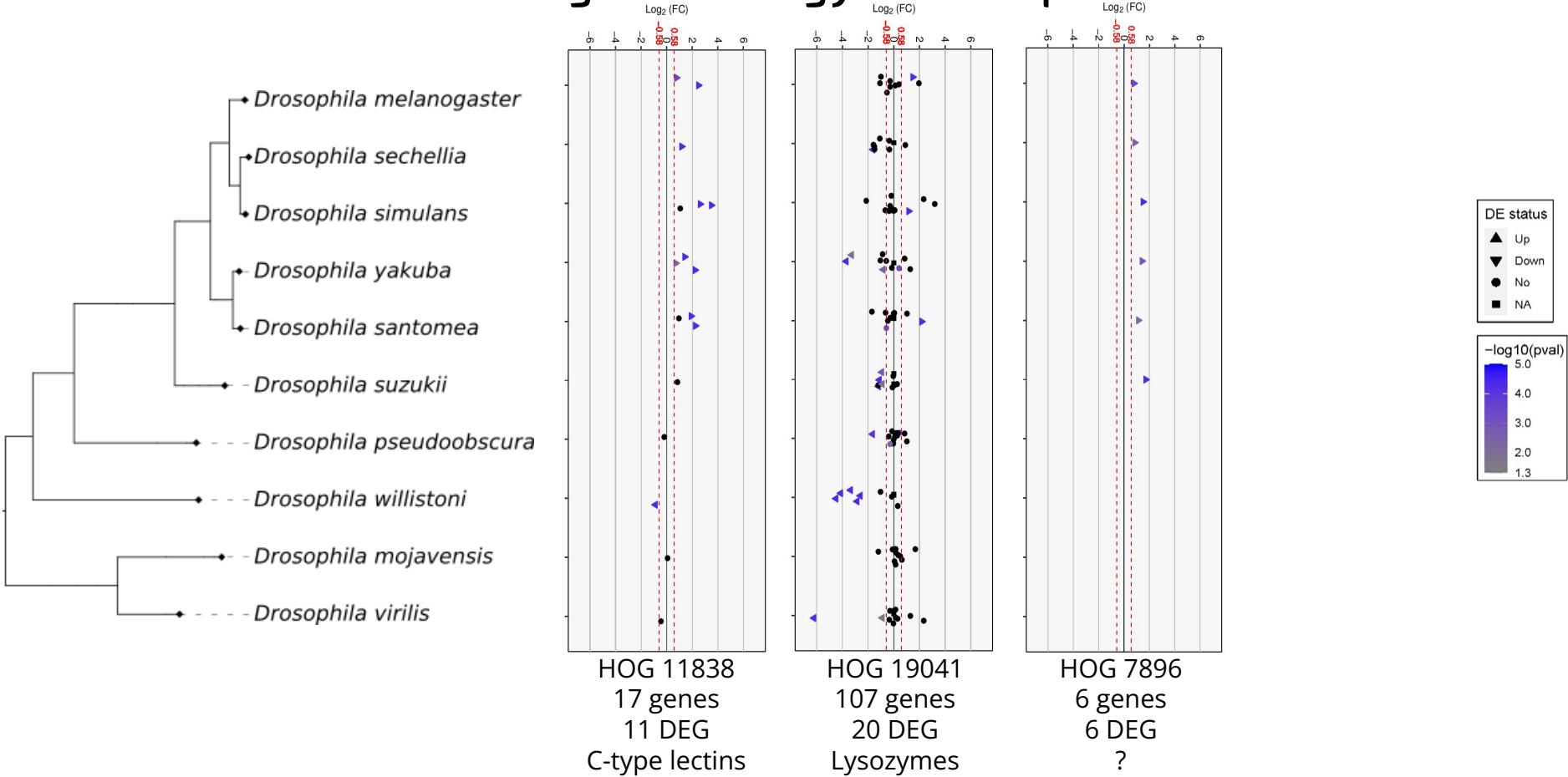
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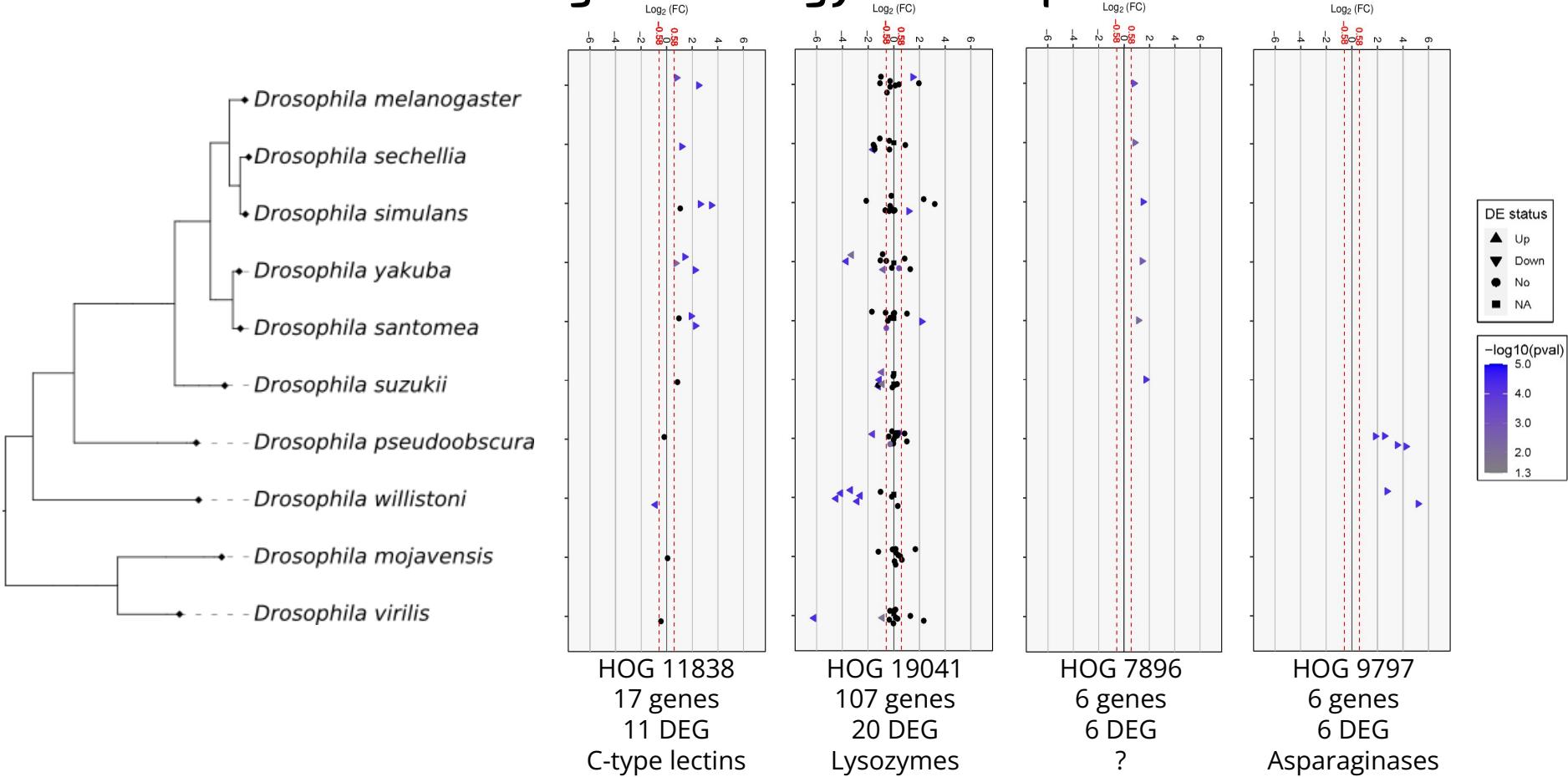
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Questions?