

Summary

Glyphosate is the most widely used herbicide in the world and accounts for 37% of global pesticide use (Gaba et al. 2016). Glyphosate forms a stable complex with 5-enolpyruvylshikimate-3-phosphate synthase (EPSPS), which directly inhibits the shikimate pathway (Sammons and Gaines 2014). As a PhD candidate I work with glyphosate resistance, off-targets and mechanisms of transport using yeast as a model organism. Therefore, I chose a dataset from the canadian horseweed, an organism frequently exposed to glyphosate, to explore which cellular processes are upregulated or downregulated upon glyphosate treatment (Yang et al. 2021).

Methods are explained in the README file.

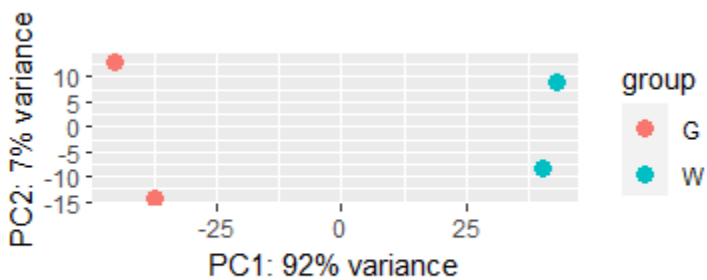


Figure 1: Principal Component Analysis (PCA) plot

This PCA plot (Fig1) shows that the glyphosate-treated group (G) and the water-treated group (W) have distinct expression profiles.

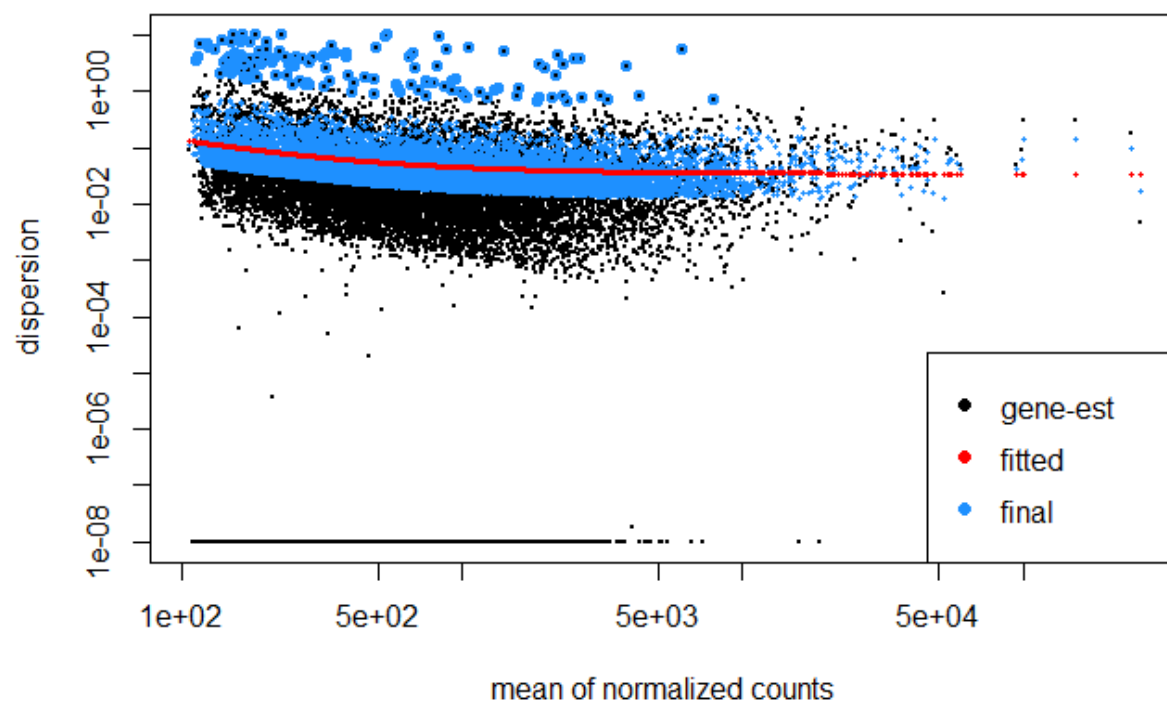


Figure 2: Dispersion Estimates

This step (Figure 2) is essential to determine if the dataset is a good fit for a DESEQ2 analysis. The red line falls below 1, which is a good sign, and the variance is overall concentrated around the trendline. This indicates that this dataset indeed is a good fit for DESEQ2.

Volcano plot

Enhanced Volcano

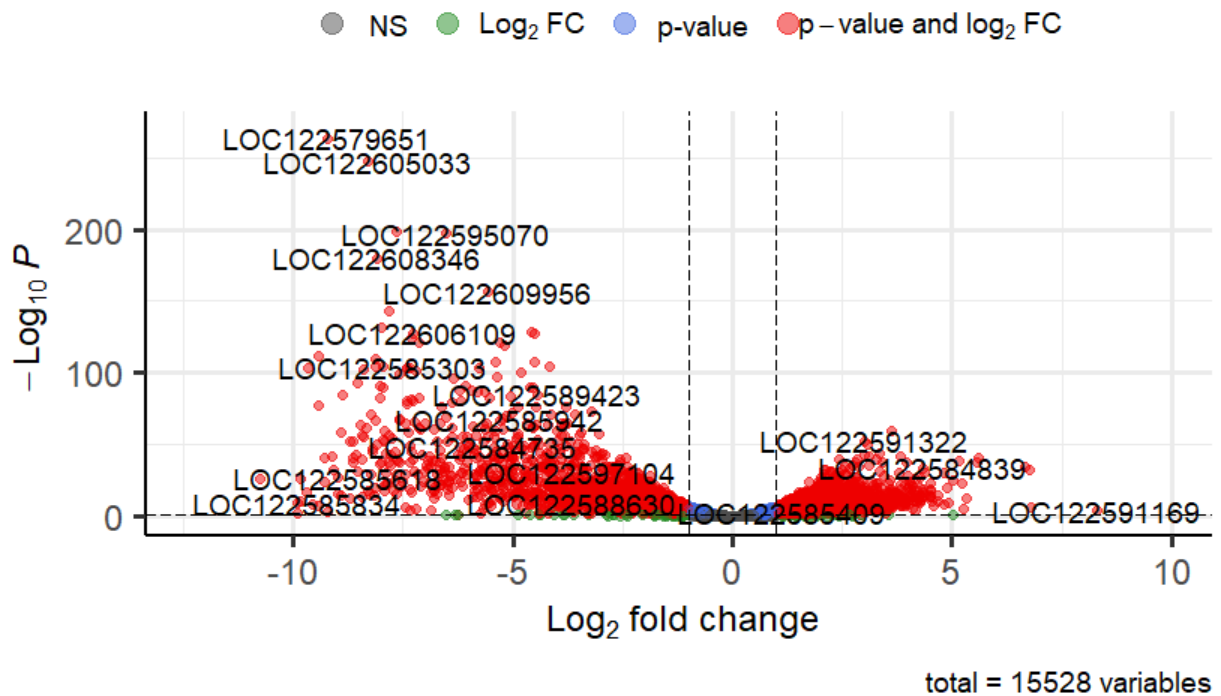


Figure 3: Volcano plot of fold change (log2) in gene expression following glyphosate treatment.

A quick look in the most upregulated genes (LOC122591169, LOC122591168, LOC122592964, LOC122582803, LOC122593962, LOC122595647, LOC122591170, LOC122601546, LOC122585140) shows that the majority consists of chlorophyll a-b binding proteins. This could be a result of a regulation mechanism attempting to bypass the growth inhibition effects of glyphosate by upregulating photosynthetic genes. The set of the most highly upregulated genes includes lipid binding proteins and a short-chain hydrogenase, functions associated with cellular metabolism. The most downregulated genes are uncharacterized, but a blast search offers a quick annotation and indicates that some are related to urticatoxin biosynthesis. Even though these toxins are defense mechanisms for plants, upon growth inhibition stress, it might be tremendously costly for a plant to synthesize these large molecules. Therefore, downregulation of these pathways could be an economical way to preserve resources.

References

- Gaba, Sabrina, Edith Gabriel, Joël Chadœuf, Florent Bonneu, and Vincent Bretagnolle. 2016. "Herbicides Do Not Ensure for Higher Wheat Yield, but Eliminate Rare Plant Species." *Scientific Reports* 6 (July): 30112. <https://doi.org/10.1038/srep30112>.
- Sammons, Robert Douglas, and Todd A. Gaines. 2014. "Glyphosate Resistance: State of Knowledge." *Pest Management Science* 70 (9): 1367. <https://doi.org/10.1002/PS.3743>.
- Yang, Yongil, Cory Gardner, Pallavi Gupta, Yanhui Peng, Cristiano Piasecki, Reginald J. Millwood, Tae-Hyuk Ahn, and C. Neal Stewart. 2021. "Novel Candidate Genes

Differentially Expressed in Glyphosate-Treated Horseweed (*Conyza Canadensis*).”
Genes 12 (10): 1616. <https://doi.org/10.3390/genes12101616>.