

Effects of Chalcone 17, 25 and 30 on global gene expression in *Caenorhabditis elegans* using RNAseq Analysis

Eema Quadri, Guadalupe Robledo, Keyora Wharry, Quynh Nguyen
Ramakrishna Kandi, and Alejandro Calderón-Urrea

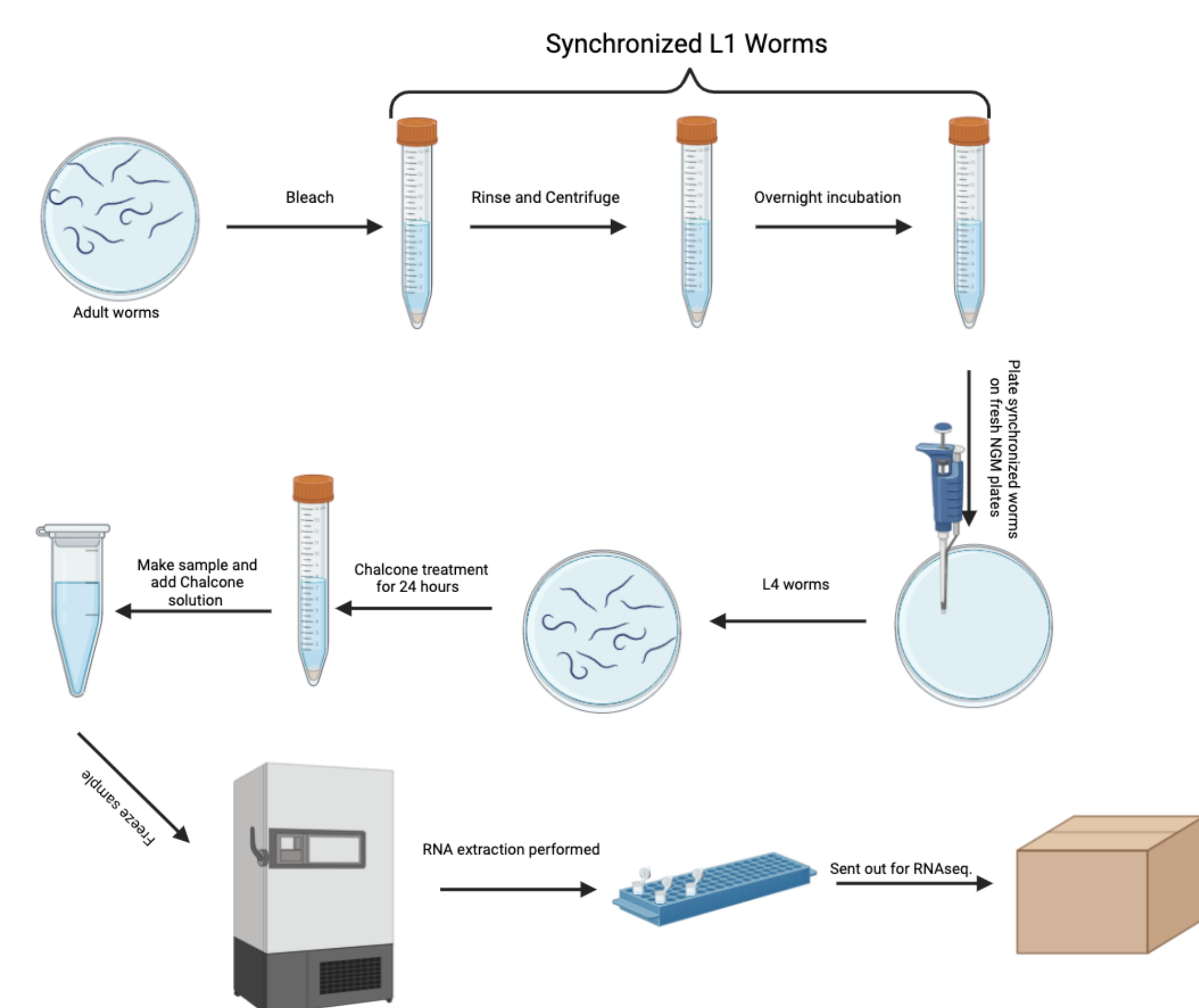
Department of Biology
California State University, Fresno



Introduction

Plant Parasitic Nematodes (PPNs) are major agricultural pests that cause significant economic damage each year. Traditional control methods, including soil management and chemical treatments, have limitations for example some are ineffective while others harm the environment. **Chalcones** have appeared to be a promising alternative, showing high effectiveness against PPNS at low concentrations without environmental harm. Despite their potential, the exact mechanism of action (MOA) chalcones kill nematodes remains unknown. To address this, our research investigates how Chalcone **17**, **25**, and **30** affect global gene expression in *Caenorhabditis elegans*; our hypothesis is that we should be able to identify pathways that might be over-expressed or under-expressed due to chalcone exposure and therefore point to a possible MOA. During our study, we identified the “Longevity Regulating Pathway” as well as the “Defense Response” and “Immune Response” pathways as the pathways with upregulated genes after exposure to chalcones. The long-term goal of Dr. Calderón-Urrea’s lab is to explore the common gene products targeted by chalcones to better understand their MOA and advance the development of new and effective nematicides.

Research Method



Results

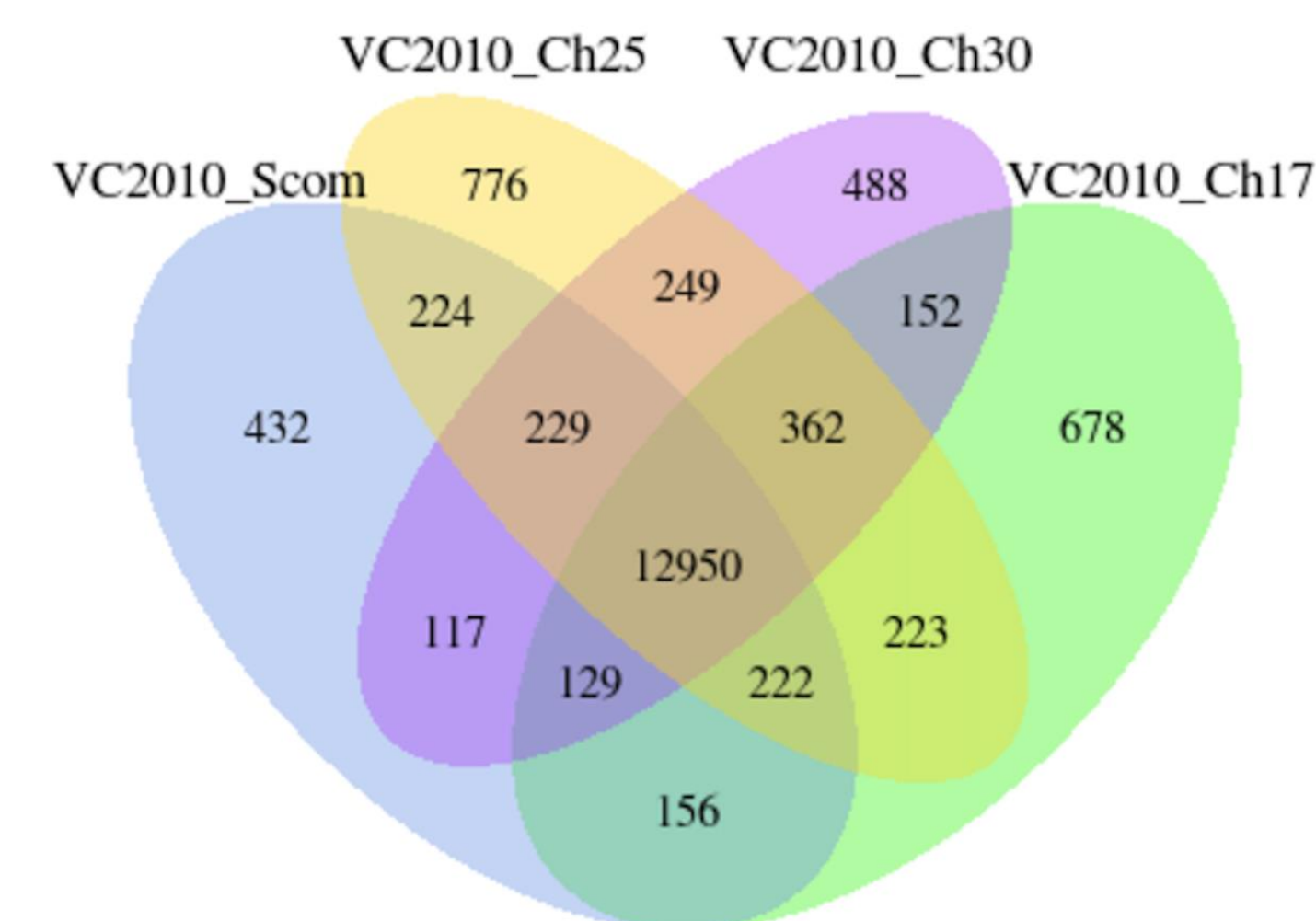


Figure 1: The co-expression Venn diagram shows the number of genes uniquely expressed in each group or sample. The overlapping areas represent the number of genes that are co-expressed in two or more groups.

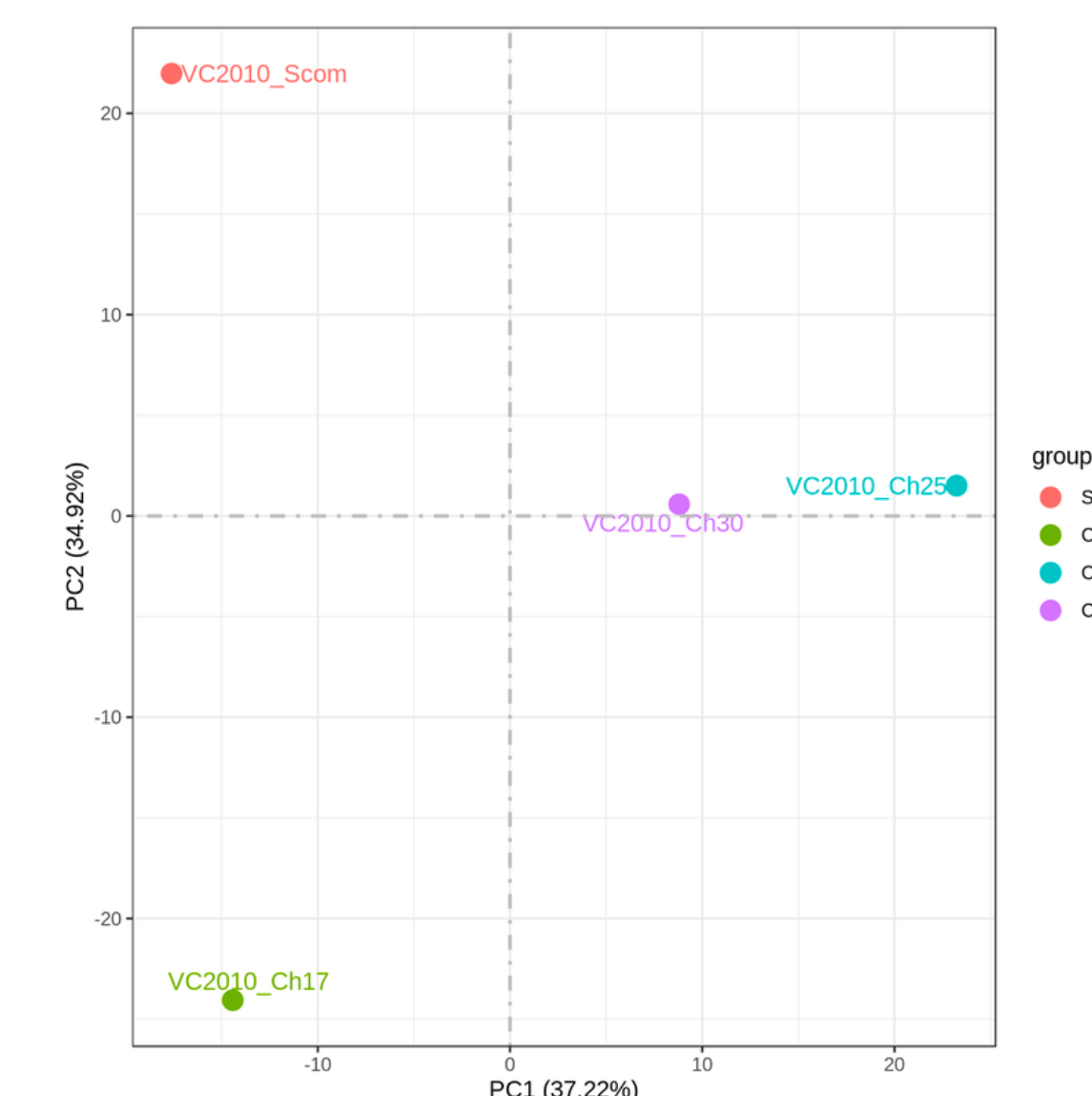


Figure 2: PCA of gene expression (FPKM) showing how samples from different groups spread out. Each group is a combination of three biological replicates.

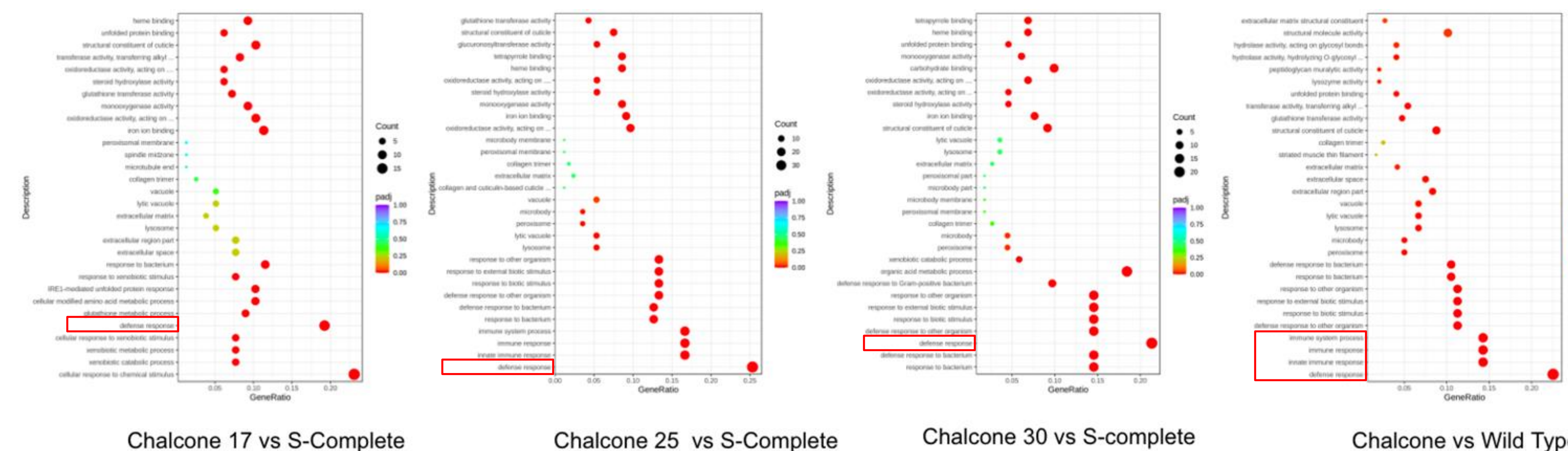


Figure 3: GO Enrichment Analysis Scatter Plot. The x-axis shows the ratio of differential genes linked to each GO term versus the total number of differential genes. The y-axis lists the GO terms. Point size indicates the number of genes associated with each GO term, and color gradient from red to purple represents the significance level of enrichment.

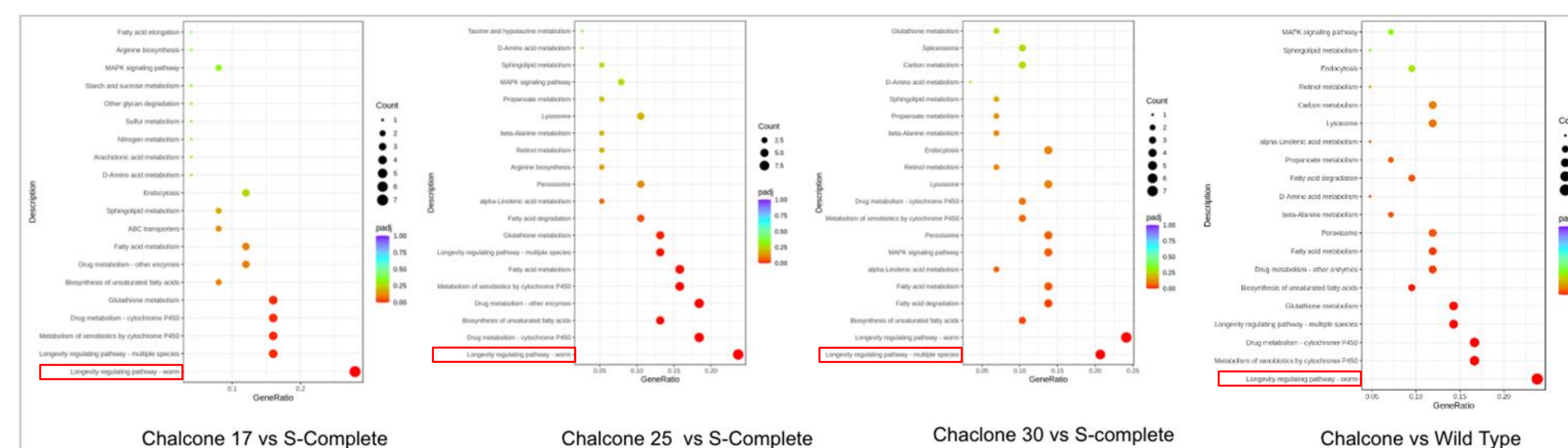


Figure 4: Kyoto Encyclopedia of Genes and Genomes (KEGG) Enrichment Analysis. Gene Ratio is the ratio of differentially expressed genes to the total genes involved in the pathway terms. Padj is the transformed p-value after adjustment for different concentrations and read counts between each sample.

Conclusions

By investigating the effects of Chalcone **17** and **30** on global gene expression in *Caenorhabditis elegans*, we identified the gene Clec-9 as a potentially crucial player in the nematicidal process. The analysis indicates notable up-regulation and down-regulation of genes across the samples. The results show differences in gene expression among the samples, as seen in the Principal Component Analysis (PCA) plot, which separates the groups clearly. The Venn diagram shows which genes are unique to each group and which are shared. The GO and KEGG analysis highlight important biological processes and pathways affected by changes in gene expression. During our study, we identified the “Longevity Regulating Pathway” as well as the “Defense Response” pathway and the two pathways with upregulated genes after exposure to chalcones. These changes suggest these biological functions heavily involved in response to chalcone exposure. Understanding these changes can help us learn more about the biological responses being studied and could be useful for future research or treatments.

Literature cited

Wang Z, Gerstein M, Snyder M. RNA-Seq: a revolutionary tool for transcriptomics[J]. Nature Reviews Genetics, 2009, 10(1): 57-63.
Mihaela Pertea, Geo M Pertea, Corina M Antonescu 1, et al. String Tie enables improved reconstruction of a transcriptome from RNA-seq reads[J]. Nat Biotechnol. 2015 March; 33(3):290-295(String Tie)
Robinson M D, McCarthy D J, Smyth GK. edgeR: a Bioconductor package for differential expression analysis of digital gene expression data[J]. Bioinformatics, 2010, 26(1): 139-140.(edgeR)

Acknowledgments

This work was supported by an NIH grant to ACU (1R16GM145429). EM and GR were supported by a Summer Research Experience of the Finish in Five Grant at Fresno State funded by the USDE (P031M210039) and to all the members of The ACU laboratory at Fresno State.