



Comparative Transcriptomic Analysis of Drought-Responsive Genes in Maize (*Zea mays*) and Sorghum (*Sorghum bicolor*)

Nisa Fitriani Nur Azizah¹

¹ Study Program of Biology, Faculty of Military Mathematics and Natural Sciences, The Republic of Indonesia Defense University. Kompleks Indonesia Peace and Security Center (IPSC) Sentul, Bogor 116810, Indonesia.

* Correspondence: nisafitriani412@gmail.com

Abstract

Drought is one of the most severe abiotic stresses limiting cereal crop productivity worldwide and is expected to intensify under ongoing climate change conditions. Maize (*Zea mays*) is highly susceptible to drought stress, whereas sorghum (*Sorghum bicolor*) exhibits superior drought tolerance mechanisms. Therefore, this study aimed to perform a comparative transcriptomic analysis of maize and sorghum under drought stress conditions using an RNA-seq workflow implemented on the Galaxy platform. Differential expression analysis revealed substantial transcriptomic changes in both species under drought stress conditions. In maize, drought stress predominantly induced genes associated with oxidative stress responses, abscisic acid (ABA) signaling, lipid metabolism, and stress-responsive signaling pathways, including MAPK signaling and plant hormone signal transduction. In contrast, sorghum showed enrichment in pathways related to translation, ribosome organization, photosynthesis, carbon metabolism, glycolysis/gluconeogenesis, and amino acid biosynthesis, indicating the maintenance of fundamental metabolic and photosynthetic activities during drought stress. Overall, the results suggest that sorghum possesses a more coordinated and efficient drought tolerance mechanism compared with maize. This study provides valuable insights into the molecular mechanisms underlying drought tolerance in cereal crops and highlights potential targets for the development of drought-resilient cultivars.

Keywords: comparative transcriptome, drought-stress, *Sorghum bicolor*, *Zea mays*

1. Introduction

Drought is widely recognized as one of the most severe abiotic stresses limiting agricultural productivity worldwide (Fracasso et al., 2016). Among environmental stress factors, drought has a particularly detrimental effect on cereal crops, resulting in an average global yield reduction of approximately 10.1% (Lesk et al., 2016). Moreover, ongoing climate change is projected to increase global temperatures, thereby intensifying water scarcity and further threatening the productivity and sustainability of major staple crops (Waititu et al., 2021). Given the increasing frequency and severity of drought events, a comprehensive understanding of the molecular and physiological mechanisms underlying drought tolerance in cereal crops is essential for the development of climate-resilient agricultural systems and the maintenance of global food security.

Maize (*Zea mays*) and sorghum (*Sorghum bicolor*) are among the world's most important C4 cereal crops (Fontanet-Manzanegue et al., 2025). However, maize is highly susceptible to drought stress throughout its growth cycle, particularly during the reproductive stage, where water deficit conditions can severely reduce yield potential (Liu et al., 2021). Drought stress negatively affects plant physiological processes by reducing transpiration rates and inducing stomatal closure, which consequently decreases photosynthetic efficiency and inhibits plant growth (Zhang et al., 2018). In contrast, sorghum is widely cultivated in semi-arid and arid regions of Africa, South Asia, and the Americas due to its superior drought

tolerance mechanisms (Venkateswaran et al., 2019). In addition to its adaptability to water-limited environments, sorghum has considerable potential as an alternative staple crop because of its relatively high protein content and lower water requirements compared with other major cereals (Davis et al., 2018). Therefore, investigating the molecular responses of maize and sorghum to drought stress is essential for elucidating the regulatory mechanisms underlying drought tolerance in cereal crops.

RNA sequencing (RNA-seq) has emerged as a powerful and cost-effective approach for transcriptome profiling and the comprehensive analysis of gene expression. Unlike conventional methods, RNA-seq does not rely on the availability of reference genomic sequences and enables the identification of differentially expressed genes across a wide dynamic range of expression levels (Lu et al., 2017a). In recent years, numerous transcriptomic studies have employed RNA-seq analysis to investigate plant responses to abiotic stresses, including osmotic stress and abscisic acid (ABA) treatment, thereby providing valuable insights into the molecular mechanisms underlying stress adaptation (Fracasso et al., 2016b). In this context, comparative transcriptomic approaches can provide deeper insights into species-specific responses and regulatory mechanisms associated with drought tolerance in cereal crops. Therefore, this study aimed to perform a comparative transcriptomic analysis of *Zea mays* and *Sorghum bicolor* under drought stress conditions using an RNA-seq workflow implemented on the Galaxy platform to identify differentially expressed genes and enriched biological pathways associated with drought tolerance mechanisms.

2. Materials and Methods

Comparative transcriptomic analysis of *Zea mays* and *Sorghum bicolor* was conducted to identify drought-responsive genes using the [Galaxy](#) platform. Raw RNA-seq data in Sequence Read Archive (SRA) format were obtained from the [National Center for Biotechnology Information](#) (NCBI) database (Table 1). The raw sequencing data were uploaded to the Galaxy platform and subjected to quality assessment using FastQC to evaluate sequence quality, GC content distribution, read length distribution, and adapter contamination. The quality control results from all samples were subsequently summarized using MultiQC to facilitate simultaneous evaluation of overall sequencing quality. Adapter trimming and removal of low-quality reads were then performed using Trim Galore to obtain high-quality clean reads. The trimmed reads were re-evaluated using FastQC and MultiQC to confirm improvements in sequencing quality prior to downstream analyses.

The high-quality RNA-seq reads were aligned to the reference genomes of *Zea mays* and *Sorghum bicolor* obtained from [Ensembl Plants](#) using HISAT2. The alignment process generated Binary Alignment Map (BAM) files containing information on read positions within the respective reference genomes. Gene expression quantification was subsequently performed using featureCounts with corresponding gene annotation files in Gene Transfer Format (GTF) obtained from [Ensembl Plants](#). The resulting count tables representing the number of mapped reads per gene for each sample were used as input for differential gene expression analysis.

Differential gene expression analysis was carried out using DESeq2 by comparing drought stress (DS) and well-watered (WW) conditions within each species. Treatment condition was used as the primary experimental factor, while biological samples were treated as replicates. The analysis generated normalized gene expression values, log₂ fold change values, p-values, and adjusted p-values or false discovery rates (FDR). Genes were considered significantly differentially expressed genes (DEGs) when they met the criteria of $FDR < 0.05$ and $|\log_2 \text{fold change}| \geq 1$. The outputs included normalized expression matrices, statistical result tables, and graphical visualizations.

Visualization of differential expression results was performed using volcano plots and heatmaps. Volcano plots were generated to illustrate the distribution of upregulated and downregulated genes based on log₂ fold change values and statistical significance levels. Heatmaps were constructed using normalized expression data of 50 top DEGs to visualize gene expression clustering patterns among DS and WW samples. Hierarchical clustering analysis was applied to evaluate similarities in gene expression profiles across treatments and between species.

Functional characterization of significant genes was performed through Gene Ontology (GO) enrichment analysis and KEGG pathway analysis using [ShinyGO 0.85](#). Significant gene lists from each species were analyzed separately to identify enriched biological processes, molecular functions, cellular components, and metabolic pathways associated with drought stress responses. The enrichment analysis revealed pathways related to abscisic acid (ABA) signaling, carbohydrate metabolism, energy metabolism regulation, amino acid biosynthesis, ribosome synthesis, and oxidative stress defense mechanisms. Finally, all transcriptomic results were comparatively evaluated between *Zea mays* and *Sorghum bicolor* to identify differences in drought-responsive transcriptional mechanisms between the two species.

Table 1. List of SRA from NCBI

No.	SRA	Species	Treatment ¹	Reference
1	SRR3105594	<i>Zea mays</i>	WW1	Lu et al., 2017
2	SRR3105595	<i>Zea mays</i>	WW2	Lu et al., 2017
3	SRR3105598	<i>Zea mays</i>	DS1	Lu et al., 2017
4	SRR3105599	<i>Zea mays</i>	DS2	Lu et al., 2017
5	SRR3452717	<i>Sorghum bicolor</i>	WW1	Fracasso et al., 2016
6	SRR3452718	<i>Sorghum bicolor</i>	WW2	Fracasso et al., 2016
7	SRR3452720	<i>Sorghum bicolor</i>	DS1	Fracasso et al., 2016
8	SRR3452721	<i>Sorghum bicolor</i>	DS2	Fracasso et al., 2016

¹ WW= well-watered (control), DS= drought-stress, 1= replicate 1, 2= replicate 2

3. Results

3.1. Differentially Expressed Genes (DEGs)

The results of the Principal Component Analysis (PCA) showed a clear separation between drought stress (DS) treatment samples and well-watered (WW) control samples in both species, indicating differences in gene expression patterns between treatment conditions. The PCA plots demonstrate clear clustering between treatment groups, indicating distinct transcriptomic responses under drought stress conditions. The PCA visualization is presented in Figure 1.

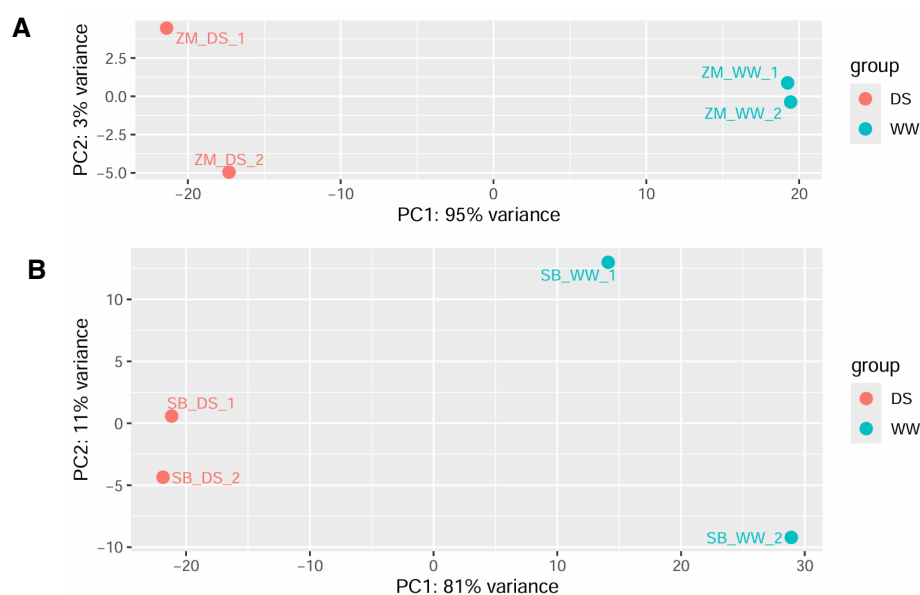


Figure 1. Principal Component Analysis (PCA) of differentially expressed genes (DEGs) in *Zea mays* (A) and *Sorghum bicolor* (B) under drought stress (DS) and well-watered (WW) conditions.

To further evaluate the similarity among samples, hierarchical clustering based on sample-to-sample distances was performed using gene expression profiles. The clustering analysis showed that biological replicates from the same treatment group clustered closely together, indicating good reproducibility and distinct transcriptomic differences between drought stress and control conditions. The heatmap visualization is presented in Figure 2.

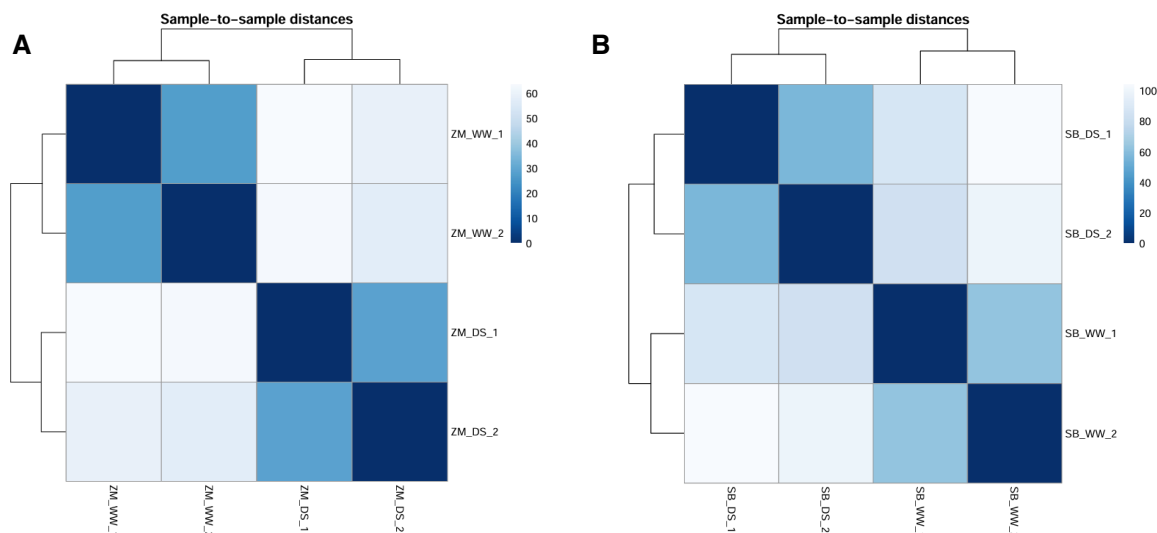


Figure 2. Heatmap of sample-to-sample distances and hierarchical clustering analysis in *Zea mays* (A) and *Sorghum bicolor* (B) under drought stress (DS) and well-watered (WW) conditions.

Dispersion analysis was performed to evaluate the variability of gene expression across samples and to estimate the relationship between mean normalized counts and dispersion values. The results showed an appropriate fitting of dispersion estimates, indicating reliable variance modeling for downstream differential expression analysis. Black dots represent gene-wise dispersion estimates, red dots indicate fitted dispersion values, and blue dots represent final dispersion estimates used for differential expression analysis. The dispersion plots are presented in Figure 3.

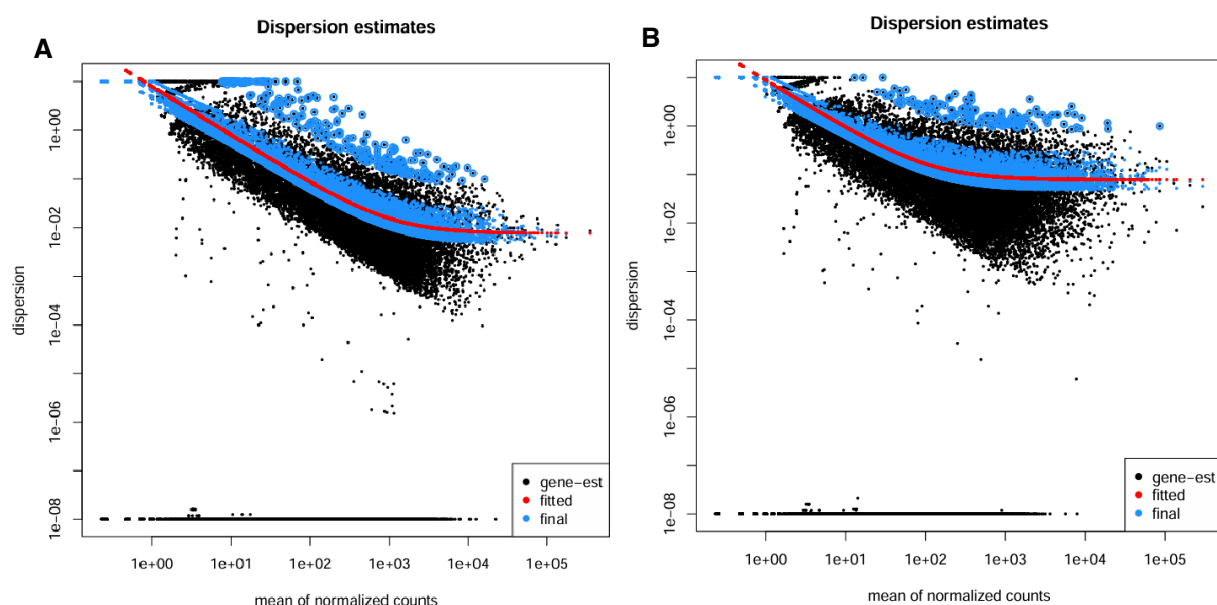


Figure 3. Dispersion estimates of gene expression data in *Zea mays* (A) and *Sorghum bicolor* (B) under drought stress analysis.

The distribution of p-values obtained from differential gene expression analysis was evaluated to assess the statistical significance of gene expression changes under drought stress conditions. The histogram showed an

enrichment of low p-values, indicating the presence of differentially expressed genes between well-watered (WW) and drought stress (DS) treatments. The p-value distributions are presented in Figure 4.

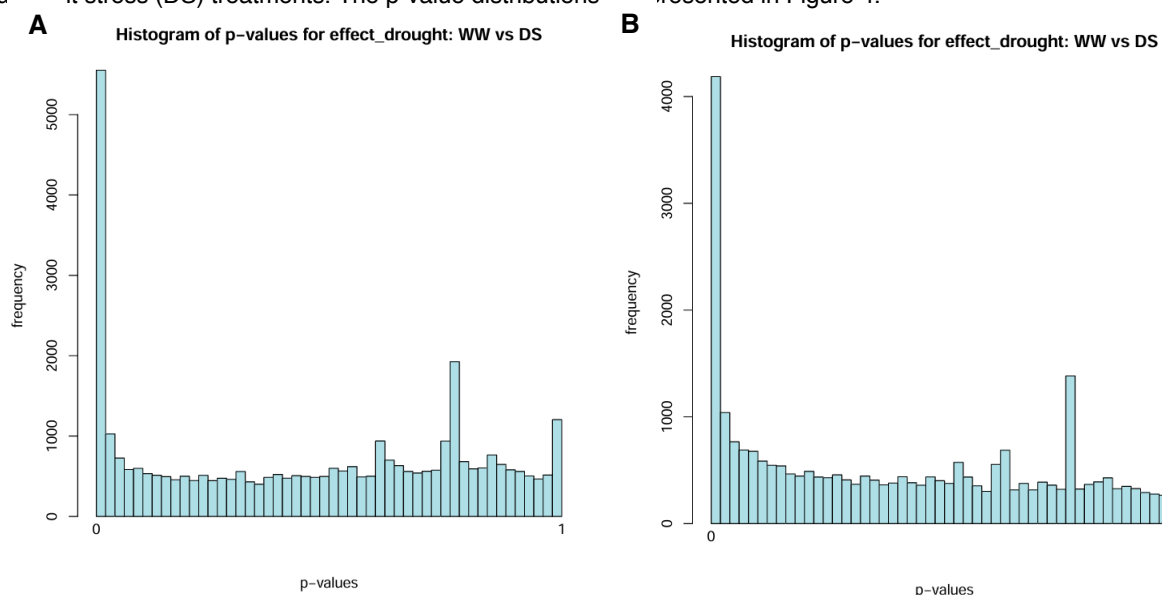


Figure 4. Histogram of p-value distributions from differential expression analysis in *Zea mays* (A) and *Sorghum bicolor* (B) comparing well-watered (WW) and drought stress (DS) conditions.

MA-plot analysis was conducted to visualize the distribution of gene expression changes between well-watered (WW) and drought stress (DS) conditions. The plot illustrates the relationship between mean normalized expression values and $\log_2$ fold changes, enabling the identification of significantly upregulated and downregulated genes under drought stress treatment. The MA-plots are presented in Figure 5.

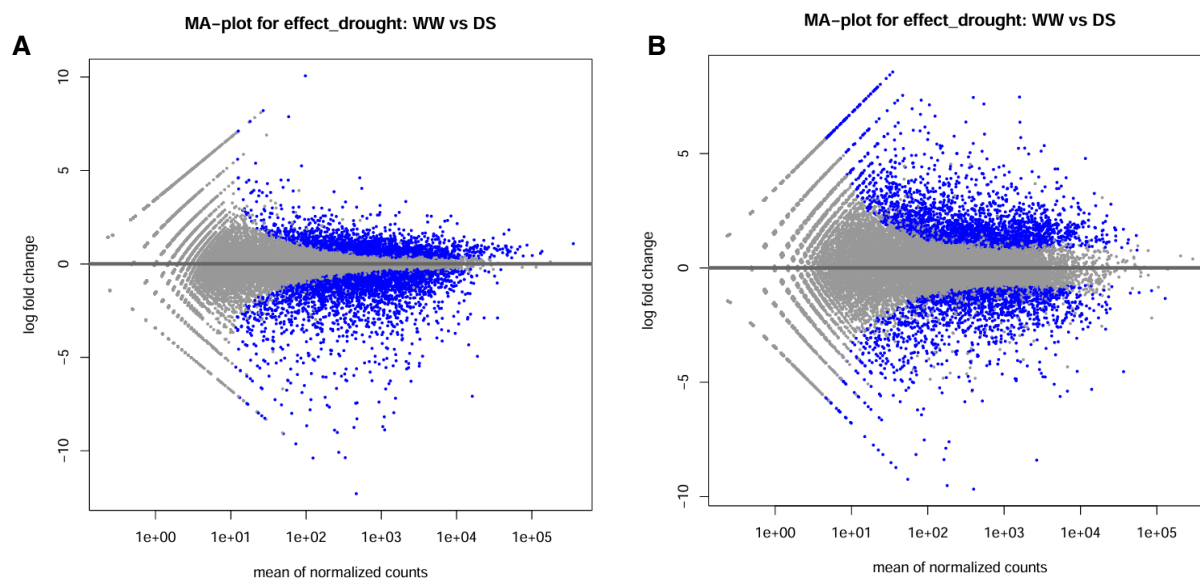


Figure 5. MA-plots of differentially expressed genes in *Zea mays* (A) and *Sorghum bicolor* (B) under well-watered (WW) and drought stress (DS) conditions. Blue dots represent differentially expressed genes (DEGs).

3.2. Volcano Plots Visualization

Volcano plot analysis was performed to visualize the distribution of significantly upregulated and downregulated genes under drought stress conditions. This analysis combines $\log_2$ fold change and statistical significance to identify differentially expressed genes between well-watered (WW) and drought stress (DS) treatments. The volcano plots are presented in Figure 6.

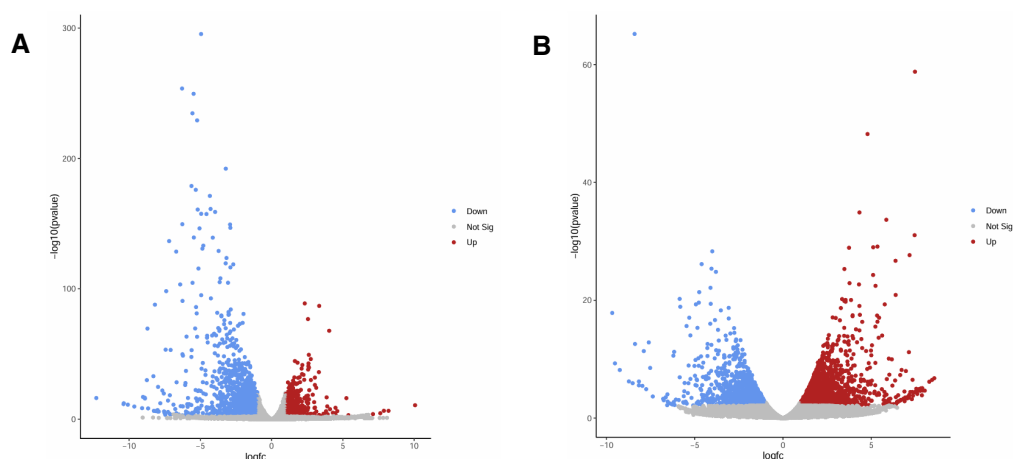


Figure 6. Volcano plots of differentially expressed genes in *Zea mays* (A) and *Sorghum bicolor* (B) under well-watered (WW) and drought stress (DS) conditions. Red and blue dots indicate significantly upregulated and downregulated genes, respectively.

3.3. Heatmaps Visualization

Heatmap analysis was performed to visualize the expression patterns of differentially expressed genes under drought stress conditions. Heatmaps were generated using normalized gene expression data to illustrate variations in gene expression levels between well-watered (WW) and drought stress (DS) conditions. Hierarchical clustering analysis was applied to group genes and samples based on similarities in expression profiles, allowing the identification of transcriptional patterns associated with drought stress responses in both species. The heatmaps are presented in Figures 7 and 8.

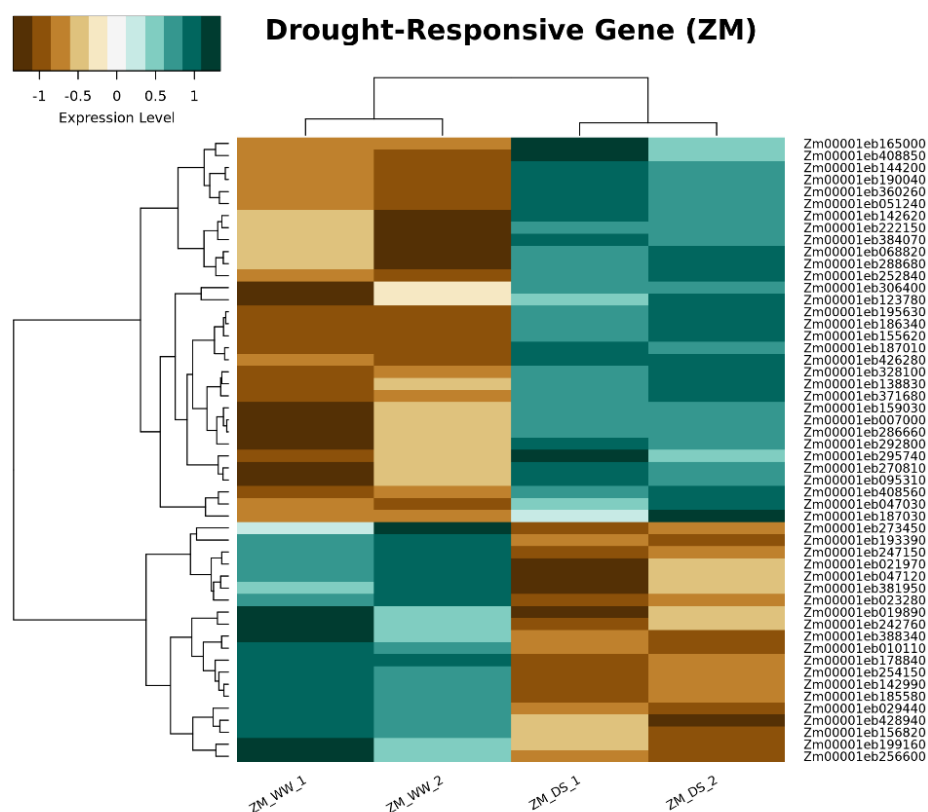


Figure 7. Heatmap of differentially expressed drought-responsive genes in *Zea mays* under WW and DS conditions.

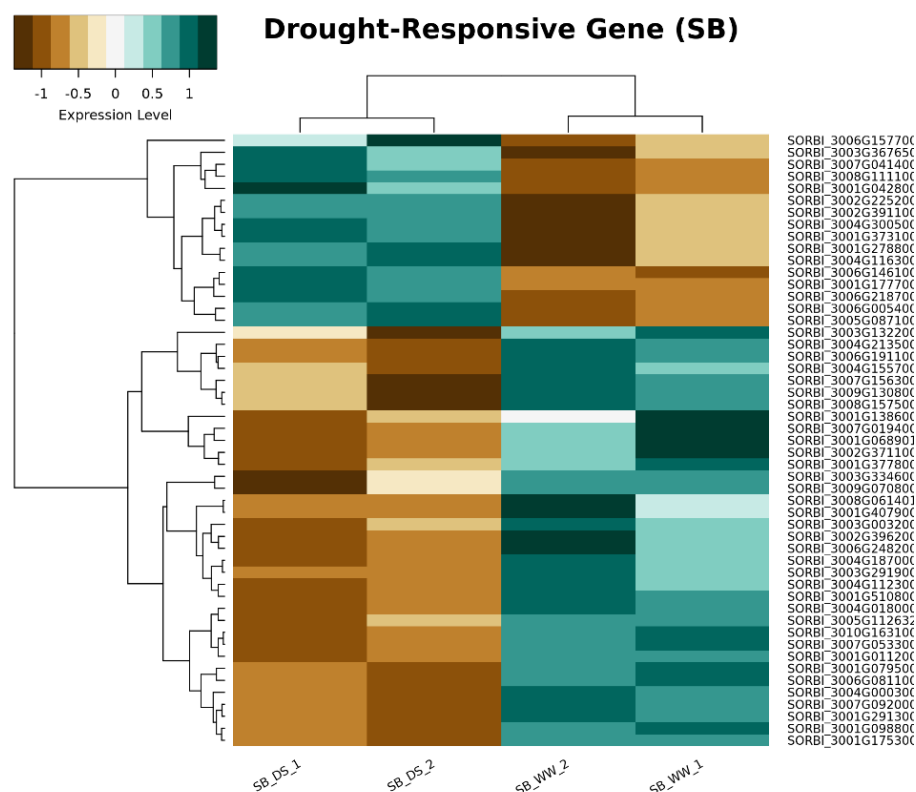


Figure 8. Heatmap of differentially expressed drought-responsive genes in *Sorghum bicolor* under WW and DS conditions.

3.4. Gene Ontology (GO) Enrichment

Gene Ontology (GO) enrichment analysis was performed to identify significantly enriched biological processes associated with drought-responsive genes in *Zea mays* under drought stress conditions. The analysis revealed that several stress-related biological processes were significantly enriched, including responses to hydrogen peroxide, heat, salt stress, osmotic stress, abscisic acid, and oxidative stress-related compounds. In addition, metabolic regulation, transcriptional regulation, and lipid metabolic processes were also enriched, indicating the activation of multiple molecular mechanisms involved in drought stress adaptation. The enrichment results suggest that drought stress induces complex physiological and transcriptional responses in maize to maintain cellular homeostasis and stress tolerance, as presented in Figure 9.

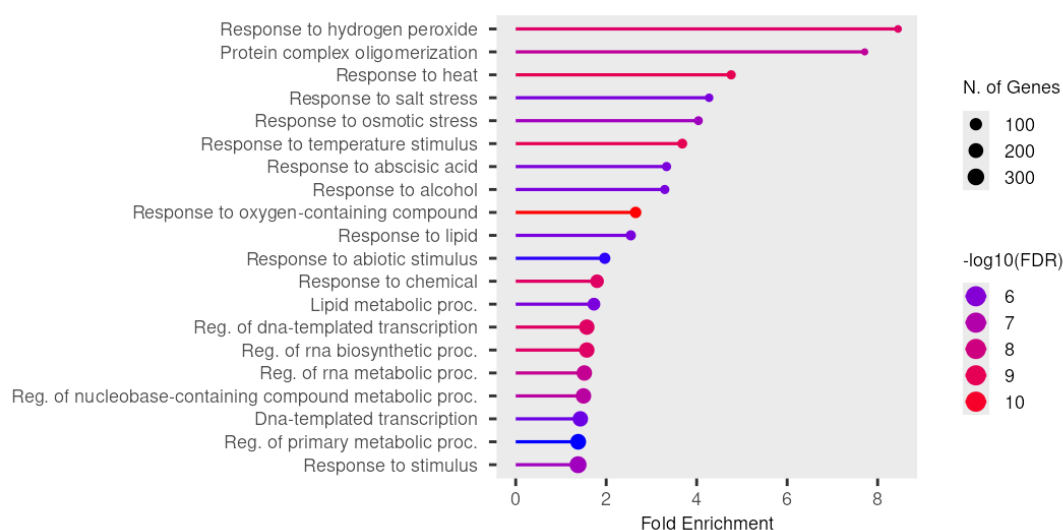


Figure 9. GO enrichment analysis of biological process categories associated with differentially expressed genes in *Zea mays* under drought stress condition.

Similarly, GO enrichment analysis of biological process categories was also conducted for *Sorghum bicolor* to identify the major biological mechanisms involved in drought stress responses. The analysis showed significant enrichment of processes related to ribosome assembly, translation, RNA metabolic processes, protein complex organization, and energy metabolism. Several metabolic processes, including organic acid metabolism and carbohydrate metabolism, were also enriched, indicating active cellular regulation and metabolic adaptation under drought stress conditions. These findings suggest that sorghum activates diverse transcriptional and metabolic pathways to maintain cellular function and enhance drought tolerance, as presented in Figure 10.

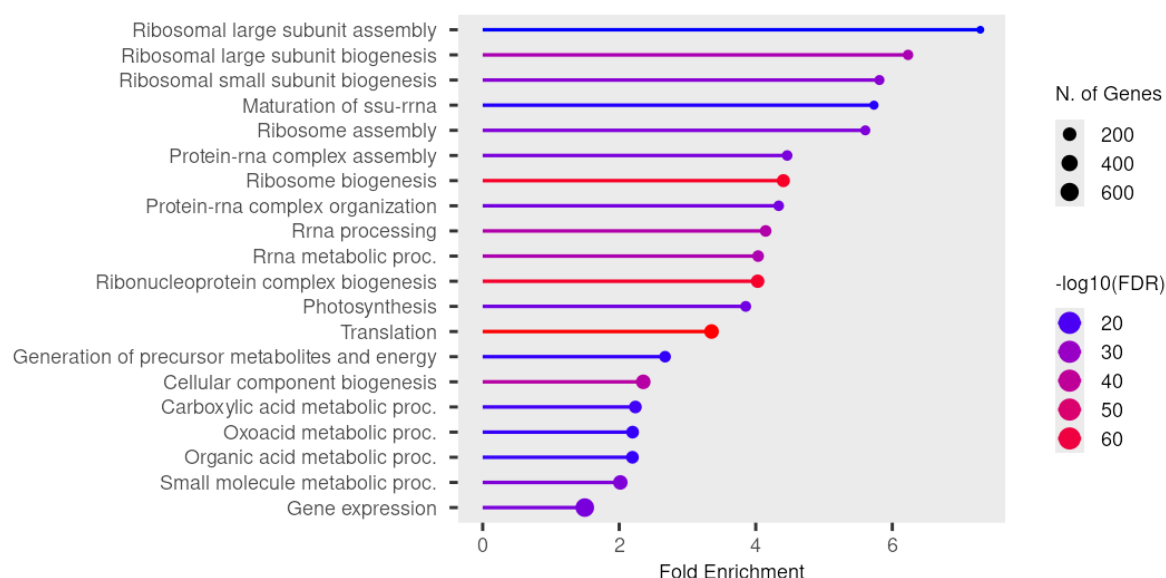


Figure 10. GO enrichment analysis of biological process categories associated with differentially expressed genes in *Sorghum bicolor* under drought stress condition.

3.5. KEGG Pathway Enrichment

KEGG pathway enrichment analysis was performed to identify significantly enriched metabolic and signaling pathways associated with drought-responsive genes in *Zea mays* under drought stress conditions. The analysis revealed significant enrichment of pathways related to carotenoid biosynthesis, alpha-linolenic acid metabolism, MAPK signaling pathway, plant hormone signal transduction, carbohydrate metabolism, amino acid metabolism, and secondary metabolite biosynthesis. These enriched pathways indicate the activation of multiple metabolic and signaling mechanisms involved in drought stress adaptation in maize, as presented in Figure 11.

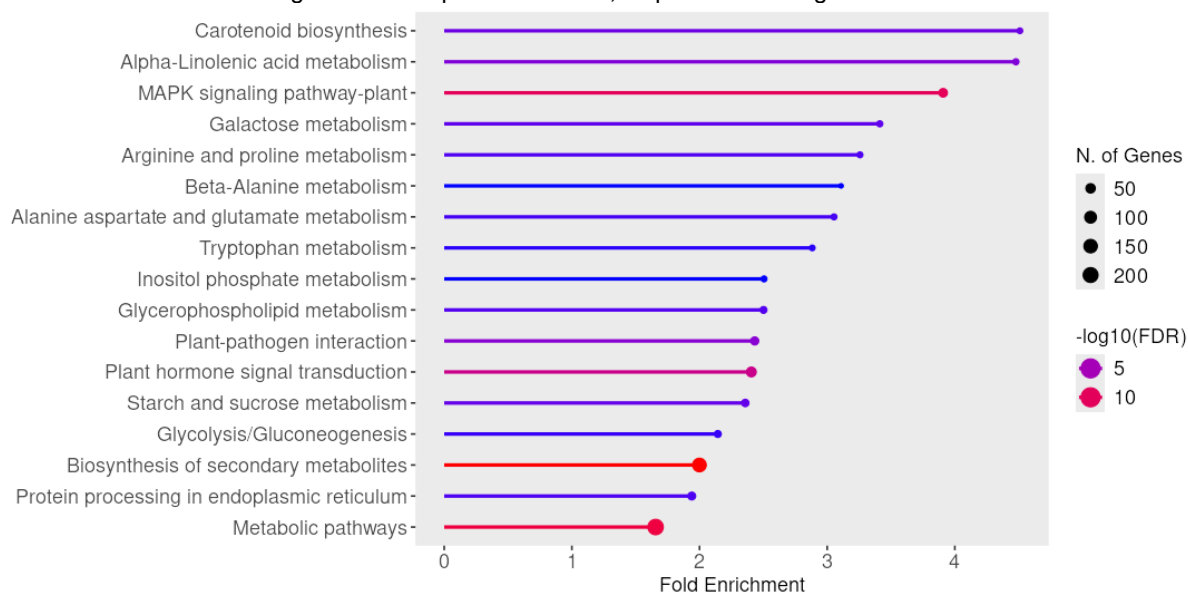


Figure 11. KEGG pathway enrichment analysis associated with differentially expressed genes in *Zea mays* under drought stress conditions.

KEGG pathway enrichment analysis was also performed to identify significantly enriched metabolic and signaling pathways associated with drought-responsive genes in *Sorghum bicolor* under drought stress conditions. The analysis revealed enrichment of pathways related to ribosome function, photosynthesis, amino acid metabolism, carbon metabolism, glycolysis/gluconeogenesis, starch and sucrose metabolism, and secondary metabolite biosynthesis. Several pathways involved in energy production and protein biosynthesis were also significantly enriched, indicating active metabolic regulation and cellular adaptation during drought stress. These findings suggest that sorghum maintains drought tolerance through coordinated regulation of metabolic, photosynthetic, and translational pathways, as presented in Figure 12.

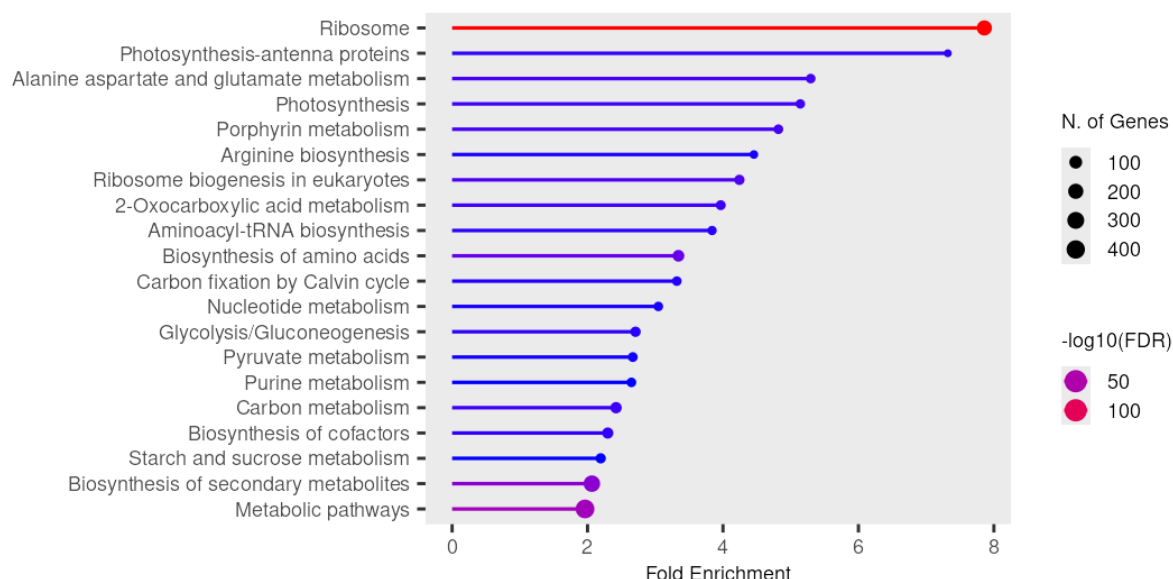


Figure 12. KEGG pathway enrichment analysis associated with differentially expressed genes in *Sorghum bicolor* under drought stress conditions.

4. Discussion

The validation results demonstrated that biological replicates within the same treatment group exhibited similar gene expression patterns in *Zea mays* and *Sorghum bicolor*. Furthermore, differential expression analysis using MA plots revealed significant transcriptomic changes in both species under drought stress conditions. The MA plots showed that most genes were closely distributed around the horizontal zero line (Figure 5.), indicating the absence of large expression changes between groups (Dawadi et al., 2025). In addition, differences in DEG distribution between maize and sorghum may reflect variations in drought adaptation mechanisms and tolerance capacities between the two species, supporting further downstream analyses.

Volcano plot analysis further illustrated the distribution and statistical significance of upregulated and downregulated differentially expressed genes based on log2 fold change and adjusted p-values (Figure 6.). In *Zea mays*, drought stress induced substantial changes in gene expression, with numerous genes exhibiting strong differential expression, indicating active responses to drought-induced cellular stress. Meanwhile, *Sorghum bicolor* also displayed significant transcriptional changes; however, the expression patterns suggested a more coordinated and efficient regulatory response to drought stress. Heatmap analysis further confirmed distinct gene expression patterns between well-watered (WW) and drought stress (DS) conditions in both species. Hierarchical clustering grouped samples with the same treatment into similar clusters, demonstrating consistency among biological replicates and good overall data quality. Heatmaps are capable of clustering samples and genes based on similarities in expression patterns (McDermaid et al., 2019). Several genes showed increased expression under drought stress conditions, which are likely associated with stress responses, osmotic regulation, and antioxidant defense mechanisms.

Differences in Gene Ontology (GO) biological process enrichment between *Zea mays* and *Sorghum bicolor* indicate variations in the molecular mechanisms underlying drought stress responses in the two species. In maize, GO biological process enrichment was predominantly associated with stress-responsive processes, including response to hydrogen peroxide, osmotic stress, salt stress, heat stress, and abscisic acid (ABA) response. Hydrogen peroxide (H_2O_2) at low concentrations functions as a signaling molecule involved in stress signal transduction and the induction of stress tolerance; however, excessive accumulation of H_2O_2 can lead to cellular damage and programmed cell death (Bhattacharyya et al., 2025). In addition, abscisic acid (ABA) is one of the most important phytohormones involved in plant responses to water deficit by regulating plant growth, inhibiting seed germination, inducing stomatal closure, and promoting leaf senescence (Yang et al., 2021). These enriched processes suggest that maize experiences enhanced oxidative stress responses and activation of hormone-mediated signaling pathways to maintain cellular homeostasis under drought conditions. Furthermore, the enrichment of lipid metabolic processes and transcriptional regulation indicates the involvement of membrane protection mechanisms and stress-responsive gene regulation. Lipids play essential roles in maintaining membrane integrity and fluidity by forming protective structures such as cuticular waxes to reduce water loss, serving as signaling molecules such as jasmonic acid, and contributing to reactive oxygen species (ROS) scavenging during stress conditions (Maryam et al., 2025). In contrast, GO enrichment in *Sorghum bicolor* was mainly associated with translation, ribosome organization, RNA metabolic processes, and protein complex assembly (Fracasso et al., 2016). These findings indicate that sorghum tends to maintain fundamental metabolic activities and protein biosynthesis during drought stress, suggesting a more stable and efficient drought tolerance mechanism compared with maize.

Differences in response patterns were also observed in the KEGG pathway enrichment analysis between *Zea mays* and *Sorghum bicolor* under drought stress conditions. In maize, the enriched pathways were mainly associated with stress signaling and stress response mechanisms, including the MAPK signaling pathway, plant hormone signal transduction, carotenoid biosynthesis, and alpha-linolenic acid metabolism. Carotenoids play essential roles in photosynthesis, photoprotection, and phytohormone production, particularly abscisic acid and strigolactones (Sathasivam et al., 2021). The mitogen-activated protein kinase (MAPK) cascade, which is widely conserved among eukaryotes, has been reported to participate in ABA signaling and drought stress responses, including ABA- and hydrogen peroxide-mediated stomatal closure mechanisms (Chen et al., 2021). In addition, alpha-linolenic acid metabolism in maize functions not only as a strong antioxidant system but also as a precursor for jasmonic acid biosynthesis, which acts as a signaling molecule that stimulates subsequent anti-stress responses (Zi et al., 2022). The enrichment of these pathways suggests that maize activates stress signaling pathways and hormone-regulated mechanisms intensively in response to drought stress conditions.

In contrast, the enriched pathways in *Sorghum bicolor* were mainly related to ribosome, photosynthesis, carbon metabolism, glycolysis/gluconeogenesis, and amino acid biosynthesis. These findings indicate that sorghum possesses a greater ability to maintain photosynthetic activity, energy production, and protein synthesis during drought stress conditions (Fracasso et al., 2016). Prolonged drought stress in sorghum has been reported to trigger compensatory responses that enhance stress tolerance following the accumulation of stress signals during earlier stress exposure. Plant hormone signal transduction and starch and sucrose metabolism pathways are considered important regulatory strategies involved in plant adaptation to abiotic stress. In parallel, glycolysis and gluconeogenesis pathways contribute to carbohydrate production required for sorghum growth and development under stress conditions (Ma et al., 2026).

5. Conclusions

In conclusion, comparative transcriptomic analysis revealed distinct drought response mechanisms between *Zea mays* and *Sorghum bicolor*. Maize predominantly activated stress-responsive signaling pathways, hormone-mediated responses, and oxidative stress regulation under drought conditions, whereas sorghum maintained more stable metabolic activities, photosynthesis, and protein biosynthesis.

These findings suggest that sorghum possesses a more efficient and coordinated drought tolerance mechanism compared with maize.

Acknowledgments: The author would like to express sincere gratitude to Dr. Rizky Dwi Satrio, S.Si., M.Si. as lecturer of the bioinformatics course, for their valuable guidance, insightful discussions, and constructive feedback throughout the learning process and the completion of this study. Their academic support and encouragement have greatly contributed to the development of this work.

References

- Bhattacharyya, S., Bleker, C., Meier, B., Giridhar, M., Rodriguez, E. U., Braun, A. M., Peiter, E., Vothknecht, U. C., & Chigri, F. (2025). Ca²⁺-dependent H₂O₂ response in roots and leaves of barley - a transcriptomic investigation. *BMC Plant Biology*, 25(1), 232. <https://doi.org/10.1186/s12870-025-06248-9>
- Chen, X., Ding, Y., Yang, Y., Song, C., Wang, B., Yang, S., Guo, Y., & Gong, Z. (2021). Protein kinases in plant responses to drought, salt, and cold stress. In *Journal of Integrative Plant Biology* (Vol. 63, Number 1, pp. 53–78). Blackwell Publishing Ltd. <https://doi.org/10.1111/jipb.13061>
- Davis, K. F., Chiarelli, D. D., Rulli, M. C., Chhatre, A., Richter, B., Singh, D., & Defries, R. (2018). *Alternative cereals can improve water use and nutrient supply in India*.
- Dawadi, P., Pokharel, B., Shrestha, A., Niraula, D., Naeem, A., Miura, S., Roy, M., & Nepal, S. (2025). From bench to bytes: a practical guide to RNA sequencing data analysis. *Frontiers in Genetics*, Volume 16-2025. <https://doi.org/10.3389/fgene.2025.1697922>
- Fontanet-Manzanque, J. B., Hernández, D. M., Giordano, A., & Caño-Delgado, A. I. (2025). Sorghum as a monocot model for drought research. *Frontiers in Plant Science*, Volume 16-2025. <https://doi.org/10.3389/fpls.2025.1665967>
- Fracasso, A., Trindade, L. M., & Amaducci, S. (2016b). Drought stress tolerance strategies revealed by RNA-Seq in two sorghum genotypes with contrasting WUE. *BMC Plant Biology*, 16(1). <https://doi.org/10.1186/s12870-016-0800-x>
- Lesk, C., Rowhani, P., & Ramankutty, N. (2016). Influence of extreme weather disasters on global crop production. *Nature*, 529(7584), 84–87. <https://doi.org/10.1038/nature16467>
- Liu, S., Zenda, T., Dong, A., Yang, Y., Wang, N., & Duan, H. (2021). Global Transcriptome and Weighted Gene Co-expression Network Analyses of Growth-Stage-Specific Drought Stress Responses in Maize. *Frontiers in Genetics*, 12. <https://doi.org/10.3389/fgene.2021.645443>
- Lu, X., Zhou, X., Cao, Y., Zhou, M., McNeil, D., Liang, S., & Yang, C. (2017a). RNA-seq analysis of cold and drought responsive transcriptomes of *Zea mays* ssp. *Mexicana* L. *Frontiers in Plant Science*, 8(FEBRUARY). <https://doi.org/10.3389/fpls.2017.00136>
- Lu, X., Zhou, X., Cao, Y., Zhou, M., McNeil, D., Liang, S., & Yang, C. (2017b). RNA-seq analysis of cold and drought responsive transcriptomes of *Zea mays* ssp. *Mexicana* L. *Frontiers in Plant Science*, 8(FEBRUARY). <https://doi.org/10.3389/fpls.2017.00136>
- Ma, Q., Wang, R., He, F., Wan, W., Liu, X., Zhang, J., Li, K., & Ren, M. (2026). Response of sorghum (*Sorghum bicolor* (L.) Moench) to various-duration of drought: physiology, transcriptome, and weighted gene co-expression network analysis. *BMC Plant Biology*, 26(1), 488. <https://doi.org/10.1186/s12870-026-08297-0>
- Maryam, A., Khan, R. I., Abbas, M., Hussain, K., Muhammad, S., Sabir, M. A., Ahmed, T., & Khalid, M. F. (2025). Beyond the membrane: the pivotal role of lipids in plants abiotic stress adaptation. *Plant Growth Regulation*, 105(6), 1869–1887. <https://doi.org/10.1007/s10725-025-01363-x>
- McDermaid, A., Monier, B., Zhao, J., Liu, B., & Ma, Q. (2019). Interpretation of differential gene expression results of RNA-seq data: review and integration. *Briefings in Bioinformatics*, 20(6), 2044–2054. <https://doi.org/10.1093/bib/bby067>
- Sathasivam, R., Radhakrishnan, R., Kim, J. K., & Park, S. U. (2021). An update on biosynthesis and regulation of carotenoids in plants. *South African Journal of Botany*, 140, 290–302. <https://doi.org/https://doi.org/10.1016/j.sajb.2020.05.015>
- Venkateswaran, K., Elangovan, M., & Sivaraj, N. (2019). Chapter 2 - Origin, Domestication and Diffusion of *Sorghum bicolor*. In C. Aruna, K. B. R. S. Visarada, B. V. Bhat, & V. A. Tonapi (Eds.), *Breeding Sorghum for Diverse End Uses* (pp. 15–31). Woodhead Publishing. <https://doi.org/https://doi.org/10.1016/B978-0-08-101879-8.00002-4>
- Waititu, J. K., Zhang, X., Chen, T., Zhang, C., Zhao, Y., & Wang, H. (2021). Transcriptome analysis of tolerant and susceptible maize genotypes reveals novel insights about the molecular mechanisms underlying drought responses in leaves. *International Journal of Molecular Sciences*, 22(13). <https://doi.org/10.3390/ijms22136980>
- Yang, X., Lu, M., Wang, Y., Wang, Y., Liu, Z., & Chen, S. (2021). Response mechanism of plants to drought stress. In *Horticulturae* (Vol. 7, Number 3). MDPI AG. <https://doi.org/10.3390/horticulturae7030050>
- Zhang, X., Lei, L., Lai, J., Zhao, H., & Song, W. (2018). Effects of drought stress and water recovery on physiological responses and gene expression in maize seedlings. *BMC Plant Biology*, 18(1), 68. <https://doi.org/10.1186/s12870-018-1281-x>
- Zi, X., Zhou, S., & Wu, B. (2022). Alpha-Linolenic Acid Mediates Diverse Drought Responses in Maize (*Zea mays* L.) at Seedling and Flowering Stages. *Molecules*, 27(3). <https://doi.org/10.3390/molecules27030771>