



# **ABSTRACT BOOK**

## **Crop Adaptation to Climate Change Congress**

**17-19 September 2025**

**Samsun/TÜRKİYE**



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**17 September 2025- Wednesday**

| Time        | Event                         | Title                                                                                                                                               |
|-------------|-------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------|
| 09:30-10:00 | Opening Ceremony              |                                                                                                                                                     |
| 10:00-10:30 | Dr. Ekrem Gürel               | Impacts of Global Climate Change on Agricultural Production: The Case of Sugar Beet in Turkey                                                       |
| 10:30-11:00 | Dr. Hakan Özkan               | <i>Triticum araraticum</i> as a Genetic Resource for Climate-Smart Wheat: Future Perspectives Including De Novo Domestication                       |
| 11:00-11:30 | Dr. Sotirios Fragkostefanakis | Beat the heat: What tomato evolution teaches us about plant thermotolerance mechanisms                                                              |
| 11:30-12:00 | Dr. Bernd Mueller-Roeber      | Tissue-specific mechanisms of heat stress tolerance in plants                                                                                       |
| 12:00-13:15 | Lunch                         | Omtel                                                                                                                                               |
| 13:15-13:40 | Dr. Antonio Granell Richart   | Genomics and NGTs for tomato fruit quality and increase resilience                                                                                  |
| 13:40-14:00 | Dr. Nejdet Kandemir           | Genetic Improvement of Drought Adaptation in Cereal Crops                                                                                           |
| 14:00-14:20 | Dr. Ece Turhan                | Impact of Sucrose Supply on Chilling Tolerance in Tomato Seedlings                                                                                  |
| 14:20-14:40 | Dr. Musa Kavas                | Genome Editing Approaches in Tomato: Insights from CRISPR Applications                                                                              |
| 14:40-15:00 | Dr. Kubilay Yıldırım          | CRISPR-Mediated Genome Editing as a Strategic Tool for Enhancing Biotic Stress Tolerance in Crops Under Climate Change and Global Warming Scenarios |
| 15:00-15:15 | Coffee Break                  |                                                                                                                                                     |
| 15:15-15:45 | Dr. Fredy Altpeter (Online)   | Comparison of heat-inducible promoters for biotech                                                                                                  |





## Crop Adaptation to Climate Change – Strengthening Crops for a Changing World

|             |                    |                                                                                                                                                                                                       |
|-------------|--------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
|             |                    | approaches in sugarcane improvement                                                                                                                                                                   |
| 15:45-16:05 | Dr. Ertan Yıldırım | Ameliorative effects of strigolactone on tolerance to lead stress on lettuce ( <i>Lactuca sativa</i> L.) plants                                                                                       |
| 16:05-16:25 | Dr. Melek Ekinci   | Determination of the contribution of humic substances to plant growth in lettuce under flooding conditions                                                                                            |
| 16:25-16:45 | Dr. Bayram Çevik   | Involvement of MYB transcription factors in biotic and abiotic stress response in plants and the expressions analysis of some tomato MYBs in response to Tomato spotted wilt virus and drought stress |
| 16:45-17:00 | Dr. Çağla Sönmez   | Sequential cold and heat stresses establish an intergenerational stress memory in rapeseed ( <i>Brassica napus</i> L.)                                                                                |
| 17:00-17:30 | Poster Session     |                                                                                                                                                                                                       |
| 18:00-19:00 | Wellcome Dinner    | Samsu Börek Restaurant                                                                                                                                                                                |





## 18 September 2025- Thursday

| Time        | Event                                  | Title                                                                                                                                                           |
|-------------|----------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 09:15-09:45 | Dr. Goetz Hensel                       | Precision Plant Editing: From Barley to Amaranth with CRISPR in Hand                                                                                            |
| 09:45-10:15 | Dr. Frank Van Breusegem                | Decrypting the plant oxidative stress response                                                                                                                  |
| 10:15-10:35 | Dr. Sara Izquierdo Zandalinas (Online) | Unraveling plant responses to multifactorial stress combinations under climate change scenarios                                                                 |
| 10:35-10:45 | Flash Talks                            | 1-2                                                                                                                                                             |
| 10:45-11:00 | Coffee Break                           |                                                                                                                                                                 |
| 11:00-11:20 | Dr. Muhammad Aasim                     | Computational and Machine Learning Models for Optimizing Germination Under Cold Stress Conditions of Common Bean with Titania (TiO <sub>2</sub> ) Nanoparticles |
| 11:20-11:40 | Dr. Murat Aydın                        | Inhibitory effect of exogenous methionine on drought stress in tomato seedlings                                                                                 |
| 11:40-12:00 | Dr. Emre Aksoy                         | Planetary Resilience by Design: Pan-Omics and AI-Driven Gene Editing for Climate-Smart Crop Breeding Roadmap to 2075 beyond Europe's Green Deal                 |
| 12:00-13:15 | Lunch                                  | Peçko Restaurant                                                                                                                                                |
| 13:15-13:35 | Dr. Filiz Vardar                       | Microorganisms and Biofertilizers: Eco-Friendly Approaches for Sustainable Agriculture                                                                          |
| 13:35-13:55 | Dr. Selman Uluişik                     | Plant Growth-Promoting Rhizobacteria in Action: Enhancing Almond Resilience to Drought                                                                          |
| 13:55-14:15 | Dr. Fatma Aydınoğlu                    | Unrevealing microRNA Roles in Maize ( <i>Zea mays</i> L.) Leaf                                                                                                  |





## Crop Adaptation to Climate Change – Strengthening Crops for a Changing World

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|-------------|-------------------------|------------------------------------------------------------------------------------------------------------------------------------------------------------------|
|             |                         | Growth Response to Chilling Stress by miRNomics and VIGS-based STTM approach                                                                                     |
| 14:15-14:35 | Dr. Nataliia Kutsokon   | Salinity tolerance of fast-growing Salicaceae species                                                                                                            |
| 14:35-14:45 | Flash Talks             | 3-4                                                                                                                                                              |
| 14:45-15:00 | Coffee Break            |                                                                                                                                                                  |
| 15:00-15:20 | Dr. Nihal Öztolan Erol  | Potassium Deficiency Induces Cellulose synthase A 4 Expression in <i>Arabidopsis thaliana</i> and <i>Triticum aestivum</i>                                       |
| 15:20-15:40 | Dr. Yılmaz Kaya         | Drought Stress Mitigation via Plant-Endophyte Interactions                                                                                                       |
| 15:40-16:00 | Dr. İsmail Bezirganoğlu | Investigation of the Effect of Melatonin and Endophytic Bacteria Administration on Salt Stress Tolerance in <i>Lotus corniculatus</i> Plants in Vitro Conditions |
| 16:00-16:20 | Dr. Sedat Serçe         | Utilization of Berry Crop Plant Genetic Resources to Cope with Changing Environment                                                                              |
| 16:20-17:30 | Flash Talks             | 5-11                                                                                                                                                             |
| 18:00-20:00 | Gala Dinner             | Hoşkadem Restaurant                                                                                                                                              |





**19 September 2025- Friday**

| Time        | Event                                                  | Title                                                                                                                                                       |
|-------------|--------------------------------------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 09:15-09:35 | Dr. Utku Avcı                                          | Plant Cell Walls in a Changing Climate                                                                                                                      |
| 09:35-09:55 | Dr. İskender Tiryaki                                   | Genome-Wide Identification of DELLA Genes in Flax ( <i>Linum usitatissimum</i> L.) and Determination of Physiological Responses to Drought Stress by GABA   |
| 09:55-10:15 | Dr. Şeyma Gökdemir                                     | Genome-wide Analysis and Role of miR167 and miR398 in the Regulation of Cold Stress and Hydrogen Peroxide Acclimation in Tomato Plants                      |
| 10:15-10:25 | Flash talks                                            | 12                                                                                                                                                          |
| 10:25-10:45 | Coffee Break                                           |                                                                                                                                                             |
| 10:45-11:05 | Dr. Hatice Şelale Yıldız                               | Divergent Transcriptional Programs Underlie Salt Tolerance in <i>Solanum pennellii</i> Introgression Lines                                                  |
| 11:05-11:25 | Dr. Gültunay Eren                                      | Determination of the Effects of Global Climate Anomalies on Apricot Orchards in Malatya Province                                                            |
| 11:25-11:45 | Dr. Esmâ Yiğider                                       | Effects of dopamine on reducing salt stress damage in pepper ( <i>Capsicum annuum</i> L.) at morphological, physiological, biochemical and molecular levels |
| 11:45-12:00 | Dr. Ahmad Alsaleh                                      | Accelerating Climate-Resilient Hemp Breeding through Molecular Marker Technologies                                                                          |
| 12:00-12:15 | Closing Ceremony                                       |                                                                                                                                                             |
| 12:15-17:00 | Samsun City Tour-Kızılırmak Delta Bird Sanctuary Visit |                                                                                                                                                             |







## Flash Talks

| No | Presenter             | Title                                                                                                                                                                                            |
|----|-----------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 1  | Tuğçe Er              | Determination of Groundwater Microbial Diversity by Metabarcoding Approach and Potential Use in Agricultural Applications                                                                        |
| 2  | Momna Mehmood         | CRISPR/Cas9-Mediated Knockout of sly-miR9469 for Functional Analysis of Drought Tolerance in Tomato ( <i>Solanum lycopersicum</i> L.)                                                            |
| 3  | Erdem Emre DELİGÖZ    | Competitive endogenous RNAs (ceRNAs) involving miR396 and miR319 regulate maize leaf growth during pathogenic fungus <i>Fusarium verticillioides</i> infection                                   |
| 4  | Sena KIZILBOĞA        | Cross-Kingdom RNA Interference-Mediated Interactions Between Pathogenic Fungus <i>Fusarium verticillioides</i> and Maize ( <i>Zea mays</i> ): Morphological, Biochemical, and Molecular Insights |
| 5  | Oğuz Kaan Yaşar       | Transcriptional Profiling in lox3 mutant <i>Arabidopsis thaliana</i> Under Severe Boron Toxicity                                                                                                 |
| 6  | Damla TURAN BÜYÜKDİNÇ | In vitro Screening for Salt and Drought Tolerance in <i>Cichorium endivia</i> L. and <i>Cichorium intybus</i> L.                                                                                 |
| 7  | Ayşenur BOZKURT       | A Multiplexed Genome Editing Approach for Climate-Resilient Iron Biofortification in Potato                                                                                                      |
| 8  | Selçuk ÇETİN          | Genome-Wide Identification and Characterization of the GABA Pathway Gene Family in Alfalfa ( <i>Medicago sativa</i> ): Insights into Stress Response                                             |





## Crop Adaptation to Climate Change – Strengthening Crops for a Changing World

|    |                      |                                                                                                                                                  |
|----|----------------------|--------------------------------------------------------------------------------------------------------------------------------------------------|
|    |                      | and Developmental Regulation                                                                                                                     |
| 9  | Enes Gökhan YILMAZ   | Assessing Drought Tolerance and its Relationship with Seed Size in Lentil ( <i>Lens culinaris</i> Medik.) Cultivars                              |
| 10 | Dilruba TABAY SÜMBÜL | Impact of Copper Oxide Nanoparticles on Growth, Oxidative Stress and Antioxidant Gene Expression in Maize ( <i>Zea mays</i> L.) Seedlings        |
| 11 | Neslihan Yaşar       | Single-nucleus RNA sequencing reveals gene regulatory networks in <i>Arabidopsis thaliana</i> roots under drought stress                         |
| 12 | Olha Yaroshko        | Enhancing shoot regeneration efficiency under PEG-modulated drought stress conditions in <i>Solanum lycopersicum</i> cultivars Micro-Tom and M82 |





## Poster Presentation

| No | Presenter           | Title                                                                                                                       |
|----|---------------------|-----------------------------------------------------------------------------------------------------------------------------|
| 1  | Ece FİDAN           | Evaluation of Tolerance to the Combination of Salt and High Temperature in Five Winter Wheat Genotypes                      |
| 2  | Aybüke Didenur SAK  | Salicylic Acid Modulation of ABA-Induced MAPK Signaling in Quinoa under Drought Stress: Insights from the Titicaca Genotype |
| 3  | Muhammed Fatih KAYA | Overexpression of the SLAIMI gene encoding the R2R3 MYB transcription factor triggers drought tolerance in potatoes         |
| 4  | Muhammed Yakup İPEK | Genome-wide identification of YSL gene family in quinoa and amaranth and expression patterns under high soil pH             |
| 5  | Burçin KIYAK        | Role of N-Acetylcysteine in Enhancing Antioxidant Activity and Productivity of Drought-Sensitive Bread Wheat                |
| 6  | Elif Azra ATAR      | Prediction of Iron Deficiency Tolerance Pathways in Quinoa Using Artificial Intelligence-Assisted Multiple Dataset Analysis |
| 7  | Necdet Mehmet ÜNEL  | Brassinosteroid–Jasmonic acid–Ethylene Crossover Communication and Fiber Biogenesis in <i>Cannabis sativa</i>               |
| 8  | Mustafa ÖÇAL        | Drought-Induced Modulation of Bioactive Compounds and Antimicrobial Potential in <i>Echinacea purpurea</i>                  |
| 9  | Muhammed TATAR      | Patulin Toxin-Producing Isolates in <i>Penicillium expansum</i> Link, (1809)                                                |





## Crop Adaptation to Climate Change – Strengthening Crops for a Changing World

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|----|--------------------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
|    |                    | Populations Isolated from Apples                                                                                                                                       |
| 10 | Büşra YAZICILAR    | The Role of Vitamin D in the Salt Stress Tolerance of <i>Arabidopsis thaliana</i>                                                                                      |
| 11 | Merve ŞİMŞEK GEYİK | Nanotechnology-Endophyte Interaction in Alfalfa Plants Against Drought Stress                                                                                          |
| 12 | Salma Naimatullha  | Integrating Design of Experiment (DOE) for Optimizing the Impact of Multiwalled Carbon Nanotubes on Seed Germination Indices in Cotton ( <i>Gossypium hirsutum</i> L.) |
| 13 | Sabeen Rehman      | Improving germination indices of biofortified cowpea using ZnO <sub>2</sub> nanoparticles and a design of experiments approach                                         |
| 14 | Noor Ul Ain        | Functional Analysis and Determination of Potyvirus Resistance in Tomato Plants Developed by Overexpression and Silencing of the eIF(iso)4E Gene                        |
| 15 | Beyza Altay        | Development of multiple resistance to fungal diseases in sunflower ( <i>Helianthus annuus</i> L.) via CRISPR-mediated mutation in MLO genes                            |
| 16 | Sılanur Aydoğdu    | Functional Characterization of Solyc02g077790 Reveals Its Role in Tomato Fruit Ripening, Quality, and Stress-Linked Pathways                                           |
| 17 | Yavuz Delen        | Transcriptome Meta-Analysis Uncovers Core Susceptibility Genes Shaping Broad-Spectrum Stress Responses in Sunflower                                                    |





## Crop Adaptation to Climate Change – Strengthening Crops for a Changing World

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|----|------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 18 | Şeyma Gökdemir         | Toxic boron responsive regulations of <i>lox3</i> mutant <i>Arabidopsis thaliana</i> at physiological and biochemical levels                                            |
| 19 | Hümeysra Yoldaş        | Unveiling the Stress-Responsive KCS Gene Family in Tomato: Insights from Genome-Wide and In Silico Expression Analyses                                                  |
| 20 | Sevtap Doksöz Boncukçu | Seaweed Applications Enhance Salt Stress Tolerance in Cucumber ( <i>Cucumis sativus</i> L.)                                                                             |
| 21 | Bayram Ali Yerlikaya   | Development of Tomato Lines with Visual Markers and Enhanced Stress Tolerance through CRISPR/Cas9-Mediated Targeting of a Negative Regulator in the Anthocyanin Pathway |





## Oral Presentations

### Biotechnological Advances in Sugar Beet for Climate-Resilient Agriculture in Türkiye

Ekrem Gürel<sup>1,2</sup>, Songul Gürel<sup>1,2</sup>, Mehmet Cengiz Baloglu<sup>3</sup>

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**Keywords:** *Beta vulgaris*, Biotechnological approaches, Climate resilience, Abiotic and biotic stress, Molecular markers

#### Abstract

Sugar beet (*Beta vulgaris*) is a key industrial crop in Türkiye, contributing significantly to national sugar production and rural economies. However, climate change poses multiple challenges to sugar beet cultivation, including drought stress, soil salinization, disease outbreaks, and shortened growing seasons. To ensure sustainable productivity under these conditions, modern biotechnological approaches are increasingly being integrated into breeding and crop improvement programs. This review provides an overview of recent biotechnological advancements in sugar beet research in Türkiye, with a particular focus on enhancing resistance to abiotic and biotic stress factors exacerbated by climate change. Key strategies include the development of molecular markers associated with drought tolerance and disease resistance (notably against rhizomania, *Cercospora beticola*, and beet cyst nematode), high-throughput genotyping, and genome-wide association studies (GWAS). These approaches are paving the way for the identification and deployment of multi-stress-tolerant genotypes. In addition, transcriptome and epigenome analyses are providing deeper insights into the gene expression patterns and regulatory networks involved in stress responses. Genetic transformation techniques are also emerging as powerful tools for functional gene validation and precise trait improvement in elite cultivars. Integration of these tools within national breeding programs represents a critical step toward developing climate-resilient sugar beet varieties. Among the most notable achievements is the development of Türkiye's first national sugar beet cultivars, Türkşeker 2023 and Türkşeker 2053, introduced to Turkish farmers in 2025. These varieties exemplify the successful integration of classical breeding with advanced molecular technologies, representing a significant milestone in domestic crop improvement. They not only demonstrate enhanced resilience to environmental stressors but also contribute to yield stability and sugar quality under increasingly variable climatic conditions. Additionally, advances in functional genomics and biotechnological tools such as CRISPR/Cas9 are opening new avenues for precise trait improvement and the validation of candidate genes in elite breeding lines.





## Crop Adaptation to Climate Change – Strengthening Crops for a Changing World

Supported by national research initiatives and public–private collaborations, these advancements reflect Türkiye’s proactive stance in adapting agriculture to climate change. This contribution highlights both the current progress and future directions of sugar beet biotechnology, underlining its strategic importance for sustainable and resilient agricultural systems.





***Triticum araraticum* as a Genetic Resource for Climate-Smart Wheat: Future Perspectives Including De Novo Domestication**

Hakan Özkan

*Department of Field Crops, Faculty of Agriculture, Çukurova University, Adana 01330, Türkiye*

**Abstract**

Wild genetic resources are pivotal for advancing crop evolution and breeding by expanding the genetic diversity of cultivated cereals. Turkey, a global hotspot for wild cereal relatives, harbors a rich array of species that exhibit valuable traits, such as tolerance to abiotic stresses like drought and salinity, resistance to biotic stresses including pests and diseases, and adaptability to diverse agroecological environments. Among these, *T. araraticum*, a wild tetraploid wheat, stands out for its unique genetic variation, offering significant potential to enhance modern wheat varieties for improved yield and resilience. This presentation will explore the genetic diversity of Turkey's cereal germplasm, with a particular focus on *T. araraticum*, and elucidate its applications in cereal breeding. By integrating these wild relatives into breeding programs, we can address challenges in crop improvement and support global food security through advancements in crop evolution studies.







**Beat the heat: What tomato evolution teaches us about plant thermotolerance mechanisms**

Sotirios Fragkostefanakis

*Molecular and Cell Biology of Plants, Institute of Molecular Biosciences, Goethe University Frankfurt, 60438, Frankfurt am Main, Germany*

**Abstract**

Plants have evolved a remarkable capacity to sense and survive elevated temperatures, but crop species differ greatly in their ability to cope with heat stress. Tomato, a globally important crop and a model for fleshy fruit development, provides unique insights into the evolutionary strategies that underpin thermotolerance. One example comes from the natural variation of the transcription factor HSFA2, which acts as a central hub in heat stress response. Allelic diversity in HSFA2 among tomato wild species and modern cultivars has shaped differences in acclimation capacity, enabling tomato cultivars to ensure long-term thermotolerance. This highlights how natural variation in regulatory genes contributes to adaptive resilience. A second story emerges from the recent discovery of a novel transcription factor that links heat stress to floral morphology in warmer climates. By modulating stigma exertion in response to high temperature, this regulator influences reproductive success under stress and opens new possibilities for breeding varieties with improved heat resilience. Together, these evolutionary lessons from tomato illustrate how genetic diversity in regulatory networks underpins both short- and long-term survival strategies, while providing novel targets for breeding programs aimed at sustaining crop productivity in a warming world.





## Tissue-Specific Mechanisms of Heat Stress Tolerance in Plants

Bernd Mueller-Roeber

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### Abstract

Plants are sessile organisms that must complete their life cycle in a fixed location, in some cases persisting for decades or centuries. To survive under fluctuating environmental conditions, they have evolved diverse molecular, cellular, and biochemical strategies. In the context of climate change, plants, including staple crops, are increasingly challenged by heat and drought. Securing future food production requires a deeper understanding of the mechanisms underlying stress resilience and the development of approaches to strengthen these adaptive traits.

As multicellular organisms, plants form specialized organs with distinct functions: leaves enable photosynthesis, roots provide anchorage and nutrient acquisition, and reproductive tissues ensure genetic transmission and yield. To maintain organ function under stress, plants rely on tissue- and organ-specific response programs. These mechanisms likely reflect evolutionary adaptations that optimize stress resilience across the whole organism.

Despite significant progress in identifying general pathways of stress perception and tolerance, knowledge of tissue-specific mechanisms remains limited. Emerging evidence suggests that stress responses in reproductive tissues, meristems, or vascular systems may differ substantially from those in photosynthetic or absorptive organs, with profound implications for productivity and survival.

In this presentation, I will emphasize the importance of considering tissue-specificity in plant stress biology. I will summarize current knowledge on organ-level responses to environmental stress, with a particular focus on heat tolerance, and highlight open questions that need to be addressed. Advancing this research will be critical for designing crops with enhanced stability under future climate conditions.





## Crop Adaptation to Climate Change – Strengthening Crops for a Changing World

### Genomics and NGTs for tomato fruit quality and increase resilience

Antonio Granell

*Instituto de Biología Molecular y Celular de Plantas, Consejo Superior de Investigaciones Científicas – Universidad Politécnica de Valencia, Spain*

Tomato Breeders and scientists face similar challenges as always, it only seems that the extent of the challenges seem to be more profound and occurring at a faster rate. Threats like Climate Change, emerging Pests and Diseases affect yield dramatically and the demand for more environmentally friendly cultural practices (ie less pesticides, herbicides and fertilizers) have then to be combined with strategies for increase productivity in low input conditions while increasing the fruit quality, nutritional, health and organoleptic tomato quality despite the increase in production costs. For this breeders need to use all the materials, knowledge and techniques available. It is important to realized that breeder have increasingly used knowledge to guide the breeding process and this reaches its acme point with new breeding techniques

A few examples will be present on how the use of new tools (genome), approaches (QTL mapping, genomics, reverse genetics) and knowledge / and data availability / gain from the use of natural diversity (genetic resources) or man- generated diversity have helped is helping to selected for the best alleles and combination to cope with those challenges. Examples will be presented on how new genomic techniques including genome editing, cisgenesis, intragenesis and transgenesis not only contribute to increase our understanding on gene to trait relationship but also provide us with plants with the desired traits with no linkage drag.





## **Genetic Improvement of Drought Adaptation in Cereal Crops**

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### **Abstract**

Drought is a significant agricultural risk factor exacerbated by global climate change. Significant differences exist in drought tolerance among different members of the plant kingdom, and transferring genes governing these differences to cultivated plants can reduce the severity of the negative effects of drought. Drought tolerance is a mega-trait determined by traits such as root system architecture, flowering time, stomatal aperture, osmotic adjustment, carbon isotope discrimination, high chlorophyll content, and cell membrane integrity. Improving drought tolerance can be achieved through a wide range of methods, ranging from classical plant breeding technologies to modern genetic engineering approaches. Using modern breeding approaches such as DNA markers and genetic engineering is particularly advantageous in breeding studies for drought tolerance, a quantitative trait influenced by numerous genes. While DNA marker technology could use genes from only close relatives of the crops, genetic engineering approaches involving transgenic and genome editing techniques can offer much more effective applications, such as overexpressing genes from distant sources. It appears that techniques such as RNA interference can be highly effective in improving drought tolerance, where epigenetic factors are also crucial. Our group has successfully improved drought tolerance in barley, a major cereal crop, by transferring three different quantitative trait loci into different varieties. In wheat, we are currently working on transferring four different drought tolerance genes to a Turkish wheat variety using functional markers. Considering that high temperature stress, in addition to drought, has caused significant losses in many crops, especially cereals, due to global climate change in recent years, it is highly beneficial to initiate studies on high temperature tolerance and/or integrate this trait into drought tolerance studies. Because the prediction of the extent of the drought in the future is difficult, it is urgent to initiate efforts to implement all agricultural production in climate-controlled production systems, such as vertical farming, where water can be used more efficiently and productivity is very high. Because this production system will have its own unique plant ideotypes, it would also be beneficial to initiate breeding efforts to develop the crop varieties used in these systems.





## Impact of Sucrose Supply on Chilling Tolerance in Tomato Seedlings\*

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**Key words:** carbohydrate-active enzymes, carbohydrate-related genes, low temperature stress, seedling tolerance, sugar metabolism, *Solanum lycopersicum* L.

### Abstract

Tomato plants are subjected to cold temperatures during various growth phases. Although studies have suggested that sugars may be linked to cold stress (chilling and frost stress) tolerance, the mechanism by which sugars influence plant cold tolerance remains unknown. In this study, we tested whether providing plants with exogenous sucrose could improve their ability to cope with chilling conditions. Tomato seedlings of the cultivar ‘Gülpembe’ were supplied with different concentrations of sucrose and then exposed to chilling stress for three days. Ion leakage, carbohydrate metabolites (sucrose, glucose, fructose, maltose), starch, and the activities of five key enzymes (acid invertase, neutral invertase, sucrose synthase, sucrose phosphate synthase, and  $\beta$ -amylase) were evaluated. In addition, the expression of sucrose phosphate synthase and  $\beta$ -amylase-related genes (BAM1, BAM3) was analyzed at 48 and 72 hours. The findings revealed that sucrose supply altered carbohydrate metabolism at both enzymatic and transcriptional levels, implying a function for sucrose in stress responses. Overall, these findings highlight the potential contribution of sucrose to chilling tolerance mechanisms in tomato seedlings.

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## Genome Editing Approaches in Tomato: Insights from CRISPR Applications

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**Keywords:** CRISPR/Cas, tomato genome editing, stress resistance, nematode resistance, *Tuta absoluta*, grafting, genome-edited plants

Tomato (*Solanum lycopersicum*), an essential horticultural crop and a model for fruit development studies, has become a leading system for genome editing research. Conventional breeding and mutagenesis have contributed to tomato improvement, yet their limited precision has accelerated the adoption of CRISPR-based tools. These technologies provide efficient, targeted, and cost-effective strategies for crop modification and adaptation under environmental challenges. We have validated the functions of key regulatory genes in tomato using CRISPR systems, demonstrating their critical roles in stress response and development. Recent works extend beyond single-gene studies: for example, CRISPR-Combo technologies and ACT3-based approaches have been applied to enhance resistance against major threats such as root-knot nematodes and *Tuta absoluta*. These strategies illustrate the potential of multiplex editing and advanced CRISPR platforms to engineer broad-spectrum resistance. In addition, innovative methods have been introduced to overcome bottlenecks in plant regeneration. By employing mobile carrier elements and grafting-based delivery, genome-edited tomato plants can be obtained while bypassing traditional tissue culture stages. This approach not only increases efficiency but also provides a path toward transgene-free edited plants with direct agricultural applicability. Together, these advances highlight the transformative potential of CRISPR technologies for precise trait improvement, disease resistance, and the development of climate-resilient tomato varieties essential for future food security.





## CRISPR-Mediated Genome Editing as a Strategic Tool for Enhancing Biotic Stress Tolerance in Crops Under Climate Change and Global Warming Scenarios

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**Keywords:** Biotic stress, CRISPR, Global Warming, pathogen resistance

### Abstract

Global warming has emerged as one of the most significant challenges to agriculture in the twenty-first century. Rising global temperatures, shifting precipitation regimes, and the growing frequency of extreme weather events are profoundly altering crop growth, development, and yield stability across diverse agroecological regions. Beyond their direct impact, climate change also intensifies biotic stresses, including viral, bacterial, and fungal pathogens, as well as insect pests and parasitic weeds. Warmer climates and altered rainfall patterns frequently expand the geographic range and severity of these threats, creating novel challenges for farmers and breeders. The effects of biotic stressors highlight the urgency of developing resilient crop varieties and sustainable production systems to ensure global food security under rapidly changing environmental conditions.

Addressing these challenges requires innovative approaches that go beyond the limits of conventional breeding. Unlike traditional mutagenesis or transgenic methods, CRISPR enables precise, efficient, and relatively low-cost modifications in plant genomes, allowing scientists to dissect complex regulatory networks and design crops with enhanced tolerance to both abiotic. The technology allows targeted inactivation of susceptibility (S) genes, precise editing of resistance (R) genes, and modulation of gene expression to strengthen plant defense responses. Moreover, the speed and accuracy of CRISPR greatly accelerate the functional validation of candidate genes, significantly reducing the time required to transfer laboratory discoveries into practical breeding outcomes.

This presentation will highlight several successful and ongoing applications of CRISPR in addressing biotic stress under the context of global warming. In sugar beet, CRISPR/Cas systems have been used to develop resistance against curly top virus, a severe pathogen whose incidence is increasing under warmer climates. In sunflower, targeted editing approaches are being applied to improve resistance against broomrape (*Orobancha cumana*), a parasitic weed that causes devastating yield losses in many production regions. In addition, CRISPR has been employed to generate loss-of-function mutations in MLO genes, a well-known strategy to confer durable resistance against powdery mildew and other fungal pathogens across multiple crop species. These examples demonstrate the versatility of genome editing tools in tackling a wide spectrum of biotic stresses that are aggravated by climate change. These innovations highlight the potential of genome editing as a cornerstone technology for sustainable agriculture in the era of global warming.







## Comparison of Heat Inducible Promoters for Biotech Approaches in Sugarcane Improvement

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### Abstract:

Sugarcane is a prime target crop to drive the emerging bioeconomy due to its efficient photosynthesis and enormous biomass production. Sugarcane stems are able to accumulate high levels of sucrose that can be diverted to alternative carbon products by metabolic engineering. We recently developed oilcane, a genetically modified sugarcane that was engineered to significantly enhance its capacity to accumulate triacylglycerol (TAG) in its vegetative biomass. Inducible expression system provides the flexibility to turn on/off the gene expression at will and at a time when critical stages of plant development are already completed. Sugarcane tolerates elevated temperatures up to 45°C for an extended period of time. Therefore, our objective was to explore the combination of heat inducible and constitutively expressed lipogenic factors to accelerate DTBL cycles in oilcane metabolic engineering. Spatial and temporal control of transgene expression are critical for both transgene and agronomic performance. Inducible promoters allow transgene expression at will, which is of particular importance when synergism between several factors needs to be explored. Therefore, our objectives were to: (1) compare leakiness, activation temperature and activation level of different heat inducible promoters at the transcriptional and the translational level in sugarcane leaf, stem, and root; (2) exploit the heat inducible promoters to drive lipogenic transcription factor (LTF) in oilcane metabolic engineering and (3) used heat inducible excision of CRISPR editing tools with site specific cre/lox recombination to minimize off-target effects. The heat inducible promoters driving  $\beta$ -glucuronidase (GUS), cre-recombinase or LTFs, along with *nptII* selectable marker were delivered to sugarcane calli via biolistic transformation, followed by selection and plant regeneration. Data describing GUS protein expression in sugarcane leaf, stem, root before and after the heat induction, the GUS/TF transgene expression, lipid content with and without the heat induction, CRISPR editing and transgene excision will be reported.







## Ameliorative effects of strigolactone on tolerance to lead stress on lettuce (*Lactuca sativa* L.) plants

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**Keywords:** Phytohormones, antioxidant metabolism, nitrogen metabolism, gene expression levels

### Abstract

Among all heavy metals, lead (Pb) is known as a persistent heavy metal that has a significant toxicological effect on ecosystems. Mobility of Pb from soil to plant system is a major concern for its bioaccumulation in plants and its stability in the food chain which may eventually disrupt the related biosystems. Strigolactones (SLs) play an important role in imparting tolerance ability to various abiotic stresses in plants. The study was carried out to determine the effects of external applications of SL (0, 10 and 20  $\mu$ M) at different doses on plant development and some physiological, biochemical and molecular levels under Pb stress [ $\text{Pb}(\text{NO}_3)_2$  (0 and 300 ppm)] on lettuce. At the end of the experiment, it was determined that Pb stress negatively affected plant growth, but SL applications positively affected plant growth both under normal and Pb stress. While Pb stress increased the electrical conductivity (EC), malondialdehyde (MDA) and hydrogen peroxide ( $\text{H}_2\text{O}_2$ ) content, SL applications caused a decrease in these parameters. Pb stress also negatively affected the amount of chlorophyll, whereas SL applications reduced this negative effect. Pb stress caused an increase in superoxide dismutase (SOD), catalase (CAT), peroxidase (POD) ascorbate peroxidase (APX), glutathione reductase (GR), glutathione s-transferase (GST) activities and Glucose-6-Phosphate Dehydrogenase (G6PD), 6-Phosphogluconate Dehydrogenase (6GPD). SL treatments significantly increased the activity of antioxidant enzymes in both control and Pb stress conditions. However, Pb stressed plants had lower nitrate reductase activity (NRA) than the control plants while SL treatments increased NRA compared to the non-treatments. Pb stress significantly reduced the uptake of essential nutrients in lettuce seedlings, whereas exogenous SL applications improved nutrient accumulation, particularly under Pb-stressed conditions. Additionally, mRNA expression profiles of nine stress-related genes in different tissues of lettuce were determined. Only Pb stress significantly decreased the expression of genes, particularly *LsCCD8* and *LsD14*, in both tissues. The combined Pb and SL treatment significantly increased the expression of *LsMAX2* in both tissues. These results suggest that exogenous SL applications can be an effective strategy to mitigate Pb-induced stress in lettuce by enhancing plant tolerance at physiological, biochemical, and molecular levels.





## Determination of the contribution of humic substances to plant growth in lettuce under flooding conditions

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**Key words:** flooding, lettuce, humic acid, fulvic acid, stress

### Abstract

In some regions of our world, where the effects of climate change are felt severely, flooding resulting from heavy rainfall damages crops in plant production and causes major economic losses. Various practices are being considered to help plants recover quickly and continue growing after flooding. Therefore, this study examined the effects of humic substances on lettuce that has experienced flooding. The effects of humic acid and fulvic acid applied to plants before and after flooding were investigated on plant morphology, physiology, biochemistry, and mineral nutrient content. While plant height, plant diameter, stem diameter, plant fresh and dry weight, root fresh and dry weight, chlorophyll (a, b and total) content and mineral content decreased significantly with flooding, the effects of humic acid and fulvic acid were similar in terms of these parameters and alleviated the damage by increasing in both applications compared to the control. With stress, an increase in H<sub>2</sub>O<sub>2</sub>, MDA, proline and antioxidant enzyme activity was observed and the increase in humic substances was evident. In the study, it is thought that humic substances are effective in reducing the flooding effect and promoting plant growth after stress, and that humic acid and fulvic acid have almost similar effects, and therefore both can be easily used in this sense.





**Involvement of MYB transcription factors in biotic and abiotic stress response in plants and the expressions analysis of some tomato MYBs in response to Tomato spotted wilt virus and drought stress**

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**Key Words:** Tomato, TSWV infection, Drought stress, MYB Transcription Factors, Gene expression

**Abstract**

Abiotic and biotic environmental stresses are the major factors adversely affecting the plant production. The climate changes associated with global warming further increased the frequency, severity and duration of these stresses. Plants developed different coping and adaptation mechanism to survive these stresses. Plants response to biotic and abiotic stresses activates similar pathways and interactions and cross talks between these pathways are common. In recent years, several molecular networks have been identified, including perception of stress, signal transduction, regulatory elements and molecular mechanisms involved in the response to abiotic and biotic stresses in plants. Molecular and biochemical pathways involve in abiotic biotic stress pathways are regulated by transcription factors (TFs) such as WRKY, NAC, bZIP, AP2 and MYB. Among these MYB TFs play a key role in regulation of growth and development as well as plants' response both abiotic and biotic stresses. Tomato is one of the most economically important agricultural crops faced with many abiotic and biotic stresses drought and Tomato spotted wilt virus (TSWV). About 140 MYB TFs encoded in tomato genome and some of these MYBs shared functional homology with MYBs involved in abiotic and or biotic stresses in other plants. In this study, some tomato MYB TFs including *S/MYB44*, *S/MYB73*, *S/MYB96*, *S/MYB101* were selected and their expression in response to TSWV infection, and drought stress as well as combination of TSWV infection and drought stress were evaluated into different tomato cultivars showing differential resistance to TSWV and drought stress. Seedlings of both cultivars were inoculated with TSWV or treated with drought separately or seedlings were first inoculated with TSWV and then treated with drought. The leaf samples were taken from tomato seedlings on the 7., 14. and 21. days of TSWV infection and on the 0., 3., 5. and 7. days of drought treatment and TSWV and drought treatments. Changes in gene expression levels were determined by real-time RT-PCR using  $2^{-\Delta\Delta CT}$  method. As a result, some changes were observed in the expression of *S/MYB44*, *S/MYB73*, *S/MYB96*, and *S/MYB101* in response to virus inoculation or drought or combination of both stresses.





## Sequential cold and heat stresses establish an intergenerational stress memory in rapeseed (*Brassica napus* L.)

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**Keywords:** *Brassica napus*; Temperature stress; Cross-tolerance; Priming; Intergenerational stress memory

### Abstract

Plants frequently experience temperature extremes that threaten growth and reproduction, yet their ability to retain and transmit stress responses across generations remains poorly understood. In this study, we investigated whether early cold exposure primes rapeseed seedlings for enhanced heat tolerance and whether such effects are inherited by the next generation. Seedlings were subjected to cold stress (4 °C for 3 weeks), heat stress (38 °C for 2 days), or sequential cold followed by heat stress. Control plants were grown under optimal conditions. We evaluated physiological, biochemical, and molecular traits in both the treated plants and their first-generation progeny.

Temperature stress influenced flowering time, seed weight, seed oil content, and fatty acid composition. Genes involved in fatty acid metabolism, including *BnaFAD2*, *BnaFAD5*, *BnaFATB*, *BnaMCOA*, and *BnaWD40*, were differentially expressed. In the progeny of sequentially stressed plants, total phenolics, flavonoids, antioxidant activity, chlorophyll content, fresh seedling weight, and leaf relative water content were significantly elevated, indicating the presence of intergenerational stress memory.

Our findings show that sequential cold – heat stress not only enhances immediate stress tolerance but also induces heritable metabolic and physiological adaptations. These results provide new insights into the mechanisms of cross-tolerance and the potential for exploiting intergenerational stress memory in crop improvement.





**Precision Plant Editing: From Barley to Amaranth with CRISPR in Hand**

Goetz Hensel

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**Abstract**

Targeted mutagenesis and gene editing employing customised endonucleases, such as CRISPR/Cas technology, have become the preferred methods for functional genomics and crop improvement, including barley and amaranth. While barley is one of the main European crops, amaranth, despite its numerous favourable properties, remains an orphan crop. Barley boasts a longer history of successful genetic transformation and precise mutagenesis, whereas amaranth still lacks such tools. The talk will discuss tools developed and supported by examples that address genes involved in plant architecture, stress tolerance, and pigmentation.





## Decrypting the plant oxidative stress response

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### Abstract

Reactive oxygen species are produced metabolically when excessive energy input exceeds the reducing potential. It is now widely recognized that plants adopted fluctuating perturbations in hydrogen peroxide (H<sub>2</sub>O<sub>2</sub>) homeostasis as a first line alerting and signaling system to adjust organellar and cellular metabolism during stress conditions. Unfortunately, our understanding of the signaling network that governs H<sub>2</sub>O<sub>2</sub> sensing, transduction and eventually trigger transcriptional response remains fragmentary. Earlier transcriptomic and genomic-centered studies, provided us first with extra insights in the regulatory networks that govern the oxidative stress response. Recently, tailoring various proteomics technologies allowed us to assess oxidative stress dependent changes at the posttranslational level. Through combined multi-omics efforts, we aim towards a better understanding of how cells interpret the oxidative signals that arise from developmental cues and stress conditions.





**Unraveling plant responses to multifactorial stress combinations under climate change scenarios**

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**Abstract**

Each year, abiotic stress conditions such as drought, heat, salinity or high light intensity, together with the harsh soil conditions due to the human activity (herbicides, pH changes or different contaminants such as microplastics), and especially their different combinations (*i.e.*, multifactorial stress combinations, MFSC), inflict a heavy toll on crop productivity worldwide. The effects of these adverse conditions on plant efficiency are becoming even more alarming in recent years in light of the increased rate and intensity of global climatic changes. Improving crop tolerance to abiotic stress conditions requires a deep understanding of the response of plants to changes in their environment and especially to combinations of many of them. Our work aims at establishing a comprehensive framework for identifying key stress regulatory networks and/or metabolic pathways to enhance tomato tolerance to MFSC. By using omics correlation analysis, our work uncovers functional links among hormone signalling, photosynthetic efficiency, and key MFSC-related transcripts and metabolic hubs in tomato plants. Together, we reveal a coordinated and complexity-dependent molecular program in tomato, offering new insights into plant adaptation to MFSC and identifying candidate regulatory and metabolic markers for engineering climate-resilient crops.







## Computational and Machine Learning Models for Optimizing Germination Unders Cold Stress Conditions of Common Bean with Titania (TiO<sub>2</sub>) Nanoparticles

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**Key words:** Taguchi, Response surface methodology, Machine learning, common bean, Stress.

### Abstract

Common bean (*Phaseolous vulgaris*) is an important edible legume that is sensitive to cold stress especially at germination and seedling stage leading to low germination and seedling vigour. Application of external stimulants can help to alleviate cold stress in plants at early stages. Titanium dioxide (TiO<sub>2</sub>) is one of the nanoparticles that can be used for this purpose. In this study, different concentration of TiO<sub>2</sub> (0, 50, and 100 mg/L) were added in the Murashige and Skoog (MS) medium. Surface sterilized seeds were cultured on the TiO<sub>2</sub> enriched medium and transferred to 0 and 4 °C for 120 and 240 hr followed by transfer to growth room automated at 24 °C. The germination data was recorded on the daily basis and analyzed by GerminAR package using R-statistical program. Nine different germination parameters named germination percentage (grp), mean germination time (mgt), mean germination rate (mgr), germination speed (gsp), uncertainty (unc), synchronization (syn), coefficient of variation in germination time (vgt), seedling vigour (sdg), and coefficient of velocity of germination (cvg) were analyzed by Taguchi design and response surface regression analysis (RSRA). Results of Taguchi design revealed Temperature-time- TiO<sub>2</sub> as most significant factor based on signal to noise (S/N) ratio. Whereas RSRA revealed the significant impact of TiO<sub>2</sub>, time, and TiO<sub>2</sub> x time on grp and mgr. Whereas TiO<sub>2</sub> x time was found significant for mgt and cvg. The unc factor was also regulated by temp., time and temp. x time. The results were also analyzed with ML models using multiple metrics which revealed the variable prediction accuracy of all germination parameters. This study allows to understand the germination pattern under cold stress conditions and can be used for testing other crops.







## Inhibitory effect of exogenous methionine on drought stress in tomato seedlings

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**Keywords:** amino acid, stress, water, tomato, methionine

### Abstract

Drought is one of the most frequently discussed issues that poses a threat to the future of the world, especially because of the damage it causes to agricultural production. Researchers are working on alternatives for areas and situations where water is scarce in crop production. One of these is exogenous plant treatments. Methionine has also recently begun to be used for this purpose. In this study, which investigated the effects of different doses of methionine, an amino acid, on plant growth and development in water-deficient tomato seedlings, solutions prepared in 3 doses as 0, 10 mg/L and 20 mg/L were applied as sprays to the leaves, and the plants were irrigated at 100% of the field capacity (control) and 60% of the field capacity to create drought stress. Water stress reduced plant height, stem diameter, and leaf area by 22%, 5%, and 32%, respectively, while methionine application showed higher values for these parameters under both normal and water stress conditions. Water stress also reduced plant fresh weight, root fresh weight, plant dry weight, and root dry weight by 38%, 8%, 32%, and 5%, respectively. Methionine application increased these parameters, but the decrease under stress was less pronounced. In the study, water stress increased H<sub>2</sub>O<sub>2</sub>, MDA, proline, and sucrose contents, and CAT, POD, and SOD enzyme activities, while these parameters varied with methionine applications. Furthermore, methionine application under drought stress resulted in increased expression levels of the *SISOD*, *SIHKT1.1*, *SIPRI*, *SILOXI*, *SIWRKY8*, *SIWRKY31*, *SIP5CS*, and *SICAT* genes in tomato shoot tissue compared to controls. The study results indicate that methionine may play an important role in providing water stress tolerance, and its effectiveness varies among doses. It is thought that further studies are needed to detail the mechanism of action.





**Planetary Resilience by Design: Pan-Omics and AI-Driven Gene Editing for Climate-Smart Crop Breeding Roadmap to 2075 beyond Europe's Green Deal**

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**Keywords:** pangenomics, artificial intelligence, life cycle analysis, gene editing, speed breeding, Green Deal, Pan-Eco-Genome platform

**Abstract**

As climate volatility escalates, Europe's 2030 Green Deal and 2050 climate neutrality targets necessitate a transformative shift in crop breeding, toward systems intentionally engineered for planetary resilience. This review introduces a visionary 2075 roadmap grounded in Planetary Resilience by Design (PRD), integrating pangenomics, multi-omics, AI-guided gene editing, and speed breeding within a unified, data-centric breeding pipeline. We present the Pan-Eco-Genome platform, an innovative framework for constructing annotated pan-genomes of crops and their wild relatives, enriched with sustainability metrics such as carbon/water footprints and nutrient use efficiency, thus aligning precision breeding with planetary boundaries. Key components include: (1) structural variant discovery across pan-genomes to identify resilience alleles; (2) integrated multi-omics atlases, spanning transcriptomics, epigenomics, phenomics, and single-cell omics, to decode genotype-to-phenotype links; (3) AI-driven CRISPR-CasX base and prime editing to rewire metabolic hubs for abiotic stress tolerance and enhanced nutrition; (4) speed breeding factories equipped with digital twins simulating future climates; (5) life cycle analysis (LCA)-embedded selection to promote low-GHG, soil-regenerative, circular bioeconomy traits. We propose digitally powered breeding hubs combining phenotyping, omics, and in silico design to compress cultivar development cycles to under five years. Case studies, including perennial wheat and nitrogen-efficient barley, demonstrate practical feasibility. We assess enabling EU regulatory frameworks, such as the Revised GMO ED Policy, facilitating precise and ethical gene editing. Finally, we chart a policy–science roadmap: omics node development (2025–2040), integrated breeding hubs (2040–2060), and monitored field deployment (2060–2075), culminating in resilient, climate-smart crops ethically aligned with sustainability, equity, and food security goals.





## Microorganisms and Biofertilizers: Eco-Friendly Approaches for Sustainable Agriculture

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**Keywords:** Climate change, sustainable agriculture, biofertilizer, microorganisms.

### Abstract

The increasing global demand for food, coupled with the negative impacts of chemical fertilizers on soil quality and the environment, has created an urgent need for sustainable agricultural practices. Microorganisms, due to their metabolic diversity and ecological significance, are key players in developing biofertilizers that provide an eco-friendly alternative to conventional inputs. Beneficial microbes such as nitrogen-fixing bacteria (e.g., *Rhizobium*, *Azotobacter*), phosphate-solubilizing microorganisms, potassium-mobilizing bacteria, and mycorrhizal fungi have the potential to enhance nutrient cycling, improve soil fertility, and stimulate plant growth through natural processes. Unlike chemical fertilizers, biofertilizers not only supply essential nutrients but also contribute to maintaining soil microbial diversity, improving soil structure, and reducing greenhouse gas emissions and water contamination. Furthermore, biofertilizers strengthen plant resilience to biotic and abiotic stresses, thereby supporting sustainable crop production under changing climatic conditions. Recent advances in microbial biotechnology, including the use of microbial consortia and genetic engineering, have further expanded the efficiency and applicability of biofertilizers in modern agriculture. This presentation will provide an in-depth overview of the functional roles of microorganisms in biofertilizer development, highlight case studies of successful applications in different cropping systems, and discuss the challenges and future prospects of integrating biofertilizers into large-scale sustainable farming practices.





**The Effect of ACC deaminase-producing rhizobacteria on almond tree performance under drought stress: Revealing physiological, biochemical, and molecular mechanisms**

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**Key words:** PGPR, drought, almond, morphological, physiological, biochemical, transcriptome

**Abstract**

Drought is one of the major constraints to crop production and food security worldwide. This increases the need for environmentally sustainable solutions to ensure global food security. In this context, the application of plant growth-promoting rhizobacteria (PGPR) becomes important for beneficial plant and environmental health. PGPRs living in plants growing under harsh ecosystems help in tolerance to abiotic stress factors by positively influencing plant physiology, development and environmental adaptation. PGPRs increase the tolerance of plants to drought through changes in the morphology and architecture of the root system, production of phytohormones, accumulation of extracellular polysaccharides, ACC 1-(aminocyclopropane-1-carboxylate) deaminase, volatile chemicals and osmolytes. In addition, PGPRs strengthen the antioxidant defense system and induce transcriptional regulation of stress response genes. This study involves four different applications using Makako/GF677 almond trees: Control (i.e., irrigated farming), control + bacteria, drought (i.e., dry farming), and drought + bacteria. As a bacterial application, the ACC deaminase-producing *Aeromonas hydrophila* iehthiosmia AE425 rhizobacteria strain is used. The study includes drought conditions, where only rainwater is used, and a control application corresponding to the amount of evaporated water. The effects of bacterial applications on almond trees under drought stress is examined morphologically, physiologically, and biochemically. In order to determine the effects of the treatments within the scope of the study, important morphological criteria such as trunk cross-sectional area, shoot length, and leaf area are examined. In addition to biochemical analyses such as malondialdehyde, hydrogen peroxide, and proline, physiological parameters related to stress, such as leaf water potential, photosynthesis, and stomatal conductance, are also be examined. Additionally, on a molecular level, transcriptomic profiling is performed on samples taken from the root and leaf tissues of the plants, aiming to provide a new perspective





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on almond tree molecular breeding studies by identifying potential drought-related genes. As a result, the study aims to uncover the relationship between almond trees, drought, and PGPR, and to investigate the compatibility of morpho-physiological data with data obtained from transcriptomic analysis.





## Unrevealing microRNA Roles in Maize (*Zea mays* L.) Leaf Growth Response to Chilling Stress by miRNomics and VIGS-based STTM approach

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**Keyword:** Maize, miRNomics, Virus Induced Gene Silencing, Short Tandem Target Mimic

**Abstract:** Maize (*Zea mays* L.) is the third most consumed crop worldwide, being used as food, feed, and industrial raw material. However, due to its tropical origin, maize is highly sensitive to low temperatures during seed germination and the seedling stage, resulting in growth reduction and yield loss. Although the effect of low temperature on the morphology and physiology of maize has been well-studied, the genetic regulation behind leaf growth under chilling stress is poorly understood. In this context, microRNAs (miRNAs), which are a class of small non-coding RNAs (~22 nt), gain attention due to their regulatory role in gene expression. Therefore, this study aims to evaluate the function of miRNAs in the maize leaf growth regulation under chilling stress. To this end, a miRNomics analysis was performed to assign the 321 known maize miRNAs to any growth processes, which are cell division, cell expansion, and cell differentiation, based on their expression profiles between the maize growth zones. Then, differentially expressed miRNAs were selected for in silico target prediction. For functional analysis, a candidate miRNA was transiently silenced by using virus-induced gene silencing (VIGS) combined with short tandem target mimic (STTM) approaches. To this end, STTM-miR408a/b was designed and synthesized for the treatment of maize seedlings subjected to chilling stress. As a result, STTM-miR408a/b-treatment successfully downregulated the expression of endogenous mir408a/b and antagonistically upregulated their predicted targets Basic Blue Protein (BBP) and Blue Copper Protein (BCP) in response to chilling. These caused a reduction of the elongation rate of the STTM-miR408a/b-treated second and third leaves by 10% and 19% leading to 19% and 11% shortening, respectively. On the other hand, there was no significant difference in the elongation rate and final leaf length of the maize seedlings under chilling stress between STTM-miR408a/b-treated and non-treated groups, pointing out the regulatory role of miR408 in leaf growth during stress tolerance. This study represented the efficiency of miRNomics and VIGS-based STTM approach for the functional study of maize miRNAs employed in leaf growth regulation under chilling stress.

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## Salinity tolerance of fast-growing *Salicaceae* species

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**Key words:** salt stress tolerance, bioenergy trees, *Salicaceae*

Soil salinisation is an important stress factor influencing plant growth and productivity. This study investigates the impact of sodium chloride (NaCl) salinisation on six clones of bioenergy trees, *Populus* and *Salix*, cultivated *in vitro*. Since different clones vary in their responses to salt stress, identifying salt-tolerant clones is an important biotechnological objective for biomass production on marginal saline soils, particularly in short rotations. This is also relevant for urban landscaping, where salt accumulation in soil can occur during winter due to the use of de-icing agents on roads and pathways.

Focusing on growth parameters such as shoot height, root number, plant status, and survival rate on the 30<sup>th</sup> day of growing under salt stress, a two-way ANOVA revealed that both salinity and genotype significantly influenced tree growth traits, with a stronger effect of salinity compared to genotype. Survival rate was the least sensitive trait, with significant differences from the control only observed at the highest salinity concentration (100 mM).

Salt tolerance varied among the studied clones of poplar and willow. The most salt-tolerant clones were common aspen (*Populus tremula*), hybrid aspen ‘INRA 353-38’, and the *Salix* clone ‘Olympic Fire’. The hybrid poplar *P. tremula* × *P. alba* cv. ‘INRA 7I7-1B4’ showed moderate salt tolerance. In contrast, the hybrid poplar *P. pyramidalis* × *P. laurifolia* cv. ‘Novoberlinska-7’ and the willow clone ‘Zhytomyrska-1’ were the least salt-tolerant, exhibiting growth inhibition even at the lowest sodium chloride concentration in the nutrient medium (25 mM).

The results obtained can be applied to the cultivation of fast-growing trees in short rotations for biomass production on marginal saline plots, as well as for urban landscaping. Clonal variability in response to salinisation could contribute to progress in the breeding of bioenergy trees for tolerance to this type of stress.





**Potassium Deficiency Induces *Cellulose synthase A 4* Expression in *Arabidopsis thaliana* and *Triticum aestivum***

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**Keywords:** *Triticum aestivum*, *Arabidopsis thaliana*, *Cellulose synthase A 4* (*CesA4*), potassium deficiency, and stem strength.

**Abstract**

Potassium (K) is essential for plant metabolism, playing a central role in the production and allocation of photoassimilates, osmoregulation, cell division, and enzyme activation. K is also known as the most abundantly accumulated nutrient in stems and is critical for stem strength and stability. Despite the significant role of K in stem stability, its impact on the production of lignocellulosic compounds and the underlying molecular mechanisms remain largely unexplored. This study investigated how the regulation of cellulose synthase genes, particularly *Cellulose synthase A 4* (*CesA4*), is associated with the K nutritional status of plants. The results obtained from this study showed that low K nutrition significantly enhances *CesA4* expression both in *Arabidopsis thaliana* and *Triticum aestivum* as revealed by phenotyping, elemental quantification using ICP-OES, and gene expression analysis using RT-qPCR. The results suggest that K deficiency induces *CesA4* expression in *A. thaliana* and *T. aestivum*, which might be one plausible molecular explanation for why plants are susceptible to lodging under low K nutrition. To our knowledge, this is the first evidence establishing a molecular link among K nutrition, cellulose synthesis, and stem stability.







## Drought Stress Mitigation via Plant-Endophyte Interactions\*

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**Keywords:** Endophytes; Abiotic stress; Drought tolerance; Climate change; Sustainable agriculture; Plant–microbe interactions

### Abstract

Climate change and global warming are reshaping environmental conditions in farming, making them increasingly unpredictable. Among the many stressors, drought is one of the most severe threats to plant development and crop productivity. Conventional mitigation practices rely heavily on chemical inputs, often generating undesirable side effects for ecosystems and human health. Against this backdrop, endophytic microorganisms — capable of forming symbiotic associations with plants — have attracted considerable interest as environmentally friendly and sustainable alternatives. By regulating phytohormone activity, maintaining osmotic balance, strengthening antioxidant defenses, and facilitating water and nutrient uptake, these microbes can substantially enhance plant tolerance to drought. This review discusses how endophytes contribute to abiotic stress adaptation under changing climatic conditions. Special attention is given to their molecular, physiological, and ecological roles in shaping plant responses to stress. In particular, their influence on water relations and osmotic adjustment under drought is emphasized. Current findings suggest that endophyte–plant partnerships hold significant promise as biotechnological tools for strengthening drought resilience in agricultural systems. A deeper understanding of these interactions will be vital for designing climate-resilient farming strategies, which, in turn, are crucial for safeguarding global food security in the decades ahead.

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## Investigation of The Effect of Melatonin And Endofithic Bacteria Administration On Salt Stress Tolerance In *Lotus corniculatus* Plants In Vitro Conditions

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**Keywords:** *Lotus corniculatus*, Melatonin, Endophytic bacteria, Salt stress

### Abstract

The use of melatonin and plant growth-promoting endophytic bacteria in improving plant stress responses is among the promising strategies for sustainable agriculture. This study aimed to investigate the effects of combined application of melatonin and endophytic bacteria on salt (NaCl) stress tolerance in *Lotus corniculatus* (bird's-foot trefoil) under in vitro conditions. *L. corniculatus* plants, grown under sterile conditions, were subjected to treatments including 1 and 5 mM melatonin, 75 and 100 mM NaCl, endophytic bacteria isolated from cacti, and combinations of these treatments. Morphological and physiological parameters (root and shoot length, fresh and dry biomass) as well as biochemical responses (malondialdehyde, reducing sugar, H<sub>2</sub>O<sub>2</sub>, and proline levels) were analyzed. In addition, the expression levels of stress related NAC and SOS genes were determined using real-time PCR (RT-PCR). The combined application of melatonin and endophytic bacteria enhanced plant growth and strengthened antioxidant defense mechanisms. The findings suggest that the combination of melatonin and endophytic bacteria may serve as an effective biological protection strategy against salt stress in forage crops such as *L. corniculatus*.





## **Utilization of Berry Crop Plant Genetic Resources to Cope with Changing Environment**

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During agricultural production, all crops face the effect of changing environment conditions due to climate change. These changes include extreme temperatures, frost and drought. For example, the Turkish temperate fruit production has suffered from the effect of an extreme late frost in 2025. The plants researchers are constantly working on the production techniques to mitigate the effects of the extreme conditions. Also, developing more resilient cultivars by breeding activities is one of the sustainable approaches to cope with changing environment.

The crop species are cultivated in their optimal conditions. As these conditions change, these crops are exposed to stress conditions. One of the models on global environment changes postulate that the average temperatures will rise 2 °C in a short time period. This rise would adversely affect strawberry production, for example, in several ways. However, when strawberry plant genetic resources are considered, they are sampled from Alaska to Patagonia where the average temperatures vary much more than 2 °C. Thus, utilizing progenitor species of cultivated strawberry in cultivar development offer a great potential to crop researchers. Introduction of day-neutrality trait in strawberry revolutionized the production by extending the harvesting season for example. Similar to strawberries, other berry species, blackberries, raspberries and blueberries offer source of resistance against abiotic stress conditions. Introduction of florican traits in brambles and cycle-flowering traits in blueberries are other examples to have great effects on production. In this talk, studies on sampling, evaluation and utilization of berry plant genetic resources will be discussed.





## Plant Cell Walls in a Changing Climate

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**Key words:** biotechnology, climate change, plant cell walls, plant stress

### Abstract

Climate change poses profound challenges to global agriculture, exposing crops to elevated temperatures, drought, salinity, and fluctuating CO<sub>2</sub> levels. Central to plant adaptation is the cell wall, a dynamic and polysaccharide-rich structure that not only maintains cellular integrity but also acts as a major sink for photosynthetically fixed carbon. Stress-induced remodeling of cell wall components—including cellulose, hemicelluloses, pectins, and glycoproteins—plays a pivotal role in regulating growth, photosynthesis, and stress tolerance. Elevated CO<sub>2</sub> can enhance photosynthetic rates and biomass accumulation, yet drought and salinity alter wall plasticity, while high temperatures disrupt polymer composition and integrity. Advances in biotechnology, including genome editing, synthetic biology, and cell wall-targeted engineering, offer strategies to enhance resilience by modifying wall composition and regulatory networks. Successful applications in cereals (rice, wheat, barley, maize) and dicots (soybean, tomato, cotton, brassicas) highlight the potential of targeted wall manipulation to improve tolerance against climate stressors. Integrating knowledge of carbon allocation, wall biosynthesis, and stress-responsive pathways will be critical for developing climate-resilient crops and sustaining agricultural productivity in the face of global warming.





## Genome-Wide Identification of *DELLA* Genes in Flax (*Linum usitatissimum* L.) and Determination of Physiological Responses to Drought Stress by GABA

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### Abstract

The goal of this study was to use bioinformatic approaches to identify *DELLA* genes that have not previously been studied in flax and to assess the effects of drought stress and exogenous Gamma-aminobutyric acid (GABA) treatments on flax's antioxidant defense system. Under stress conditions, five members of the *LuDELLA* gene family, which represses the gibberellin signaling pathway, were identified, and the presence of the characteristic *DELLA* signature motif in all members was confirmed. The *LuDELLA* genes were found to be localized on chromosomes 8, 13, and 14. Phylogenetic analyses demonstrated that *LuDELLA1*, *LuDELLA2*, and *LuDELLA3* clustered in the same group with Arabidopsis *AtRGL1*, *AtRGL2*, and *AtRGL3* genes, indicating close evolutionary relationships, whereas *LuDELLA4* and *LuDELLA5* clustered together in a separate group. Gene structure analyses revealed that all *LuDELLA* genes possess a single exon, although the exon architectures exhibited variability. Cis-acting regulatory element analyses indicated that these genes contain regulatory sequences associated with tissue-specific expression, hormonal responses, and various abiotic stress conditions. Protein-protein interaction network predictions suggested that *LuDELLA* proteins exhibit strong putative interactions with Gibberellin Receptor Proteins (GID1). Transcriptome analyses showed that *LuDELLA1-LuDELLA2* and *LuDELLA4-LuDELLA5* gene pairs display similar expression profiles, whereas *LuDELLA3* was not expressed in tissues other than leaves. Additionally, in drought-tolerant and sensitive flax varieties, proline, malondialdehyde, and superoxide dismutase activities-key components of the antioxidant defense system-were analyzed on days 0 (control), 1, 2, and 3 under drought stress and drought stress + 10 mM GABA treatments. The results demonstrated that the stress tolerance profile of the flax varieties, the applied treatments, and the duration and intensity of stress induced significant differences in the antioxidant defense system. Keywords: Flax (*Linum usitatissimum* L.), Drought stress, GABA, *DELLA* genes, Antioxidant defense

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## Genome-wide Analysis and Role of *miR167* and *miR398* in the Regulation of Cold Stress and Hydrogen Peroxide Acclimation in Tomato Plants

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**Keywords:** *Solanum lycopersicum*, cold stress, *Sly-miR167* and *Sly-miR398*, hydrogen peroxide pretreatment.

### Abstract

Cold stress is one of the important abiotic stresses that negatively affect plant growth and crop yield. Previous studies have shown that H<sub>2</sub>O<sub>2</sub> pretreatment in tomato plants (*Solanum lycopersicum* Mill) promotes cold acclimation. miR167 affects root and fruit development through the auxin response pathway, while miR398 helps manage oxidative stress by converting superoxide radicals. In this study, an *in-silico* genome-wide identification and characterization of members of the miR167 and miR398 families of tomato plants was performed, followed by the investigation of changes in gene expression after H<sub>2</sub>O<sub>2</sub> pretreatment. *In silico* analyses were performed using sequences from the pmIREN and snoRNA databases. Target genes, chromosomal localization, promoter elements, and phylogenetic relationships were then determined. The roots of H<sub>2</sub>O<sub>2</sub> acclimatized tomato seedlings (H2274) were immersed in a 1 mM H<sub>2</sub>O<sub>2</sub> solution for 1 h at 28°C. The stressed plants were incubated at 4°C for 16 hours, while the non-stressed plants were incubated at 28°C for the same period. The expression levels of *Sly-miR167* and *Sly-miR398*, along with biomarkers of oxidative stress (MDA levels, NBT staining), were examined using semi-quantitative polymerase chain reaction (qPCR). Analysis of the cis-regulatory elements within the *Sly-miR167* and *Sly-miR398* gene families has identified a total of 62 distinct cis-regulatory elements, including those responsive to abscisic acid, anaerobic conditions, light, auxin, MeJA regulation, low temperature, drought, and salicylic acid. H<sub>2</sub>O<sub>2</sub> acclimation decreased cold induced oxidative damage as evidenced by MDA levels in the leaves and roots of the seedlings. Expression analyses demonstrated that *Sly-miR398* exhibited an approximate 1.8-fold increase, while *Sly-miR167* demonstrated a 1.6-fold increase in leaf tissue of plants treated with H<sub>2</sub>O<sub>2</sub> and subjected to cold stress. Conversely, expression levels exhibited a decline in the root tissue. Hydrogen peroxide has been shown to facilitate the reprogramming of stress-responsive gene networks, thereby enhancing the plant tolerance to subsequent low temperature stress. The present study demonstrates that H<sub>2</sub>O<sub>2</sub> pretreatment mitigates cold stress-induced oxidative damage in tomato seedlings, and that miR167 and miR398 play a regulatory role in post-transcriptional responses during adaptation.







## Divergent Transcriptional Programs Underlie Salt Tolerance in *Solanum pennellii* Introgression Lines

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**Keywords:** tomato, salinity, *Solanum pennellii*, gene expression, transcriptional regulation

### Abstract

Soil salinity severely limits tomato (*Solanum lycopersicum*) productivity, but its wild relative *Solanum pennellii* carries alleles that enhance tolerance. To dissect transcriptional mechanisms underlying salt adaptation, we compared gene expression responses to severe stress (200 mM NaCl) in the cultivated parent M82 and two contrasting *S. pennellii* introgression lines (ILs): IL2-5 and IL7-4-1. IL2-5 maintained low toxic ion levels and essential ion balance with sustained shoot and root growth, whereas IL7-4-1 showed a high-root phenotype with elevated ion accumulation, representing fundamentally different responses to salinity stress.

IL2-5 showed strong up-regulation of vacuolar ion transporter genes (*NHX1*, *NHX3*) and the Na<sup>+</sup>/K<sup>+</sup> transporter *HKT1.2*, supporting an ion exclusion strategy. Among antioxidant genes, *APX1* was induced, while *CAT1* and *GST* had lower expression levels relative to M82. ERF and WRKY transcription factors displayed a dampened response, suggesting that IL2-5 displaying a limited activation of downstream stress signalling.

In contrast, IL7-4-1 adopted a tolerance strategy despite high Na<sup>+</sup>/Cl<sup>-</sup> accumulation. This line up-regulated *SOD* and *NHX3*, consistent with enhanced ROS detoxification and vacuolar sequestration to preserve shoot biomass. Furthermore, higher expression of *WRKY8*, *WRKY39*, and *ERF80* indicated strong activation of stress-responsive transcriptional networks, reflecting a more severe stress perception.

These contrasting expression patterns reveal two divergent molecular strategies. IL2-5 minimizes stress impact through ion exclusion and limited stress signalling activation, whereas IL7-4-1 tolerates high ionic loads by activating antioxidant defence along with strong stress signalling induction. Together, these findings highlight the diversity of salt response and tolerance mechanisms encoded by *S. pennellii* alleles and their potential utility for breeding salt-resilient tomatoes.







## Determination of the Effects of Global Climate Anomalies on Apricot Orchards in Malatya Province

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**Keywords:** Malatya, Apricot, Climate change

### Abstract

Although it is not the genetic homeland of apricots, Malatya is the province with the highest production of dried apricots worldwide. It accounts for approximately 53% of global dried apricot production and stands out with an average annual production of 76,926 tons. Apricots are a product of strategic importance for the agricultural sector. However, due to the negative environmental factors caused by climate change, which has become increasingly apparent in recent years, they are subject to various physiological disorders. Late spring frosts in the Malatya region cause partial or total damage in certain areas every year. The frost event that occurred in April 2025 caused a much higher level of crop loss compared to previous years and caused serious damage to the morphological structures of the trees. This extreme frost event, which occurred on April 12 in particular, caused serious damage to apricot trees at different phenological stages (bud, flower, small fruit, and green fruit stages) depending on topographical differences. These damages manifested as a decrease in photosynthetic capacity, water balance disorders, irregularities in carbohydrate metabolism, and a decline in shoot development. These physiological disorders are thought to not only reduce the yield of the current year but also negatively affect tree development and yield potential in future years. On the night of April 11/12, 2025, the temperature dropped to -13.6 °C, and a severe frost lasting 10–12 hours occurred. Field studies of apricot trees revealed necrosis and browning of leaves; necrotic leaves were observed to remain mummified on branches, with leaf formation restarting approximately 20–30 days later with the emergence of new leaf buds. During August (depending on growing conditions), the leaves showed chlorosis and some trees were found to be dry. Samples taken from damaged shoots were examined under an electron microscope, revealing structural changes in the vascular bundles. Garden owners whose trees were recorded were advised to regularly perform plant nutrition and cultural maintenance procedures. It was emphasized that these practices are directly related to the healthy development of leaf buds formed on shoots, the support of chlorophyll synthesis, and the formation of a full green color in the leaves. As a result, it is thought that agronomic interventions that promote physiological and morphological development may increase the yield potential for the following year. In the 2026 studies, it is planned to conduct phenological observations of the trees and determine the yield per tree. The findings obtained from the observations are aimed to be presented in a scientific report format to reveal the effects of climate change on apricot trees.





## Effects of dopamine on reducing salt stress damage in pepper (*Capsicum annuum* L.) at morphological, physiological, biochemical and molecular levels

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**Keywords:** Pepper, salt stress, dopamine, plant growth, physiological and biochemical responses, gene expression

### Abstract

Salt stress is a major environmental challenge that significantly reduces agricultural productivity, particularly in arid and semi-arid regions. Excessive sodium chloride (NaCl) accumulation in soil negatively affects plant growth, physiological functions, and biological processes. Dopamine, a catecholamine neurotransmitter, has emerged as a potential regulator of plant stress responses. This study aimed to investigate the effects of exogenous dopamine on salt stress tolerance in pepper (*Capsicum annuum* L.) by examining morphological, physiological, biochemical, and molecular responses. Pepper seedlings were subjected to 100 mM NaCl stress and treated with dopamine at concentrations of 50, 100, and 200  $\mu$ M. Dopamine application, particularly at 100  $\mu$ M and 200  $\mu$ M concentrations, significantly improved plant growth parameters, including height, stem diameter, leaf area, and biomass accumulation. It enhanced photosynthetic efficiency by increasing chlorophyll content, stomatal conductance, and transpiration rate, while reducing oxidative stress markers such as H<sub>2</sub>O<sub>2</sub> and MDA. Dopamine also regulated the activity of antioxidant enzymes (SOD, CAT, and POD) and maintained ion homeostasis by reducing sodium (Na<sup>+</sup>) and chloride (Cl<sup>-</sup>) accumulation and promoting potassium (K<sup>+</sup>) and calcium (Ca<sup>2+</sup>) uptake. At the molecular level, dopamine influenced the expression of genes involved in ion transport (AKT1, HKT2;1, and HKT2;2) and photosynthesis (psb). This study demonstrates that dopamine is a promising plant growth regulator that enhances salt tolerance in pepper plants. It achieves this by improving growth, photosynthetic efficiency, antioxidant defense, and ion homeostasis, while modulating key molecular pathways. These findings suggest that dopamine could be utilized as a sustainable strategy to mitigate salt stress and improve crop productivity in saline-affected agricultural regions. Further research is needed to explore its application in other crops and under field conditions.





## Determination of Groundwater Microbial Diversity by Metabarcoding Approach and Potential Use in Agricultural Applications

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**Keywords:** eDNA, groundwater, metabarcoding, microbiota, agricultural biotechnology, Clostridia, Proteobacteria.

### Abstract

**Introduction:** Groundwater plays a pivotal role in public health and agriculture. It serves as a vital source of potable water and irrigation, facilitating the sustenance of ecosystems. The presence of microbial diversity within groundwater underscores its significance, as it serves as a conduit for the transportation of these microorganisms. In recent years, environmental DNA (eDNA) and 16S rRNA-based metabarcoding analyses have facilitated our understanding of microbial diversity in these environments at the molecular level. From the standpoint of agricultural biotechnology, the presence of microorganisms in groundwater has the potential to confer beneficial properties, including nitrogen fixation, phosphorus solubilization, biopesticide production, and the release of plant growth-promoting substances.

**Materials and Methods:** In this study, eDNA was extracted from a groundwater sample collected from the Kahramankazan district of Ankara. The eDNA was then subjected to 16S rRNA gene amplification targeting the V3-V4 regions. The amplified DNA was subsequently sequenced using Illumina technology. The raw data were filtered and taxonomically classified using QIIME2 and analogous bioinformatics tools.

**Results and Discussion:** The most dominant groups at the class level were *Clostridia* (26%), *Gammaproteobacteria* (18%), and *Alphaproteobacteria* (11%), according to the data obtained. The *Clostridia* class includes species that play a role in organic matter transformation, especially in anaerobic environments, and is the leading bacterial group used in biofertilizer production. *Gammaproteobacteria* and *Alphaproteobacteria* classes have bacteria with potential as biocontrol agents and nitrogen fixation. At the family level, the presence of groups such as *Lachnospiraceae*, *Comamonadaceae*, and *Ruminococcaceae*, which may be of potential benefit in agriculture, is noteworthy. In addition, a large number of unclassified taxa in the "Incertae Sedis" and "Others" categories indicate the existence of biotechnological resources





## **Crop Adaptation to Climate Change – Strengthening Crops for a Changing World**

waiting to be discovered. This study reveals that groundwater should be considered not only as a source of water, but also as a microbial resource of potential agricultural benefit. The findings suggest that microbiota-based agricultural applications (biofertilizers, biopesticides, plant growth promoters, etc.) can be supported by local resources.





## Accelerating Climate-Resilient Hemp Breeding through Molecular Marker Technologies

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**Key words:** *Cannabis sativa*, climate resilience, molecular markers, GWAS, genomic selection, CRISPR, omics integration

### Abstract:

Industrial hemp (*Cannabis sativa* L.) is experiencing renewed global interest due to its sustainability and diverse industrial applications, including textiles, bio-composites, nutraceuticals, and pharmaceuticals. As climate change intensifies, developing hemp cultivars with improved adaptation to abiotic stressors, such as drought, salinity, and extreme temperatures, has become a priority. Conventional breeding efforts are challenged by the crop's dioecious reproductive system, complex trait inheritance, and limited genomic resources. Molecular marker technologies provide powerful tools to overcome these barriers, enabling faster, more accurate selection of elite genotypes. This presentation highlights recent advances in hemp molecular breeding, focusing on marker-assisted selection (MAS), genomic selection (GS), and genome-wide association studies (GWAS) to dissect quantitative traits related to stress resilience, cannabinoid biosynthesis, and fiber quality. Various marker systems, such as SSRs, SNPs, and DArTseq, are discussed, alongside their integration with high-throughput genotyping platforms and multi-omics datasets, including transcriptomics and metabolomics. Furthermore, the application of RNA-Seq in gene expression profiling and CRISPR/Cas9 gene editing for targeted trait enhancement are explored. These strategies are instrumental for accelerating the development of hemp varieties that combine high productivity with environmental adaptability. Emphasis is placed on the urgent need for genomics-enabled breeding approaches to ensure hemp's role in climate-resilient cropping systems. This contribution aligns with the RECROP Action's overarching aim to improve crop reproductive success and resilience through cutting-edge biotechnology and integrative breeding strategies.





**Enhancing shoot regeneration efficiency under PEG-modulated drought stress conditions in *Solanum lycopersicum* cultivars Micro-Tom and M82**

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**Key words:** *Solanum lycopersicum*, polyethyleneglycol, drought, regeneration

The aim of this work was to optimize the parameters of drought tolerant tomato lines creation.

The series of experiments were conducted with *Solanum lycopersicum* varieties Micro-Tom and M82. The seeds were propagated and cultivated on MS<sub>30</sub> medium for 7 days. Then, the cotyledons were separated and cultivated on MS<sub>30</sub> medium supplemented with 1 mg/L ZT (zeatin) + 0.1 mg/L IAA (indole-3-acetic acid) for callus induction. Three-week-old calluses obtained from cotyledon explants were used for experiments with PEG (polyethyleneglycol).

The calli were cultivated in buffer with 40% PEG 4000 for 15 or 24 hours. The explants, which were incubated only in buffer without the addition of PEG, served as a negative control.

We identified that after 15 or 24 hours of incubation in PEG buffer, Micro-Tom and M82 calli can recover and later regenerate. The obtained results were evaluated by statistical analysis.

We observed that regeneration efficiency was dependent on the genotype used, PEG usage, and time of incubation in PEG.

Globular structures (which are considered drought tolerant) appeared from M82 and Micro-Tom calli (incubated for 15 hours in 40% PEG 4000) after 18 - 21 days on a medium MS<sub>30</sub> + 1 mg/L ZT + 0.1 mg/L IAA.

A higher number of *de novo* formed shoots was observed among explants incubated for 24 hours in buffer with PEG (the highest average shoot number per one explant was 5.7). However, the average regeneration percentage was higher when Micro-Tom explants were incubated in 40% PEG for 15 hours (83%), what is significantly higher than when the explants were incubated in buffer without PEG (33%).

While 24 hours of incubation was more effective to obtain a higher number of regenerated shoots, 15 hours of incubation for cv. Micro-Tom explants was more effective for the survival of explant tissues and a higher percentage of shoots regeneration.

Micro-Tom showed a higher number of regenerated shoots than M82. The shoot regeneration method created for Micro-Tom and M82 is effective for creation of drought tolerant lines and for increasing the regeneration efficiency of these varieties, what can be used in genetic transformation and gene editing experiments.







## Flash Talks

### CRISPR/Cas9-Mediated Knockout of *sly-miR9469* for Functional Analysis of Drought Tolerance in Tomato (*Solanum lycopersicum* L.)

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**Keywords:** CRISPR-Cas9, Knock-out, miRNA, *sly-miR-9469*, Drought stress, Tomato, Climate change.

#### Abstract

Tomato (*Solanum lycopersicum* L.) is a globally important crop whose productivity is severely constrained by drought stress. MicroRNAs (miRNAs) are critical post-transcriptional regulators of stress responses, and their targeted editing has emerged as a promising strategy for crop improvement. Among these, *sly-miR9469* is a drought-responsive miRNA shown to be downregulated under water deficit and predicted to regulate genes involved in NAD<sup>+</sup> biosynthesis and callose synthesis. In this study, we aimed to elucidate its functional role by generating CRISPR/Cas9-mediated knockout lines in the Crocker tomato variety. Two guide RNAs were designed against *sly-miR9469-3p* and introduced via *Agrobacterium tumefaciens*-mediated transformation using the pHSE-401 vector. T0 transgenic plants were successfully obtained and validated through PCR and Sanger sequencing, confirming targeted edits in multiple independent lines. Preliminary phenotypic observations indicated variation in plant height and leaf morphology compared to wild-type controls, suggesting possible functional consequences of miRNA disruption. Ongoing analyses include drought imposition assays and the assessment of physiological (relative water content, stomatal conductance, chlorophyll index), biochemical (proline content, antioxidant enzyme activity), and molecular responses. In particular, the expression of *sly-miR9469* and its target genes will be quantified in mutant versus wild-type lines using qPCR. These results provide the first evidence for successful knockout of *sly-miR9469* in tomato and establish a platform for dissecting its role in drought tolerance. Ultimately, this work contributes to the broader goal of enhancing crop resilience through precise miRNA editing, offering valuable implications for sustainable tomato breeding under climate stress.







**Competitive endogenous RNAs (ceRNAs) involving miR396 and  
miR319 regulate maize leaf growth during pathogenic fungus  
*Fusarium verticillioides* infection**

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**Keywords:** Leaf Growth Zones; Biotic Stress Tolerance; ceRNA Regulatory Network; miRNA; lncRNA

**Abstract**

Maize (*Zea mays*), the third most consumed crop worldwide, is essential for global food security. However, biotic stress caused by the fungal pathogen *Fusarium verticillioides* inhibits its leaf growth, affecting overall plant development. Rising global temperatures due to climate change can adversely affect photosynthesis, thereby weakening plant defenses and leading to additional yield losses. Leaf growth depends on tightly regulated processes like cell division and expansion. Recent research points out the regulatory role of non-coding RNAs (ncRNAs), especially microRNAs (miRNAs) and long non-coding RNAs (lncRNAs), through competing endogenous RNA (ceRNA) network in the regulation of stress tolerance. This study examined the effect of *F. verticillioides* infection on maize leaf growth zones, which are meristem (Me), elongation (El) and mature (Ma), focusing on ceR319 and ceR396 networks. In this context, maize lines tolerant (R) and susceptible (S) to *F. verticillioides* were subjected to soil inoculation (I) method and analyzed at the six-leaf stage compared to non-inoculated control (C) plants. As a result, the infection reduced final leaf length (FLL) by 26% for R line and 16% for S line, leaf elongation rate (LER) by 19% for S line and mature cell length (MCL) by 9% in both lines. Additionally, Ascorbate peroxidase (APX) activity increased by 314% in the Me of R line and Superoxide dismutase (SOD) activity increased by 49% in El of R line. Transcriptional analysis revealed line- and zone-specific expression of mRNAs, lncRNAs and miRNAs in ceRNA networks. miR319 and miR396 were upregulated in the El of the SI group by 4- and 8-fold, respectively, compared to Me, while miR319 was downregulated by 9-fold in the RI Ma relative to the RC Me. GRF15 was upregulated by 5- and 6-fold in the Me of RI and RC groups compared to the El and Ma, respectively. lnc319 and TCP38 were upregulated by 2-fold in the RI Ma compared to the corresponding zones of the RC group, while lnc89 was downregulated by 2-fold in the RC EL relative to the Me. Overall, this study underscores the central role of ceRNA networks in regulating maize leaf growth under pathogen attack, offering valuable insights for breeding *F. verticillioides*-resistant cultivars and supporting sustainable agriculture in the face of climate change.

*This study was supported by TUBITAK (Grant no: 221O321).*





## Cross-Kingdom RNA Interference-Mediated Interactions Between Pathogenic Fungus *Fusarium verticillioides* and Maize (*Zea mays*): Morphological, Biochemical, and Molecular Insights

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**Keywords:** Cross-Kingdom RNAi, Plant-Pathogen Interaction, Maize, *Fusarium verticillioides*, Biotic Stress, Exchange RNA

### Abstract

Maize is one of the most extensively cultivated crops globally, is facing the threat of *Fusarium verticillioides*, a widespread soil-borne maize pathogenic fungus. Even the plant-pathogen interactions are forecast to become worse due to global climate change. Therefore, it is essential to comprehend how pathogens and hosts interact to eradicate this pathogen. Recent evidence suggested the role of exchangeable RNAs in this interaction through cross-kingdom RNA interference (RNAi), an endogenous dsRNA-induced gene silencing mechanism resulting in degradation of target mRNA, through small RNA (sRNA) production. Therefore, this study aims to identify the role of cross-kingdom RNAi in the regulation of *F. verticillioides* and maize interaction. For this end, maize seedlings were subjected to the leaf inoculation method with *F. verticillioides* at the first leaf stage, and infection development was observed in the second, third, and fourth leaves morphologically, physiologically, and biochemically compared to the non-inoculated control group. To observe cross-kingdom RNAi, sRNA traveling between two organisms is predicted bioinformatically by an *in silico* target prediction tool and confirmed by gene expression analysis. As a result, the final leaf length and mature cell length of the third and fourth leaves were significantly decreased by 17% and 23%, and by 23% and 17% in the infected groups compared to the control group, respectively. There was no significant change in the parameters of leaf width, leaf area, and chlorophyll content and antioxidant enzyme activities in the third and fourth leaves. Similarly, no significant changes were detected in pigment analysis in the second leaves. However, the phenolic content of the infected group increased significantly by 166% compared to the control group in the second leaves. *Fusarium verticillioides*-derived Fv-miR1827 was up-regulated by 815-fold, leading to 5,651-fold suppression of its target gene, 3-ketoacyl-CoA synthase, in maize. Conversely, Zm-miR159 was up-regulated five-fold in response to fungal infection, but its predicted target, the vacuolar fusion protein Monensin sensitivity 1 (MON1) down-regulated by 88%. These findings support the hypothesis that small RNAs (sRNAs) mediate molecular communication between the host and the pathogen and may have significant implications for improving disease resistance through RNAi-based strategies.

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## Transcriptional Profiling in *lox3* mutant *Arabidopsis thaliana* Under Severe Boron Toxicity

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**Key words:** Boron toxicity, *Arabidopsis thaliana*, Lipoxygenase 3, Transcriptomics, RNA sequencing

### Abstract

Boron (B) is an indispensable micronutrient for higher plants, where it plays key roles in maintaining cell wall structure, membrane integrity, and reproductive development. However, its beneficial range is immensely narrow, and excess boron can cause severe growth inhibition, altered ion homeostasis, and oxidative stress. While the molecular basis of boron toxicity has been partially characterized, the contribution of lipoxygenase-mediated signaling remains poorly understood. Lipoxygenase 3 (*lox3*) of *Arabidopsis thaliana* is known for its role in jasmonic acid biosynthesis and defense regulation, yet its potential involvement in boron stress adaptation has not been fully elucidated. In this study, we investigated transcriptomic responses of *A. thaliana lox3* mutants and Col-0 wild-type plants exposed to severe boron toxicity (2mM). RNA sequencing followed by differential expression analysis revealed that *lox3* disruption significantly reshaped the transcriptional landscape under high boron conditions. Principal Component Analysis (PCA) demonstrated a clear separation of *lox3* boron treated samples from Col-0 and control groups, indicating strong genotype- and condition-specific responses. Comparative analyses identified 2,590 differentially expressed genes (DEGs) in Col-0 and 908 in *lox3*, with only minor differences between genotypes under control conditions. Functional enrichment analyses showed that upregulated DEGs in *lox3* were predominantly associated with stress-responsive biological processes, ribosome biogenesis, and redox regulation, whereas downregulated DEGs were enriched in photosynthesis-related pathways, suggesting a trade-off between growth and stress adaptation. KEGG pathway enrichment further revealed alterations in secondary metabolism, hormone signaling, glutathione metabolism, and ribosomal activity, consistent with enhanced detoxification and cellular adaptation mechanisms. These findings provide novel insights into how *lox3* disruption modulates transcriptional networks under micronutrient toxicity. By shedding light on stress-responsive regulatory pathways, this work expands our understanding of boron stress tolerance in *A. thaliana* and identifies candidate genes and transcription factors for future functional studies.





***In vitro* Screening for Salt and Drought Tolerance in *Cichorium endivia* L. and *Cichorium intybus* L.**

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**Key words:** *Cichorium endivia*; *Cichorium intybus*; *in vitro* culture; salinity tolerance; drought tolerance; oxidative stress; physiological screening

**Abstract**

Salinity and drought are among the most critical abiotic stresses limiting horticultural crop productivity worldwide. The present study aimed to evaluate and compare the tolerance levels of curly endive (*Cichorium endivia* L.) and common chicory (*Cichorium intybus* L.) under controlled *in vitro* conditions. Seeds and explants from selected cultivars were cultured on Murashige and Skoog (MS) medium supplemented with graded concentrations of NaCl (0–15–30–60–90 mM) to simulate salinity stress and PEG (0–3–6–9 %) to induce drought stress. Growth performance, dried matter content (DMC) and proline accumulation were measured after 6 weeks of culture. Malondialdehyde (MDA), hydrogen peroxide (H<sub>2</sub>O<sub>2</sub>) and antioxidant enzyme activities (SOD, POD, APX, CAT) were determined as oxidative stress indicators. Results showed significant ( $p < 0.05$ ) differences between species and among cultivars in their responses to both stress factors. *C. intybus* generally exhibited higher tolerance to salinity; lower MDA levels, while *C. endivia* demonstrated relatively higher drought tolerance, indicated by greater DMC and enhanced proline accumulation. Principal component analysis (PCA) grouped the cultivars into distinct tolerance categories, suggesting potential genetic resources for future breeding programs. These findings provide valuable insight into the physiological and biochemical mechanisms underlying salt and drought stress tolerance in *Cichorium* species, supporting targeted selection in stress-resilient cultivar development.





## A Multiplexed Genome Editing Approach for Climate-Resilient Iron Biofortification in Potato

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**Keywords:** CRISPR-Cas9, iron homeostasis, biofortification, transcriptional regulation, sustainable agriculture

### Abstract

Iron (Fe) deficiency is a widespread micronutrient disorder threatening public health, particularly in regions with limited dietary diversity. Biofortification via genome editing presents a sustainable and targeted approach to enhance the nutritional profile of staple crops. Since crops are central to human nutrition, their micronutrient composition directly influences human health. However, iron availability in plants is severely limited under abiotic stresses, which are increasingly prevalent due to climate change, further exacerbating nutrient deficiencies in food systems. In this study, we aim to boost iron content in *Solanum tuberosum* L. (potato) by modulating two critical transcriptional regulators of iron homeostasis. Using a CRISPR-Cas9-based system, a negative regulator will be silenced to improve iron redistribution, while a multiplexed activation approach will overexpress a master transcription factor controlling root-level iron uptake. Guide RNAs targeting conserved sequences in potato orthologs were designed, with constructs generated through Golden Gate and Gateway cloning. Transgenic lines will be developed via *Agrobacterium*-mediated transformation and screened for precise genome edits. This dual-targeted genome editing approach provides a promising framework for developing non-transgenic, iron-enriched potato varieties to address hidden hunger and promote sustainable agriculture.





## Genome-Wide Identification and Characterization of the GABA Pathway Gene Family in Alfalfa (*Medicago sativa*): Insights into Stress Response and Developmental Regulation

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**Keywords:** Alfalfa (*Medicago sativa*), GABA pathway, Gene family, Transcriptome profiles, Stress

### Abstract

Gamma-aminobutyric acid (GABA) is a critical metabolite involved in regulating plant defense responses against abiotic and biotic stresses, as well as coordinating growth and developmental processes. In this study, the GABA pathway gene family was comprehensively analyzed in the genome of alfalfa (*Medicago sativa*), leading to the identification of a total of 47 genes, including 19 *MsGAD*, 12 *MsGAT*, 8 *MsGABA-P*, 4 *MsGABA-T*, and 4 *MsSSADH* genes. These genes were found to be distributed across 24 different chromosomes within the alfalfa genome. Phylogenetic analyses revealed that *MsGAD* genes clustered into classes I, III, and IV; *MsGAT* genes into classes I and IV; and *MsGABA-P*, *MsGABA-T*, and *MsSSADH* genes into class I. Extensive synteny analyses demonstrated that 23, 25, 32, and 36 genes showed collinear relationships between *Medicago sativa* and *Arabidopsis thaliana*, *Medicago truncatula*, *Lens culinaris*, and *Phaseolus vulgaris*, respectively. Ka/Ks ratio analyses indicated that while the *MsGAD4-1b/MsGAD4-1c* gene pair arose through tandem duplication, the remaining gene pairs resulted from segmental duplication events, with all gene pairs evolving under purifying selection pressure. Promoter analyses revealed that GABA pathway genes harbor numerous *cis*-regulatory elements responsive to hormones, developmental processes, light, and various environmental stresses. Transcriptome data indicated variable expression levels of GABA pathway genes across different tissues, with the notable exception of *MsGAD3-2*, which was not expressed in leaf tissue. Protein-protein interaction network analyses further showed that GABA pathway proteins interact either directly or indirectly with each other, as well as with proteins involved in stress responses and developmental regulation. Collectively, these findings suggest that alfalfa GABA pathway genes exhibit tissue-specific and stress-responsive expression profiles. To our knowledge, this study represents the first genome-wide identification and characterization of the GABA pathway gene family in alfalfa.







## Assessing Drought Tolerance and its Relationship with Seed Size in Lentil (*Lens culinaris* Medik.) Cultivars

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**Keywords:** Lentil, drought, germination, seed size, tolerance

### Abstract

In the face of climate changes, the development of climate-change-ready new cultivars is an important task for plant breeders to meeting global food demand. The current study aimed to reveal the tolerance levels of 15 registered lentil (*Lens culinaris* Medik.) cultivars to drought stress during the germination period and to determine any possible association between seed size and drought tolerance level. The seeds were germinated either in the presence or absence of PEG6000 (-0.15 MPa) at  $23 \pm 0.5^{\circ}\text{C}$  in a constant dark condition. A completely randomized block design with four replications of 50 seeds was used to determine germination parameters such as the final germination percentages (FGPs), speed (G50) and span (G10-90) of germination. The seed sizes were determined by two-dimensional seed surface area (SSA) measurements. Cluster and Principal Component Analysis (PCA) were used to investigate the effect of drought stress on the cultivars' germination parameters. The results revealed significant genetic variations ( $p < 0.0001$ ) among the cultivars for the germination parameters measured. The cultivar Lc-12 showed the greatest reduction (97.47%) in FGP due to osmotic stress, while cultivar Lc-7 had the smallest (18.35%). The germination speed ranged from  $G50 = 2.77$  days (Lc-9) to  $G50 = 6.68$  days (Lc-15) while cultivar Lc-5 had the longest germination delay ( $G10-90 = 5.25$  days) under given stress conditions. The variation in germination percentages under stress conditions was greater than that observed under control conditions. Cluster analysis revealed two clusters, and the first two components explained 81.7% of the overall variation between cultivars under osmotic stress conditions. Significant ( $p < 0.01$ ) positive ( $r = 0.46$ ) and negative ( $r = -0.47$ ) correlations were determined between SSA and G50 in the presence and absence of drought stress, respectively. The results revealed that the level of drought stress utilized in this study successfully distinguished drought tolerance levels of the cultivars at germination stage. The results also indicated that the relationship between germination parameters and seed size might alter dramatically depending on the presence or absence of stress, which should be considered when evaluating stress tolerance levels of plant genotypes.







## Impact of Copper Oxide Nanoparticles on Growth, Oxidative Stress and Antioxidant Gene Expression in Maize (*Zea mays* L.) Seedlings

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**Key words:** *Copper oxide nanoparticles (CuO NPs); Zea mays* L.; oxidative stress; antioxidant enzymes; gene expression; plant stress physiology

### Abstract

This study aimed to evaluate the effects of copper oxide (CuO) nanoparticles on growth, physiological, biochemical, and molecular responses in maize (*Zea mays* L.) seedlings. CuO nanoparticles were applied at concentrations of 250, 500, and 1000 mg/L to hydroponically grown seedlings. The applications resulted in significant reductions in root and shoot lengths as well as chlorophyll a and b contents. Moreover, oxidative stress markers including malondialdehyde (MDA), hydrogen peroxide (H<sub>2</sub>O<sub>2</sub>), and superoxide anion (O<sub>2</sub><sup>-</sup>) levels increased in a dose-dependent manner. While the activities of superoxide dismutase (SOD) and catalase (CAT) decreased, the activities of peroxidase (POD) and glutathione reductase (GR) increased. A significant increase in glutathione (GSH) levels was also recorded. Gene expression analysis revealed that the expression levels of antioxidant-related genes (*sod*, *cat*, *pod*, *gr*, *gst*, and *gpx*) varied depending on the tissue type and the applied CuO concentration. The findings indicate that CuO nanoparticles induce oxidative stress in maize and activate antioxidant defense mechanisms at both enzymatic and transcriptional levels.





## Toxic boron responsive regulations of *lox3* mutant *Arabidopsis thaliana* at physiological and biochemical levels

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**Keywords:** *Arabidopsis*, boron toxicity, lipoxygenase, oxidative stress, antioxidants

### Abstract

Boron (B) is an essential micronutrient for plants; however, elevated concentrations can lead to severe toxicity symptoms. Lipoxygenases (LOXs) have been identified as pivotal regulators of oxylipin and jasmonate biosynthesis, which have been linked to stress responses. This study explores the biochemical responses exhibited by *Arabidopsis thaliana* Col-0 and *lox3* mutant plants when subjected to moderate (1 mM) and severe (2 mM) levels of boron (B) toxicity. A series of physiological and biochemical assays were performed to assess plant growth, oxidative damage, and antioxidative defense systems. Morphological analysis showed a dose-dependent reduction in growth, with *lox3* mutants displaying enhanced sensitivity at 2B, as indicated by reduced leaf surface area. Mineral analysis confirmed significant accumulation of boron in both lines, accompanied by a 25% reduction in Ca and consistent decreases in Cu, K, Mg, P, and S. Notably, Na content increased by 9–15% in *lox3* mutants, suggesting disturbed ion homeostasis linked to impaired jasmonate pathway activity. Photosynthetic pigment analysis revealed reductions in chlorophyll-a, chlorophyll-b, and carotenoids under increasing B concentrations. Col-0 exhibited greater declines compared to *lox3*, indicating higher pigment instability in wild-type. In contrast, anthocyanin accumulation was markedly induced in Col-0 under 2B, while *lox3* mutants exhibited repressed anthocyanin biosynthesis, highlighting a role for LOX3 in stress-induced pigment regulation. Proline levels increased significantly under boron stress in both lines, reaching maximum levels at 2B, but accumulation was lower in *lox3*, suggesting reduced osmotic adjustment. Thiol content and glutathione levels increased in both genotypes, with *lox3* showing higher thiol accumulation, indicating compensation through alternative antioxidant mechanisms. Enzymatic antioxidant assays showed differential responses: while APX and CAT activities increased 3–4 fold in Col-0 under 2B, no significant induction was observed in *lox3* mutants. These results demonstrate that impaired jasmonate signalling compromises enzymatic antioxidant defenses, leading to higher oxidative stress susceptibility. Overall, the findings suggest that LOX3 contributes to boron tolerance by maintaining ion balance, promoting anthocyanin and proline accumulation, and activating APX/CAT-mediated antioxidant defenses. The *lox3* mutation disrupts these mechanisms, underscoring the importance of jasmonate-dependent regulation in boron stress adaptation.





## Single-nucleus RNA sequencing reveals gene regulatory networks in *Arabidopsis thaliana* roots under drought stress

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**Keywords:** *Arabidopsis thaliana*, drought, single-nucleus RNA sequencing (snRNA-seq), stress response, transcriptome

Drought is known to be one of the main stress factors restricting crop production globally. Plants exhibit important changes in their metabolism due to stress-induced transcriptional reprogramming. In order to comprehend how plants tolerate environmental stressors, transcriptional profiling through bulk RNA sequencing is frequently utilized to uncover the effects on growth and development. Furthermore, by identifying the gene expression profiles unique to various cell types, single-cell RNA sequencing (scRNA-seq) offers a deeper investigation of cellular heterogeneity. Moreover, single-nucleus RNA sequencing (snRNA-seq) performs the same investigation without the need for protoplast isolation, which is itself a stress-causing process. In this study, snRNA-seq was used to discover cell-type-specific differentially expressed genes (DEGs) at the single-cell level in *Arabidopsis thaliana* roots exposed to drought stress using a high-throughput droplet-based microfluidics platform belonging to 10X Genomics. Here, we determined a total of 20653 genes across 5910 nuclei and annotated them into 10 distinct cell-type-specific clusters as atrichoblast, columella+cortex, cortex+endodermis, endodermis, lateral root cap, metaphloem, metaxylem, phloem, protoxylem, and trichoblast, respectively. Accordingly, DEGs, particularly in metaphloem, protoxylem, and trichoblast were linked to ribosome, ribosomal subunits, and oxidative phosphorylation. Also, DEGs in atrichoblast and lateral root cap were related to the biosynthesis of various plant secondary metabolites and some metabolic pathways. Additionally, among the DEGs, the genes and transcription factors whose expression level changed at least 3-fold in at least three different cell clusters were determined. Especially, LOX3 and CYP707A3 genes and WRKY33 transcription factor were found to be downregulated and related to each other in the biosynthesis of secondary metabolites and alpha-linolenic acid metabolism. To confirm the role of the LOX3 gene, physiological and biochemical analyses of *lox3* mutant plants grown under different drought conditions were performed. It was found that the growth of *lox3* mutants was much better compared to wild type plants under both the control and drought conditions. More research on these genes might contribute to understanding the plant stress response mechanism. As a result, to uncover the fundamental processes of drought response in *Arabidopsis thaliana*, we created a gene expression map at single-nucleus resolution for the first time in the literature.





## Poster Presentations

### Evaluation of Tolerance to the Combination of Salt and High Temperature in Five Winter Wheat Genotypes

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**Keywords:** Wheat, Salt stress, Heat stress, Abiotic stress tolerance

#### Abstract

Increasing environmental stress factors associated with climate change are among the most significant threats to agricultural production. Among these stresses, high temperatures and salinity cause yield and quality losses, particularly in strategically important cereals such as wheat. Understanding the responses of winter wheat genotypes commonly grown in Turkey to these stresses is of great importance in determining stress tolerance and contributing to breeding efforts.

This study investigates the effects of heat stress and the combination of heat and salt stress using five different winter wheat genotypes (Gerek-79, Bezostaja-1, Esperia, Bayraktar-2000, and Sönmez-01) grown in Turkey. In the experiment, two groups were formed for each genotype; one group was subjected to high temperature stress alone, while the other group was subjected to both high temperature and salinity stress. As a result of the experiment, stress responses were evaluated by measuring the relative water content (RWC), electrical conductivity (EC), shoot length, chlorophyll content, and SPAD values in the plants.

This study reveals that the winter wheat genotypes Gerek-79, Bezostaja-1, Esperia, Bayraktar-2000, and Sönmez-01 grown in Turkey have different tolerance levels to heat and salt stress. The findings obtained from this study will contribute to the identification of stress-tolerant genotypes for future breeding programs and to increasing productivity under stress conditions.





## Salicylic Acid Modulation of ABA-Induced MAPK Signaling in Quinoa under Drought Stress: Insights from the Titicaca Genotype

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**Keywords:** quinoa, drought stress, salicylic acid (SA), abscisic acid (ABA), MAPK signaling

### Abstract

Quinoa (*Chenopodium quinoa* Willd.) is a gluten-free, nutrient-rich crop with a unique protein profile encompassing all essential amino acids, alongside lipid composition comparable to oilseeds. Its resilience to harsh conditions positions it as a climate-smart crop with growing relevance for sustainable agriculture. Under drought, abscisic acid (ABA) accumulates predominantly in leaves, activating MAPK signaling cascades that regulate stomatal closure and enhance stress adaptation. Salicylic acid (SA) strengthens antioxidant defenses, mitigates cellular damage, preserves photosynthesis, and modulates stomatal behavior under drought stress. However, the mechanistic crosstalk between SA and ABA, particularly through MAPK signaling pathways, remains poorly understood. While studies suggest partially overlapping mechanisms in stomatal regulation, molecular-level interactions have yet to be fully elucidated. This study aims to investigate the molecular effects of exogenous SA application on ABA-induced MAPK signaling under drought stress in the drought-tolerant quinoa cv. Titicaca. Plants will be grown under controlled conditions, with three experimental groups: (1) drought without exogenous SA, (2) drought with SA, and (3) baseline control without drought and SA for comparison. Drought will be induced via water limitation, while SA will be administered by foliar spraying. At designated time points, leaf samples will be collected for qPCR analysis of key MAPK signaling components, with emphasis on *MAPKKK18*, *MAPKKK1/2/3*, and associated downstream transcription factors and effector genes such as ABA biosynthesis and signaling. In parallel, physiological and biochemical measurements related to drought response will be recorded across all treatments. The expected outcomes will clarify how SA modulates ABA–MAPK signaling interactions during drought, providing novel insights into the molecular adaptation strategies of quinoa. These findings will not only enhance our understanding of stress resilience in quinoa but also serve as a foundation for translating SA-based molecular tools into broader crop improvement strategies, contributing to food security under climate change.





## Overexpression of the SIAIMI gene encoding the R2R3 MYB transcription factor triggers drought tolerance in potatoes

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**Keywords:** Potato, drought stress, SIAIMI gene, transgene development

### Abstract

Potatoes encounter numerous biotic and abiotic stress factors at different growth stages. These stresses can disrupt the plant's normal growth functions and ultimately lead to a decrease in tuber yield. Plants have developed various defense mechanisms at the molecular level against stress factors. One of these defense mechanisms is changes in gene expression. Engineering genes encoding transcription factors in plants is an important approach to developing and strengthening stress-tolerant plants. MYB protein genes play a role as transcription factors that are induced or suppressed in response to different abiotic stresses. In this study, the tomato (*Solanum lycopersicum*) SIAIMI1 gene (an ABA-induced MYB transcription factor) was engineered into potato to evaluate its effects under drought tolerance. The *Agrobacterium* strain AGL1, carrying the pEarleyGate 100 vector containing the SIAIMI gene and under the control of a constitutive promoter (35S), was used to infect leaf, nodal, microtuber, and internodal explants of the potato variety Agria. When subjected to artificial in vitro stress conditions, the transgenic plants showed accumulated levels (up to a 6-fold increase) compared to the control. These results are expected to potentially contribute to efforts to increase drought tolerance in potatoes through genetic engineering of transcription factors.







## Genome-wide identification of *YSL* gene family in quinoa and amaranth and expression patterns under high soil pH

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**Keywords:** YSL, quinoa, amaranth, iron, alkalinity, climate change

### Abstract

Yellow Stripe-Like (YSL) transporters play crucial roles in metal chelate transport, especially in the uptake and translocation of iron (Fe) and other micronutrients in plants. In this study, we performed a comprehensive genome-wide identification and characterization of the *YSL* gene family in two important pseudocereals, quinoa (*Chenopodium quinoa*) and amaranth (*Amaranthus cruentus*). A total of 24 and 18 *YSL* genes were identified in the quinoa and amaranth genomes, respectively. Phylogenetic analysis grouped the YSL proteins into distinct clades, revealing evolutionary relationships with orthologs from *Arabidopsis thaliana* and *Oryza sativa*. Conserved motif analysis, gene structure examination, and chromosomal localization provided insights into the diversity and potential functions of the *YSL* genes. Promoter analysis revealed several cis-regulatory elements related to abiotic stress and metal ion responses. To investigate the functional relevance of *YSL* genes under alkaline stress, we evaluated their expression profiles in root and shoot tissues of both species exposed to high soil pH (pH 8.5). Several *YSL* genes exhibited significant tissue-specific differential expression, suggesting their involvement in metal homeostasis under alkaline conditions. These findings offer valuable insights into the molecular mechanisms of micronutrient transport in quinoa and amaranth and lay the foundation for developing stress-resilient crop varieties adapted to alkaline soils.







## Role of N-Acetylcysteine in Enhancing Antioxidant Activity and Productivity of Drought-Sensitive Bread Wheat

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**Keywords:** N-Acetylcysteine, drought stress, wheat, antioxidants, AsA-GSH cycle

### Abstract

Wheat (*Triticum aestivum* L.) is a globally important staple crop, but its yield is increasingly threatened by drought stress, which disrupts photosynthesis, cellular water balance, and redox homeostasis. Excessive accumulation of reactive oxygen species (ROS) causes oxidative damage, though plants counteract this through antioxidant systems such as the ascorbate–glutathione (AsA–GSH) cycle. N-Acetylcysteine (NAC), a thiol-containing precursor of glutathione (GSH), has been shown to strengthen antioxidant defenses under heavy metal stress, yet its role in drought tolerance in wheat remains unclear. This study aims to evaluate whether exogenous NAC application improves drought tolerance in drought-sensitive bread wheat genotypes under controlled conditions. Experiments will follow a randomized complete block design with three biological replicates. Stress will be induced by water withholding at the three-leaf stage, with NAC applied as a foliar spray at different dosages. Sampling will occur at early stress (day 3), mid-stress (day 7), and recovery (day 10). Physiological parameters such as chlorophyll content, photosynthesis rate, transpiration, stomatal conductance, relative water content (RWC), and chlorophyll fluorescence (Fv/Fm) will be recorded. Growth traits including root length, root/shoot ratio, and shoot and root fresh/dry weights will be evaluated. Biochemical analyses will include MDA, electrolyte leakage, ROS levels, GSH content, and antioxidant enzyme activities (APX, GR, MDHAR, DHAR). Gene expression analyses will focus on antioxidant-related genes (*TaAPX*, *TaGR*, *TaMDHAR*, *TaDHAR*), drought-responsive transcription factors (*DREB*, *NAC*), and ROS markers. In addition, yield-related traits such as spike length, grain weight, and harvest index will be assessed in a speed breeding–like growth room in a different setup. This work will provide the first comprehensive evaluation of NAC-mediated regulation of physiology, molecular responses, and yield components under drought in wheat. Expected outcomes include improved antioxidant activity, enhanced growth, reduced oxidative damage, and increased productivity.





## Prediction of Iron Deficiency Tolerance Pathways in Quinoa Using Artificial Intelligence-Assisted Multiple Dataset Analysis

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**Keywords:** quinoa, iron deficiency, abiotic stress, prediction models, machine learning

### Abstract

Iron (Fe) is an element essential for plant physiology, participating in photosynthesis, respiration, and chlorophyll biosynthesis. At the same time, excessive Fe can cause toxicity through hydroxyl radicals produced in the Fenton reaction. Therefore, plants must strictly regulate Fe homeostasis to balance deficiency and toxicity. Although Fe is abundant in soils, its bioavailable fraction is limited, especially in calcareous soils, often leading to chlorosis, growth inhibition, and yield reduction. Quinoa (*Chenopodium quinoa* Willd.) is a nutrient-rich pseudocereal with high levels of amino acids, fatty acids, fiber, minerals, and vitamins. Its adaptability allows cultivation in diverse climates, from arid deserts to humid tropics. While quinoa's tolerance to salinity and drought is well documented, knowledge of its molecular and physiological responses to Fe deficiency remains limited. Initial studies profiling quinoa seedlings under Fe-limiting conditions have provided valuable insights, but further integrative analyses are needed. This project aims to investigate quinoa's genomic, transcriptomic, and physiological responses to Fe deficiency. Publicly available transcriptome datasets will be combined with physiological assays to identify Fe-responsive transcription factors and antioxidant gene families. Comparative analyses with *Arabidopsis thaliana* will highlight conserved and species specific responses. In addition, Artificial Intelligence based pipelines will construct predictive models of gene regulation under Fe stress. These models will apply machine learning algorithms for grouping similar expression profiles, selecting key biomarkers, and building networks that reveal key regulatory genes. By simulating genotype-specific responses, the model will provide predictions that can later be tested in experiments. To validate these predictions, quinoa plants will be grown under controlled conditions with and without Fe deficiency to provide a wet lab confirmation of computational results. Expected outcomes include the identification of candidate genes, pathways, and regulatory modules contributing to Fe efficiency in quinoa. The findings may help improve our understanding of how quinoa adapts to nutrient stress and provide a basis for developing Fe-efficient cultivars.





## Brassinosteroid–Jasmonic acid–Ethylene Crossover Communication and Fiber Biogenesis in *Cannabis sativa*

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**Keywords:** *Cannabis sativa*, brassinosteroid, jasmonic acid, ethylene

### Abstract

Optimizing fiber length, fineness, and wall architecture in *Cannabis sativa* depends critically on phytohormonal control. In this study, how brassinosteroid (BR), jasmonic acid (JA), and ethylene (ET) signaling integrate to govern fiber development in two local genotypes (Narlı, Vezir) was interrogated. A transcriptome-wide analysis across two developmental stages and three chemical regimes—exogenous BR, the BR biosynthesis inhibitor brassinazole (BRZ), and control—was conducted, and differentially expressed genes were resolved under stringent criteria (FDR < 0.01,  $|\log_2FC| > 2$ , TPM > 50). The data delineate a BR-centered regulatory axis that tempers JA load while sustaining ET-associated growth programs. Core JA biosynthesis nodes, including OPR3 and 13-LOX, were consistently repressed by BR but strongly induced under BRZ, indicating feedback limitation of oxylipin flux during growth. AOC expression exhibited stage- and genotype-contingent modulation—pronounced BR responsiveness in early Vezir and dual (BR and BRZ) hyperinduction in late Narlı—suggesting multiple entry points for oxylipin control. Canonical JA regulators (TIFY/JAZ, MYC2) shifted upward with BRZ and attenuated under BR, consistent with a reallocation from defense toward morphogenesis. Concordantly, BR-enhanced ET/BR-responsive transcriptional modules: ERF106/ERFL1 and LBD21 increased, whereas the ET pathway repressor EBF2 rose under BRZ, implying that BR sustains ET signaling partly by suppressing negative feedback. Cell-wall remodeling genes that enable elongation—EXP10, EXPA1, EXPB2, XTH2/21—were upregulated by BR, and secondary wall programs showed genotype- and stage-dependent reinforcement: CesA4/7/8 and LAC17 increased in contexts consistent with wall thickening. Calcium signaling components (CNGC1/CNGC17, CML5) were tuned by BR, supporting coordinated ion/ROS staging during growth. Growth brakes—including BBX24, CCCH-type zinc fingers, and U-box E3 ligases—were broadly suppressed by BR. Genotype-specific response windows were resolved. Narlı exhibited a late-stage, BR-responsive secondary-wall program together with a pronounced LOX/OPR3–TIFY surge under BRZ, indicating high sensitivity to BR withdrawal. Vezir displayed an early BR-biased ERF/LBD–EXP/XTH induction that favors rapid elongation. Collectively, these patterns define a BR-anchored cross-talk that sustains elongation and timely wall strengthening by constraining JA while maintaining ET-mediated growth, offering a mechanistic basis for preserving fiber performance amid environmental variability.





## Drought-Induced Modulation of Bioactive Compounds and Antimicrobial Potential in *Echinacea purpurea*

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**Keywords:** *Echinacea purpurea*, drought stress, antimicrobial, extract, flavonoid

*Echinacea purpurea* (L.) Moench is a perennial herbaceous plant belonging to the Asteraceae family and is considered one of the economically significant medicinal plants. This study aimed to investigate the impact of drought stress—one of the most pressing challenges caused by climate change—on the phytochemical composition and certain biological activities of *E. purpurea*. Four irrigation regimes were applied to the cultivated plants at certain rates [25%, 50%, 75%, 100% (Control)] as drought stress. The drought treatments continued until visible leaf wilting occurred, after which leaf samples were collected. The collected samples were dried at 40°C and extracted using ethyl acetate, methanol, and water. Ethyl acetate and methanol extracts were obtained via maceration, while water extracts were prepared by soaking powdered plant material in pre-boiled water, followed by lyophilization. The highest total phenolic content was observed in the ethyl acetate and water extracts of plants subjected to the 25% irrigation regime. For the methanol extract, the highest phenolic content was detected in the 50% irrigation group. Regarding flavonoid content, the methanol extract from the 25% irrigation group showed the highest levels, followed by the ethyl acetate extract from the 75% irrigation group. To assess biological activity, extracts showing notable increases in phenolic and flavonoid contents—ethyl acetate (75%), methanol (25%, 50%), and water (25%)—were tested for antimicrobial activity against four Gram-negative (*Escherichia coli*, *Pseudomonas aeruginosa*, *Salmonella Typhimurium*, *Enterobacter aerogenes*) and three Gram-positive





## Crop Adaptation to Climate Change – Strengthening Crops for a Changing World

(*Enterococcus faecalis*, *Staphylococcus aureus* ATCC 25923, *S. aureus* ATCC 67101) bacterial strains. The broth microdilution method was employed, testing concentrations from 1000 to 32.15 µg/mL. However, all extracts exhibited Minimum Inhibitory Concentration (MIC) values >1000 µg/mL, indicating no significant antimicrobial activity at the tested concentrations. In conclusion, drought stress led to an increase in total phenolic and flavonoid content in *E. purpurea*, yet this increase did not enhance antimicrobial activity within the tested concentration range. Further studies are needed to evaluate whether this phytochemical enhancement influences other biological activities.

This study was supported by Kastamonu University Scientific Research Project (KÜBAP01/2022-40).





## Distribution of Patulin Toxin-Producing Isolates in *Penicillium expansum* Link, (1809) Populations Isolated from Apples

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**Abstract:** *Penicillium expansum* Link (1809) is a fungal pathogen commonly found in apples and apple products and is one of the main producers of patulin toxin, which poses a significant risk to food safety. In this study, the toxigenic potential of *P. expansum* strains isolated from apple samples collected from the provinces of Isparta, Kahramanmaraş, and Elazığ, located in different geographical regions of Turkey, was investigated.

In this study, a total of 177 isolates were obtained from apple samples collected in Isparta, Karaman, and Elazığ (Jan-Feb 2024). Species identification was confirmed by PCR using PEF-PER primers, while patulin-producing potential was detected with FC2-IDH2R primers. All isolates were identified as *P. expansum*. Patulin-positive isolates showed regional variation: Isparta 91/159 (57.2%), Karaman 5/9 (55.6%), and Elazığ 2/9 (22.2%). These results reveal significant regional differences, which may be linked to genetic variability as well as local climatic and storage conditions. High humidity favors spore germination and fungal development, while low temperatures reduce but do not fully suppress patulin production. The relatively high proportions in Isparta and Karaman could be attributed to more favorable humidity levels and storage conditions, whereas Elazığ isolates exhibited a lower toxin production capacity. This research aims to provide important data for the monitoring and control of toxigenic strains that pose a risk to food safety in apple production areas.

**Keywords:** *Penicillium expansum*, patulin, apple, toxic isolates, food safety, climate change.

This study was supported by the TÜBİTAK 1007 research project titled “Domestic Production of Analytical Mycotoxin Standards.” (Project number 119G003).







## THE ROLE OF VITAMIN D IN THE SALT STRESS TOLERANCE OF *Arabidopsis thaliana*

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**Keywords:** Vitamin D, *Arabidopsis thaliana*, Salt stress.

### Abstract

Vitamin D compounds are lipid-soluble vitamins that play a role in calcium ( $\text{Ca}^{2+}$ ) homeostasis in animals.  $\text{Ca}^{2+}$  is also an essential nutrient required for growth and development in plants. Moreover, plant responses to salt stress are thought to be closely linked to  $\text{Ca}^{2+}$  signaling.  $\text{Ca}^{2+}$  pumps regulate  $\text{Ca}^{2+}$  ion levels in plant cells, thereby enhancing plant resistance to salt stress.  $\text{Na}^+$  and  $\text{K}^+$  pumps help maintain water and ion balance, enabling plants to survive under salt stress conditions. This study aims to investigate the physiological and biochemical effects of vitamin D compounds (50 ppm D2 and 75 ppm D3) on the model organism *Arabidopsis thaliana* L. under salt stress. Under salt stress conditions (100 mM NaCl), the application of 50 ppm D2 and 75 ppm D3 to *Arabidopsis thaliana* led to an increase in root and shoot length compared to the control (2.733 cm and 0.5 cm), with values of 4.166 and 3.600 cm (roots), and 0.5 and 0.766 cm (shoots), respectively. In contrast, a decrease was observed with 100 mM NaCl alone (1.066 cm root; 0.433 cm shoot). Regarding dry weight and viability test results, the highest increase was observed with 50 ppm D2 treatment (0.077 g/seedling, 42.737%) compared to the control (0.058 g/seedling, 24%). Malondialdehyde (MDA) and hydrogen peroxide ( $\text{H}_2\text{O}_2$ ) contents increased under 100 mM NaCl stress (0.3267 nmol/mL, 0.0063  $\mu\text{g/g}$ ) compared to the control (0.2903 nmol/mL, 0.0053  $\mu\text{g/g}$ ), whereas a decrease was observed with 50 ppm D2 and 75 ppm D3 treatments (0.2495 and 0.2473 nmol/mL; 0.002 and 0.0017  $\mu\text{g/g}$ , respectively). The results of this study highlight the potential of vitamin D in enhancing plant tolerance to salt stress, contributing to the understanding of plant stress response mechanisms and aiding in the development of new strategies to improve salt tolerance in plant cultivation.

(This study was supported by TÜBİTAK within the scope of the 2218 National Postdoctoral Research Fellowship Program.)







## Nanotechnology-Endophyte Interaction in Alfalfa (*Medicago sativa* L.) Plants Against Drought Stress

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Drought stress is one of the primary abiotic factor that negatively affects plant growth and yield, posing a serious threat to global food security. Its importance is increasing due to population growth and diminishing water resources, leading to significant yield losses in agricultural production. Nanotechnology, which enables the manipulation of materials at the atomic level, offers innovative solutions in health, energy, environment, and agriculture. Endophytes are microorganisms, including fungi, bacteria, and actinomycetes, that inhabit plant tissues without causing symptoms. In this study, 40 endophytic bacterial isolates were obtained from *Opuntia ficus-indica*, *Agave americana*, and various succulent species in Turkey. These isolates were characterized based on their pathogenicity and plant growth-promoting (PGPB) traits, and two promising isolates were selected for further experiments. The viability of the isolates was confirmed using an MTT assay after treatment with SiO<sub>2</sub> nanoparticles at concentrations higher than those intended for application. Species identification was carried out using 16S rRNA sequence analysis, and the sequences were deposited in NCBI GenBank (AT3: *Bacillus proteolyticus*, PP473248; H17: *Enterobacter hormaechei* subsp. *xiangfangensis*, PP473250). The effects of endophytic bacteria and SiO<sub>2</sub> nanoparticles on physiological and biochemical responses of alfalfa under drought stress induced by PEG-6000 were then evaluated. Parameters such as root–shoot length, reactive oxygen species (ROS), and lipid peroxidation levels were measured in stressed plants. The application of the isolates increased root and shoot dry weight while reducing H<sub>2</sub>O<sub>2</sub> and MDA levels. Scanning electron microscopy (SEM) was used to determine bacterial localization within plant tissues. The presence of the inoculated bacteria was further confirmed by re-isolation and 16S rRNA analysis. The results demonstrated that the combined application of endophytic bacteria and SiO<sub>2</sub> nanoparticles represents an effective strategy to enhance drought stress adaptation in alfalfa and to mitigate the adverse effects of stress. (This research was supported by TÜBİTAK project no. 122Z810).

**Keywords:** Succulent, endophytic bacteria, drought stress





## Integrating Design of Experiment (DOE) for Optimizing the Impact of Multiwalled Carbon Nanotubes on Seed Germination Indices in Cotton (*Gossypium hirsutum* L.)

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**Keywords:** MWCNTs, Cotton, Germination, Design of Experiment (DOE), Response Surface Methodology, Taguchi

### Abstract

Cotton (*Gossypium spp.*), a major fiber and economic crop from the Malvaceae family, is globally recognized as “White Gold” for its industrial value. However, its production is affected by multiple factors, and its uniform and enhanced germination is highly critical. For this purpose, seeds were grown on MS medium enriched with different concentrations (0, 25, 50, 75, 100, 125, 150, 175, and 200 mg/L) of multi-walled carbon nanotubes (MWCNTs). Two different commercial cotton cultivars (ST-468 and Esperia) in Turkey were used as plant material, and seeds were sterilized with 0.1% HgCl<sub>2</sub>. Data regarding germination were taken daily and computed with the GerminaR statistical package for nine different germination indices, such as Germination percentage (grp), Mean germination Time (mgt), Germination speed coefficient (gsp), Mean Germination Rate (mgr), Uncertainty (unc), Synchronization (syn), Germination variance (vgt), standard germination deviation (sdg), and coefficient of variation (cvg). The generated data was subsequently computed with classical ANOVA analysis along with modern design of experiment techniques, including Taguchi Design and Response Surface Methodology (RSM). Results illustrated improved germination at lower doses, while higher doses of CNT inhibited germination and induced stress. The results demanded the significance of optimization, and both DOE models optimized the input factors significantly. RSM analysis illustrated that unc was significant, and all remaining parameters were non-significant. Whereas the Taguchi design demonstrated concentration as more significant than cultivars. Integration of multiple statistical tools proved to be efficient for optimization. The present research provides new insights into the role of MWCNTs in enhancing plant germination and development, offering an economical approach to increasing crop yields for sustainable agriculture.





## Improving germination indices of biofortified cowpea using ZnO<sub>2</sub> nanoparticles and a design of experiments approach

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**Keywords:** Nanotechnology, Germination, Biofortification, Zinc, Cowpea, Design of experiment

### Abstract

Cowpea (*Vigna unguiculata* L.) is widely cultivated for its high nutritional value. The nutritional quality can be further enhanced by biofortification like Zinc oxide nanoparticles (ZnONPs). This innovative technique enhances nutritional bioavailability in diets while also improving soil health and agricultural productivity. For this purpose, cowpea seeds were sterilized with 3.5% commercial bleach (NaOCl) for 15 minutes, followed by three rinses with sterile distilled water. Thereafter, seeds were cultured on Murashige and Skoog (MS) basal medium (Murashige & Skoog), incorporating different concentrations of (6.25- 125 mg/L) ZnONPs with also Seed germination indices of two different cultivars. Data regarding germination was taken on daily basis and computed with GerminaR statistical package for nine different germination indices. Such as Germination percentage (grp), Mean germination Time (mgt) Germination speed coefficient (gsp), Mean Germination Rate (mgr), Uncertainty (unc), Synchronization (syn), Germination variance (vgt), Standard deviation (sdg), and Coefficient of variation (cvg). The generated data was thereafter computed with classical ANOVA analysis along with modern design of experiment techniques including Taguchi Design and Response Surface Methodology (RSM). Whereas Taguchi design demonstrated concentration as more significant than cultivars. Application of ZnONPs significantly improved germination and seedling growth in most treatments compared to the control, resulting in increased seed germination and vigor. Present cultivars ANOVA results exhibited that Bodrum improved the germination rates compared with Karagoz. RSM analysis illustrated that *grp* and *unc* was significant and remaining all parameters were non-significant. Whereas Taguchi design demonstrated concentration as more significant than cultivars. Multiple statistical tools proved to be efficient for optimization. Zinc nanoparticles have been shown to increase germination rates, augment seedling vigor, and improve physiological responses, providing a cost-effective method for enhancing crop yields. This study highlights the capacity of zinc nanoparticles to sustainably resolve global food security.





## Functional Analysis and Determination of Potyvirus Resistance in Tomato Plants Developed by Overexpressing and Silencing the *eIF(iso)4E* Gene

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**Keywords:** Tomato, *eIF(iso)4E*, Potyvirus, CRISPR-Cas9, Virus resistance

### Abstract

Tomato (*Solanum lycopersicum*) is one of the most important and the second most cultivated vegetable crop worldwide, but it is highly sensitive to virus attack and its production is severely affected by potyviruses such as Potato virus Y (PVY). Infection by potyviruses leads to severe yield losses, reducing both the quality and quantity of tomato production worldwide. Plant viruses exploit host translation initiation factors to complete their infection cycle. In tomatoes, three genes encoding members of the eukaryotic translation initiation factor **4E** (*eIF4E*) family; *SleIF4E1*, *SleIF4E2*, and *SleIF(iso)4E* have been identified, all these function as key host susceptibility **factors** in a range of plant–virus interactions. Resistance to potyviruses is often conferred by recessive mutations in genes encoding eukaryotic translation initiation factors. The inability of potyviruses to utilize mutated factors leads to resistance through the loss of-susceptibility mechanism. Understanding the precise role of the eukaryotic translation initiation factor *SleIF(iso)4E* in tomato–potyvirus interactions is crucial for developing resistant cultivars. This study aims to functionally characterize *eIF(iso)4E* in tomato by employing both gene overexpression and CRISPR-Cas9-mediated knockout strategies. For overexpression, the full-length *eIF(iso)4E* coding sequence was cloned into a plant expression vector under a constitutive promoter. For gene knock-out, CRISPR-Cas9 system carrying two guide RNAs targeting three exon regions of *eIF(iso)4E* was constructed. The results demonstrated successful cloning of *eIF(iso)4E* into overexpression and knockout vectors, which was confirmed through Sanger sequencing. Both vectors were introduced into *Agrobacterium tumefaciens* for the transformation of tomato explants leading to the development of mutant T<sub>0</sub> lines. The regenerated lines are expected to exhibit contrasting phenotypes: overexpression lines with enhanced susceptibility and knockout lines with improved resistance against PVY infection. This research provides an important step toward elucidating the functional role of *eIF(iso)4E* in viral susceptibility. The anticipated findings will not only enhance our molecular understanding of tomato–potyvirus interactions but also contribute to the development of virus-resistant tomato cultivars through precise gene-editing strategies.





## Development of Broad-Spectrum Resistance Against Fungal Diseases in Sunflower (*Helianthus annuus* L.) Through CRISPR-Mediated Mutation in MLO Genes

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**Keywords:** Sunflower, CRISPR, MLO, fungal disease

### Abstract

Sunflower (*Helianthus annuus* L.) ranks among the most important plant-based oil sources worldwide and in our country. In addition to its widespread use in human nutrition, sunflower oil is also extensively utilized in the chemical and pharmaceutical industries, which further increases its importance each year. Similar to other crops, fungal diseases are among the major factors reducing seed yield and oil content in sunflower production. Particularly, downy mildew caused by the pathogen *Plasmopara halstedii* and white mold caused by *Sclerotinia sclerotiorum* are the most prevalent fungal diseases that significantly threaten sunflower cultivation both in Turkey and globally, leading to major yield losses. Therefore, the development and use of resistant sunflower varieties against downy mildew, one of the most destructive diseases limiting sunflower production, is of great importance for national production and food security. To date, genetic materials resistant to mildew have been developed through traditional breeding methods, and these resistance genes have been transferred to commercial cultivars. However, due to the rapid emergence of highly aggressive pathogen races, this resistance is often broken, making long-term resistance ineffective. Thus, the development of new methods is required to achieve durable and broad-spectrum resistance. Recent studies have shown that silencing the Mildew Locus O (MLO) genes, which are plant susceptibility factors expressed during interactions with fungal pathogens, can suppress disease mechanisms and provide resistance. Natural or induced mutations in MLO genes have been reported to confer strong resistance to fungal pathogens in many plants, including barley, wheat, tomato, potato, and pea. The CRISPR-Cas9 system, a precise and controlled genome editing tool, has recently been successfully applied to suppress MLO gene function in sunflower, providing durable resistance against multiple fungal pathogens, including downy mildew. This study highlights the potential of CRISPR-mediated MLO gene editing in developing broad-spectrum disease-resistant sunflower varieties.







## Functional Characterization of Solyc02g077790 Reveals Its Role in Tomato Fruit Ripening, Quality, and Stress-Linked Pathways\*

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**Keywords:** *Solanum lycopersicum*, fruit ripening, ethylene production, vitamin C, co-expression analysis, overexpressional study

### Abstract

Tomato (*Solanum lycopersicum*) fruit ripening involves complex regulatory networks that integrate ethylene production, sugar accumulation, firmness, and pigmentation. In this study, we characterized *Solyc02g077790* using transgenic overexpression (OE) lines and transcriptome-based co-expression analyses. OE fruits displayed markedly reduced ethylene emission but enhanced vitamin C content, higher soluble solids (°Brix), and greater firmness at the red-ripe stage, indicating a delay in softening and altered pigment profiles. Morphological assessment revealed pleiotropic effects, including increased flower numbers but reduced plant height, linking the gene to both reproductive and vegetative development. To explore its regulatory landscape, RNA-Seq co-expression analysis across 93 tissue-specific datasets positioned *Solyc02g077790* within modules enriched in phenylpropanoid and flavonoid biosynthesis. Principal component and clustering analyses confirmed tissue- and stage-specific regulation, especially in locular and seed tissues during ripening. Candidate downstream targets identified for qRT-PCR validation included ethylene biosynthesis genes (*ACS2*, *ACO1*), carotenoid metabolism (*PSY1*), cell wall remodeling factors (*EXP1*, *PG2a*), and master regulators of ripening (*RIN*, *TAGL1*). These findings suggest that *Solyc02g077790* acts as a central regulatory node modulating fruit quality traits, oxidative balance, and ripening physiology. Its manipulation may offer novel breeding strategies to improve tomato shelf life, nutritional value, and resilience under climate stress.





## Transcriptome Meta-Analysis Uncovers Core Susceptibility Genes Shaping Broad-Spectrum Stress Responses in Sunflower

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**Keyword:** Sunflower, helianthus, transcriptome meta-analysis, broad-spectrum stress resistance, differential gene expression

### Abstract

Sunflower (*Helianthus annuus* L.) is a globally important oilseed crop, but its productivity remains vulnerable to diverse abiotic and biotic stress factors. Although conventional breeding has improved stress tolerance, the rapid evolution of pathogens and climate-induced variability demand innovative approaches that extend beyond single-stress resistance. In this study, we performed a comprehensive transcriptome meta-analysis by integrating publicly available RNA-seq datasets from susceptible sunflower genotypes exposed to drought, salinity, cold, heat, flooding, fungal infection, and parasitism. Using a standardized bioinformatics workflow encompassing batch-effect correction, differential expression analysis, and p-value integration, we identified 8,234 meta-differentially expressed genes (meta-DEGs). Among these, a core set of 16 genes exhibited consistent regulation across all stress conditions, defining a conserved transcriptional signature of susceptibility. Functional annotation revealed two genes consistently upregulated and nine genes uniformly downregulated, collectively indicating a transcriptional shift from growth and photosynthesis toward stress adaptation and resource conservation. Correlation analysis further demonstrated convergence among drought, heat, salinity, and cold responses, whereas fungal and flooding stresses displayed distinct expression patterns. These findings highlight susceptibility-associated hubs that function as central regulators of sunflower stress responses. The identified genes constitute strategic targets for molecular breeding and genome editing, providing a foundation for the development of resilient sunflower cultivars with broad-spectrum stress resistance.







## Unveiling the Stress-Responsive *KCS* Gene Family in Tomato: Insights from Genome-Wide and In Silico Expression Analyses

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**Keywords:** *Biotic stress, CRISPR/Cas9, KCS gene family, Overexpression, SlKCS3, Solanum lycopersicum,*

### Abstract

Tomato (*Solanum lycopersicum*) is highly susceptible to biotic stresses, leading to substantial global losses in both yield and quality. The biosynthesis of very-long-chain fatty acids (VLCFAs) plays a central role in plant stress responses, with the 3-ketoacyl-CoA synthase (KCS) gene family acting as key regulators of this process. In this study, we focused on *SlKCS3* (*Solyc05g009270*), a member of the KCS family, to investigate its role in conferring tolerance to biotic stress. Analysis of the RNA-Seq dataset GSE123543 revealed a significant downregulation of *SlKCS3* under biotic stress, suggesting a potential regulatory function in plant defense mechanisms. To functionally validate this, we will employ a dual strategy: (i) targeted disruption of *SlKCS3* using CRISPR/Cas9-mediated genome editing, and (ii) overexpression of *SlKCS3* driven by the CaMV 35S promoter. Transgenic plants will be generated via tissue culture-based transformation and subsequently confirmed through molecular characterization. The phenotypic performance of these lines will then be evaluated under biotic stress conditions in greenhouse trials. This integrated approach will provide insights into the functional significance of *SlKCS3* in tomato defense and establish a molecular framework for breeding strategies aimed at enhancing resistance to biotic stresses. Ultimately, the findings are expected to contribute to the development of tomato cultivars with improved resilience against adverse stress conditions.





## Seaweed Applications Enhance Salt Stress Tolerance in Cucumber (*Cucumis sativus* L.)

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**Key words:** Cucumber, Abiotic Stress, Biostimulant, Yield and quality

### Abstract

Vegetable species are more sensitive to salt stress during early growth stages. Seaweed extract-based biostimulants are among the most effective modern sustainable plant growth promoters. They have been proven to maximize yield by alleviating plant diseases and abiotic stresses, and they are also listed as eco-friendly biofertilizers. The focus of the present study was the use of a commercial seaweed biostimulant as an environmentally friendly product. Cucumber (*Cucumis sativus* L.) is an important vegetable crop with wide cultivation areas. However, with the development of modern greenhouse vegetable production, excessive chemical fertilizer use and improper irrigation practices have increased soil salinity, making salt stress one of the major limiting factors in cucumber cultivation. Biostimulants are known to enhance growth and vigor in mature plants and to mitigate the adverse effects of salt stress.

The aim of this study was to determine the effects of seaweed application (200 and 400 mL/100 L water) on yield and quality in cucumber (*Cucumis sativus* L.) seedlings irrigated with different salinity levels (0, 50, and 100 mM NaCl) during the seedling growth stage, in order to improve salt tolerance. The experiment was conducted under greenhouse and laboratory conditions at the Agricultural Research and Application Center of Tokat Gaziosmanpaşa University, Faculty of Agriculture. Two cucumber cultivars, Çengelköy and Gordion F1, were used as plant material. Seedlings at the three-leaf stage were transplanted into 15 L pots filled with a peat:perlite (2:1) mixture, and throughout the growing season, two different salt concentrations and two seaweed extract doses were applied.

At the end of the experiment, plant height, number of nodes, average fruit number, average yield, leaf area, and early yield were measured. In addition, the expression levels of some stress-related genes were analyzed to evaluate the molecular responses of cucumber to salt stress and seaweed treatments.

The results demonstrated that seaweed applications not only mitigated the adverse effects of salt stress but also regulated gene expression, thereby positively influencing growth and yield parameters in cucumber.





**Development of Tomato Lines with Visual Markers and Enhanced Stress Tolerance through CRISPR/Cas9-Mediated Targeting of a Negative Regulator in the Anthocyanin Pathway\***

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**Keywords:** CRISPR/Cas9, anthocyanin pathway, abiotic stress, negative regulator, gene editing, *Solanum lycopersicum*

**Abstract**

Tomato (*Solanum lycopersicum*) is highly vulnerable to abiotic stresses such as heat, drought, salinity, and UV-B, all of which trigger excessive reactive oxygen species (ROS) accumulation and cause severe yield losses. Anthocyanins, as flavonoid-derived pigments, function both as potent antioxidants mitigating oxidative damage and as visual markers for rapid phenotypic screening. In this study, we focused on *Solyc09g055230*, identified as a candidate repressor of anthocyanin biosynthesis. Comprehensive in silico analyses, including gene–gene and protein–protein interaction networks, RNA-Seq expression profiling, BLAST homology searches, and GO/KEGG functional enrichment, consistently supported its role as a negative regulator within the anthocyanin pathway and its connection with key transcriptional regulators of flavonoid metabolism. To release this repression, we designed multiple high-specificity CRISPR/Cas9 guide RNAs targeting the exon regions of *Solyc09g055230*. The silencing of this gene is expected to enhance anthocyanin accumulation, thereby conferring multi-stress tolerance while simultaneously enabling a visual marker-based selection system. This approach integrates functional genomics with genome editing, providing a novel and practical strategy for crop improvement under climate stress conditions.

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