



## Genome editing for enhancing abiotic stress tolerance in crop plants

Sivaji Mathivanan<sup>1\*</sup>, Shakespear Sundaresan<sup>2</sup>, Chandrasekar Arumugam<sup>3</sup>

Received: 2 January 2023 / Accepted: 4 June 2023 / Published: 30 June 2023

<sup>1</sup>Agricultural Biotechnology, Agricultural College and Research Institute(AC&RI), TNAU, Vazhavachanur, Tiruvannamalai, Tamil Nadu, India.

<sup>2</sup>Plant Biotechnology, ICAR-National Institute of Biotic Stress Management, Baronda, Raipur (CG), India.

<sup>3</sup>Assistant Professor (Biotechnology), Department of Crop Improvement, SRM College of Agricultural Sciences, Vendhar Nagar, Baburayanpettai, Tamil Nadu, India.

\*Correspondence

Sivaji Mathivanan  
sivajibt@gmail.com

The globe has to treble the crop production rates in order to improve food security for future generations. However, crop production would likely become more challenging in the future since current crop types and crop development techniques might not be strong enough to withstand the rising abiotic pressures brought on by climate change. The primary cause of crop loss worldwide is abiotic stress, which reduces average yields for the majority of agricultural crops i.e., by more than 50%. The main environmental stresses that reduce crop production and productivity are drought, salinity, extreme temperatures, and cold. Crop improvement is the key element for the sustainable food production and modern crop improvement methods are very proficient that achieve remarkable improvements in plant performance against abiotic stress. One of the most important modern crop improvement method is genome editing. The advent of genome editing has generated a lot of excitement, especially among agricultural scientists, because it offers new chances to create improved crop varieties with the precise addition of beneficial traits. Genome editing is like mutational breeding; through this method, that is possible to create targeted genome modification and also possible to improve crop varieties with enhanced abiotic stress resistance. This review briefly discusses abiotic stress, genome editing, mechanisms, different types and applications in crop improvement against abiotic resistance.

**Key words:** CRISPR/Cas9, crop improvement, abiotic stress, tolerance, genome editing, rice

### Introduction

Global food security is threatened by abiotic stresses which reduce the food grain production and productivity. Drought, heat, salinity and cold are the predominant stresses that negatively affect agricultural production. These stresses independently or in interaction deleteriously affect crop production. The effect of individual stress or the interaction on crop growth is further aggravated by climate change. It is feared that in the future climate change intensify the effect and the frequency of occurrence of abiotic stress in a region which is already evident from recent reports. Unfavorable environmental conditions for plant growth are more prevailing those are water stress, heat stress, cold stress and salinity stress. Among them, drought and salinity are becoming drastically increased in many regions. (Fedoroff et al., 2010; Kundzewicz et al 2005). Cramer et al (2011) estimated that in rural areas more than 90% of the crop cultivated on agricultural land is affected by abiotic stress at any point of its growing season.

Determining how plants react to stress is crucial when trying to develop stress-tolerant cultivars that can withstand abiotic challenges and give more yield to feed the expanding population. In order to respond to the stress conditions, plants create stress signals to overcome stress conditions. In the same way, abiotic stress also produces various physiological modifications in the plant system and those act as signals and activate various specific metabolic pathways to react the specific abiotic stress. For example, hyperosmotic stress, often known as osmotic stress, is the main signal brought on by salinity and drought. In addition to osmotic stress ion toxicity also occurs in plants under salinity conditions. More complex secondary effects of salinity and drought include metabolic malfunction, oxidative

stress, and damage to cellular constituents such as membrane lipids, proteins, and nucleic acids. So both salinity and drought have distinctive and overlapping signals. In such a way, both drought and salinity disrupt homeostasis of water potential (osmotic homeostasis) and ion distribution (ionic homeostasis) at cellular and whole plant levels (Mathivanan, 2021).

Abrupt changes in water and ion balance develop molecular damage, growth arrest and finally, death of the plants. Certain cellular responses are produced by primary stress signals but most of the other responses are developed by secondary signals. An important signal of drought and salinity is a hyperosmotic signal, which leads to the accumulation of the phytohormone abscisic acid (ABA), which in turn causes several adaptive responses in plants (Zhu et al., 2005). By altering the cell structure and membrane stability, cold or chilling stress impacts plant growth and development (Orvar et al., 2000). The nature of proteins or protein complexes is disturbed by cold stress, and the activity of enzymes such ROS scavenging enzymes is decreased. As a result of these activities, photosynthesis is hampered and photo inhibition occurs. These activities cause significant membrane damage, photo inhibition, and reduced photosynthesis (Siddiqui et al., 2006; Ruelland et al., 2009). At present days so many advanced crop improvement technologies are available but there is no technology is available for making precise changes in plant genomics. After the advent of genome editing, it is now much more convenient to develop a variety with high precision and specificity. Through these methods, specific genetic alterations can be made to a plant's genetic code to alter its features. These alterations may vary in size from a little change in the gene to a major change i.e., insertion or deletion of one or more genes. The use of genome-editing techniques has sped up molecular breeding and allowed scientists to incorporate mutations into plants' genetic code with extreme efficiency and precision. Due of its simplicity, economic feasibility, and flexibility, genome editing techniques have been widely used by researchers (Shakespeare et al., 2022).

### **Genome editing**

Genome editing is a process in which new DNA can be inserted, existing DNA can be removed or replaced by using artificially engineered nucleases, or "molecular scissors". The nucleases make the specific cut at desired locations in double-stranded DNA and this will be repaired by using endogenous repairing mechanisms such as Homologous recombination & Non-homologous end joining (Deriano & Roth, 2013; Osakabe & Osakabe, 2015). Genome editing is mediated through two different systems, one is SSR (site-specific recombinase) and SSNs (site-specific nucleases) cleaving the target sequence by SSNs is followed by a cellular DNA repair mechanism. At present, there are four families of engineered nucleases are used in genome editing: those are Engineered Meganuclease (MegaN), Zinc Finger Nuclease (ZFN), Transcription Activator like Effector Nuclease (TALENs), and Clustered Regularly Interspaced Short Palindromic Repeats /CRISPR-cas9 nuclease system (Osakabe & Osakabe, 2015).

Meganucleases are one of the endonucleases occurred naturally and were first identified in the late 1980s. According to Suzuki et al. (2020), they can recognize and cut long DNA sequences (12 to 40 base pairs) that are either unique in most genomes or very nearly so. Zinc finger nucleases (ZFNs) are site-specific nucleases that cleave DNA *in vitro* in precisely specified locations. This was initially demonstrated in 1996 using protein domains such as "zinc fingers" in combination with FokI endonuclease domains. This chimeric protein contains a modular structure in which each "zinc finger" domain can recognize a single triplet of nucleotides (Joung & Sander, 2013). Continuous research efforts of various scientists led to finding new genome editing technologies like TALENs and CRISPR/Cas with more precision and simple manner when compared to the Meganuclease and Zinc finger-based genome editing. It has been demonstrated that the TALEN and CRISPR systems function in plant, animal, and human cells. By effectively manipulating genomes, such editing techniques have the potential to address a variety of challenging issues, such as the development of mutants with more precision and the production of plants with desirable traits.

### **Clustered regularly interspaced short palindromic repeats (CRISPR)**

CRISPR/Cas is one of the most powerful genome editing technology and the most notable CRISPR system is the CRISPR/Cas9 (based on Cas9 protein), which has clustered regularly interspaced short palindromic repeats. This technique makes use of the adaptive bacterial immune system, whose workings depend on the existence of unique bacterial genome regions known as CRISPR loci. Operons encoding the Cas9 protein and a repeating array of repetitive spacer sequences make up these loci. Short segments of foreign DNA (plasmid or viral) that have

undergone recombination and been integrated into the bacterial genome make up the spacers in the repeat array. The CRISPR system mainly depends on RNA-DNA binding to achieve sequence specificity not like ZFN and TALEN systems, which rely on protein-DNA binding specificity (Rath et al., 2015). The functional characterization of the CRISPR/Cas showed viral resistance mechanism along with components which are inevitable for this system such as crRNA, PAM motif, and tracrRNA (Gasiunas et al., 2012; Jinak et al., 2012). The DNA sequence that follows the protospacer adjacent motif (PAM) DNA sequence is the target of the Cas9 nuclease in the CRISPR system. PAM is a part of the plasmid or virus causing the invasion, but it is not a part of the bacterial CRISPR locus. If the PAM sequence is not immediately after the target DNA sequence, Cas9 will not successfully connect to or cleave it. Its own CRISPR locus of the bacterial genome is being protected since the PAM is a crucial targeting element not present in bacteria. RNA-guided CRISPR/Cas9 could be used for the gene editing of other species than bacteria that cause double-stranded DNA breaks (DSBs) in a site-specific manner. These DSBs was proven in plant, human, and animal cells. In this approach, RNA-DNA pairing of a 20-nt region in the chimeric single-guide RNA (sgRNA) binding on its target DNA sequence with specificity. Consequently, a RNA:DNA heteroduplex is forming and Cas9 domains cause the double strand breakage. CRISPR is quicker, less expensive, more precise, and more effective than previous genome editing technologies (Rath et al., 2015; Jinak et al., 2012; Gasiunas et al., 2012).

### **Crop plants and abiotic stresses**

Crops grown under challenging environments often encounter simultaneous occurrences of multiple abiotic stresses rather than individual stress, negatively affecting crop growth and productivity. Some abiotic stresses often co-exist together and are referred to as companion stress, for instance, drought and heat. The negative effect of the interaction of stress on crop production is more adverse than the effect of individual stress. Similarly, crop response to the combination of stress differs from the response to individual abiotic stress. Unique and overlapping pathways exist in tolerant crop plants to encounter the negative effect of abiotic stress. Ultimately the tolerant crop plants compromise with the regular source-sink relationship which affects the crop growth and productivity (Xiong et al., 2012).

### **Effect of drought, salt and cold stress in plant physiological modifications**

All three stresses predominantly create a loss of cell water leading to a decrease of cell osmotic potential, but the factor of water loss from cells varies among stresses: i) In drought, water loss from cells is due to water shortage in the soil. ii) whereas in salt stress, osmotic or water potential of the surrounding root zone is decreased by ions which prevents the uptake of water by roots. iii) In cold stress, cell water loss is mainly due to the inability of the plant to transport water inside the plant cells causing physiological drought. An increase in osmotic stress induces abscisic acid (ABA) biosynthesis, activating various drought, salt and cold stress-responsive genes in the plant system (Boudsocq & Lauriere, 2005). These three stresses reduce osmotic potential in the plant system by increasing the solute concentration (particularly Na<sup>+</sup>), which deleteriously impacts proteins and enzymes. High-volume production of low molecular weight osmolytes is a typical method of reducing the stress caused by salt, cold, and drought. Production of more low molecular weight osmolytes, such as proline (Hesham & Fahad, 2020), betain (Aziz et al., 2017), and carbohydrates (Marques & Arrabaca, 2004), can counteract this effect by preventing cellular dehydration and turgor loss (Beck et al., 2007),

### **Regulation of gene expression in response to abiotic stress**

Stresses such as drought, salinity, and cold cause a number of genes in plants to express and produce different proteins, such as chaperones or late embryogenesis abundant (LEA) proteins, etc., in different sections of the plant, leading to developing distinct abiotic stress tolerance mechanisms in plants (Kazuko & Shinozaki, 2006). Abiotic stresses produce distinctive DNA methylation patterns, which either promote or decrease gene transcription. Regulons of some stress-sensitive genes are dehydration-responsive element-binding (DREB) or C-repeat binding factor (CBF), basic-leucine zipper (bZIP), and zinc-finger proteins (Hu et al., 2006). A unique cis-acting element called the C-repeat/dehydration response element (CRT/DRE) responds to drought, cold, and high-salt stress (Yamaguchi et al., 1994). By looking for DNA-binding proteins that bind to the CRT/DRE motif, CBF proteins have been successively identified since their discovery (Stockinger et al., 1997; Liu et al., 1998). Three cold-induced CBF genes, CBF1- (CBF1/DREB1B, CBF2/DREB1C, and CBF3/DREB1A), are present in Arabidopsis and are organized in a tandem

manner on chromosome 4. According to Liu et al. (1998) and Gilmour et al. (1998), CBF1–3 are APETALA2/ETHYLENE-RESPONSIVE (AP2/ERF1) type transcription factors that directly bind to the conserved CRT/DRE motifs in the promoters of COR genes (known as CBF regulons) and activate their expression in cold stress circumstances. When its own CBF genes, specifically LeCBF1, are overexpressed, the cold-sensitive tomato (*Lycopersicon esculentum*), becomes freezing-tolerant (Zhang et al., 2004).

### **Genetic modification in plants for abiotic stress tolerance**

Despite the advantages of commercially available genetically engineered plants and their success in combating abiotic stresses, this technology is still not universally adopted due to public misconceptions, which restricts its use in developing abiotic resistant varieties. The main issue with transgenic technology may be that the gene source used to create transgenic crops is frequently acquired from unrelated organisms, such as microorganisms, plants, and animals. Genome editing technology can better handle this problem. Making small genome changes through chemical and physical mutagens in crop plants is called mutation breeding (a traditional way of crop improvement). The success rate or odds of attaining a desirable genotype are quite low since mutational breeding causes changes in the genome in a random manner. However, modifications are made in genome editing at specific locations using sequence-specific nucleases that cause double-strand breaks in the target genomic loci chosen for editing. As a result, more frequently, a desirable genotype can be obtained. TALENs and CRISPR/Cas9 are important genome editing tools (Voytas, 2013). There are many possibilities for developing crop plants with any desirable character by advanced genome editing methods using several available crop genome sequence information. Among genome editing technologies, CRISPR/Cas9 genome editing involves simple cloning and designing techniques, with the same Cas9 can be used with several guide RNAs targeting various genomic regions. Additionally, there are ways to improve the specificity and effectiveness of gene editing approaches because of the accessibility of Cas9 enzymes from various bacterial species. These methods will create non-genetically modified (Non-GMO) crops with the desired characteristic that will increase their yield potential under biotic and abiotic stress conditions (Wang et al., 2014).

### **CRISPR-Cas9**

Utilizing the CRISPR/Cas9 system allows for forward genetics, which can be used to research the genetics of abiotic stress response and contribute to the development of crop types that are resistant to stress. Using CRISPR/Cas-based genome editing techniques, Shi et al. (2017) have created a maize variety with increased yield under drought stress. The research has focused on ARGOS8, which inhibits ethylene reactions. Increased drought tolerance was reported in plants with improved ARGOS8 expression (Shi et al., 2017). In another research, truncated gRNAs (tru-gRNAs) and Cas9 were driven by a tissue-specific AtEF1 promoter, which mutated the abiotic stress-responsive gene OST2/AHA1 and increased stomatal responses in Arabidopsis. To improve salinity tolerance, rice genes OsRR22 and OsNAC041 have also been targeted (Zhang et al., 2019; Bo et al., 2019). By utilizing the RNase/DNase capabilities of *Acidaminococcus* Cas12a (Cpf1) for multiplexed genome editing, a recent work effectively targeted 25 distinct genomic targets (Campa et al., 2019). Water, urea, H<sub>2</sub>O<sub>2</sub>, and silicon are some of the most important solutes for solute transport control, and aquaporins are among the best candidates for abiotic stress augmentation (Zargar et al., 2017). Recent studies revealed that, some other transporter proteins also involved in improving abiotic stress tolerance by genome editing (Vishwakarma et al., 2019; Ahmad et al., 2019). Increased gene expression using synthetic transcriptional activators and repressors (Piatek et al., 2015). C-repeat binding factors (CBFs) are responsible for plants' adaptation to cold temperatures. Producing triple mutant CBF1,2,3 lines through conventional genetic crossing is extremely difficult because the CBF1-3 loci are all on the same chromosome.

Therefore, creating single, double, and triple mutants of the CBF genes was effectively accomplished by utilizing the genome editing technique CRISPR/Cas9. When exposed to cold, the cbfs triple mutants are the most vulnerable to the effects of freezing stress among any of the other mutants. According to RNA sequencing investigation of the triple mutants, 10–20% of COR gene expression is CBF dependent (Jia et al., 2016; Zhao et al., 2016). These results support the idea that CBFs are important regulators that perform redundant functions in plants' cold adaptation. These experimental findings suggest that the CRISPR/Cas system can be effectively used for this innovative purpose and will eventually be the method of choice for targeting minor genes of complex quantitative features associated with abiotic stress (Mushtaq et al., 2018).

## CRISPR for drought tolerance

Since drought tolerant trait is complicated and quantitative, several physiological and biochemical mechanisms are involved in developing drought tolerance (Bhat et al., 2020). To increase public acceptance of genome-edited crops, experiments are being planned to alter the genes implicated in pathways for drought tolerance by using genome editing tools (Li et al., 2022). Numerous studies have documented how CRISPR confers plant drought tolerance (Table 1).

**Table 1. Gene modification for drought tolerance through genome editing**

| Crop        | Gene                 | Modification       | Reference                                |
|-------------|----------------------|--------------------|--|
| Rice        | MYB5, DERF1          | Down-regulation    | Zhang et al., 2014                       |
| Rice        | SRL1, SRL2, and ERA1 | knockout           | Liao et al., 2019;<br>Ogata et al., 2020 |
| Rapeseed    | A6RGA                | Insertion/deletion | Wu et al., 2020                          |
| Arabidopsis | OST2                 | Insertion/deletion | Osakabe et al., 2016                     |
| Arabidopsis | STL1                 | deletion           | Wang et al., 2022                        |
| Arabidopsis | miR169a              | Knockout           | Zhao et al., 2017                        |
| Arabidopsis | AVP1                 | Activation         | Park et al., 2017                        |
| Arabidopsis | AREB1                | Activation         | Roca Paixao et al., 2019                 |
| Arabidopsis | TRE1                 | Silencing          | Nunez-Munoz et al., 2021                 |
| Maize       | Abh2                 | Suppression        | Liu et al., 2020                         |
| maize       | abh2                 | Insertion/deletion | Liu et al., 2020                         |
| Tomato      | LBD40                | Insertion          | (Liu et al., 2020)                       |
| Tomato      | GID1a                | Insertion          | (Illouz-Eliaz et al., 2020)              |

## CRISPR for salt tolerance

Plants can tolerate salinity by activating more molecular and physiological processes and pathways (Munns and Tester, 2008). To control osmotic adjustment during salt stress, genome editing technologies have been used to target genes involved in ion transport (Volkov, 2015). Several studies have been conducted to show the possibility of development of salt tolerance in plants through CRISPR (Table 2.).

**Table 2. Gene modification for salt tolerance through genome editing**

| Crop        | Gene                           | Modification           | Reference                               |
|-------------|--------------------------------|------------------------|---|
| Rice        | OsmiR535                       | Knockout               | Yue et al., 2020                        |
| Rice        | RR9, RR10                      | Deletion               | Wang et al., 2019                       |
| Rice        | SPL10                          | Insertion and Deletion | Lan et al., 2019                        |
| Rice        | RR22                           | Insertion and Deletion | Zhang et al., 2019;<br>Han et al., 2022 |
| Rice        | PQT3                           | Insertion and Deletion | Alfatih et al., 2020                    |
| Tomato      | SIHyPRP1                       | Knockdown              | Tran et al., 2021                       |
| Tomato      | ABIG1                          | deletion               | Ding et al., 2022                       |
| Arabidopsis | SOS1 (salt overly sensitive 1) | Overexpression         | Yue et al., 2012                        |
| Arabidopsis | C/VIF1                         | Insertion and Deletion | Yang et al., 2020                       |
| Barley      | HvHKT2;1                       | Overexpression         | Mian et al., 2011                       |
| Cotton      | AITR genes                     | Deletion               | Wang et al., 2021                       |
| Maize       | STL1                           | Insertion and Deletion | Wang et al., 2022                       |

## CRISPR/Cas9 for cold stress

A crop's growth and yield are negatively impacted by cold stress, which can be separated into freezing stress (0°C) and chilling stress (0-15°C) based on the temperature difference (Guo et al., 2018). Mechanical damage of cells and metabolic activity malfunction are the most prevalent symptoms of cold stress. (Yadav, 2010). Low temperatures can harm agricultural crop species, impairing their growth, production, and survival ability (Sanghera et al., 2011). Many researchers have researched several crops to generate cold-tolerant crops through CRISPR (Table.3)

**Table 3. Gene modification for cold resistance through genome editing**

| Crop   | Gene                      | Modification   | Reference          |
|--------|---------------------------|----------------|--------------------|
| Rice   | OsPRP1                    | Knockout       | Nawaz et al., 2019 |
| Rice   | OsMYB30                   | Knockout       | Zeng et al., 2020  |
| Rice   | OsAnn3                    | Knockout       | Shen et al., 2017  |
| Rice   | OsAnn5                    | Knockout       | Que et al., 2020   |
| Tomato | CBF1                      | Knockout       | Wang et al., 2017  |
| poplar | PtPYRL1 and PtPYRL5 genes | Overexpression | Yu et al. 2017     |

## Conclusion

Our understanding of genetic manipulation and optimization of genome editing technology will grow with notable advancements toward developing crop varieties with abiotic stress resistance. In due course, genome editing tools could be incorporated with conventional and marker-assisted breeding efforts to get the desired improved varieties. Identifying multiple abiotic stress tolerant genotypes are most important for developing new varieties for a changing climate. Together, these initiatives will make significant progress in mitigating the consequences of climate change, especially drought, salt stress, and cold stress, and will improve agricultural productivity, ultimately improving food security.

## Author contributions

SM, SS: Conceptualized and written this review. CA: Edited this manuscript and approve for publication.

## Competing interests

The authors have declared that no conflict of interest exists.

## Ethics approval

Not applicable

## References

- Ahmad, P., Tripathi, D.K., Deshmukh, R., Pratap Singh, V. & Corpas, F.J. (2019). Revisiting the Role of ROS and RNS in Plants under Changing Environment; Elsevier: Amsterdam, The Netherlands.
- Alfatih, A., Wu, J., Jan, S.U., Zhang, Z.S., Xia, J.Q. & Xiang, C.B. (2020). Loss of rice PARAQUAT TOLERANCE 3 confers enhanced resistance to abiotic stresses and increases grain yield in field. *Plant Cell Environ.*, 43, 2743–2754.
- Aziz, K., Daniel, K.Y.T., Muhammad, Z.A., Honghai, L., Shahbaz, A.T., Mir, A. & Fahad, S. Nitrogen fertility and abiotic stresses management in cotton crop: a review. (2017). *Environ. Sci. Pollut. Res.*, 24, 14551–14566.

- Beck, E.H., Fettig S., Knake C., Hartig K. & Bhattarai T. (2007). Specific and Unspecific Responses of Plants to Cold and Drought Stress. *Journal Biosciences*, 32(3), 501–510.
- Bhat, J.A., Deshmukh, R., Zhao, T., Patil, G., Deokar, A., Shinde, S. & Chaudhary, J. (2020). Harnessing high-throughput phenotyping and genotyping for enhanced drought tolerance in crop plants. *J. Biotechnol.*, 324, 248–260.
- Bo, W., Zhaohui, Z., Huanhuan, Z., Xia, W., Binglin, L., Lijia, Y., Xiangyan, H., Deshui, Y., Xuelian, Z. & Chunguo, W. (2019). Targeted Mutagenesis of NAC Transcription Factor Gene, OsNAC041, Leading to Salt Sensitivity in Rice. *Rice Sci.*, 26, 98–108.
- Boudsocq, M., & Lauriere, C. (2005). Osmotic Signaling in Plants: Multiple Pathways Mediated by Emerging Kinase Families. *Plant Physiology*, 138(3), 1185–1194.
- Campa, C.C., Weisbach, N.R., Santinha, A.J. Incarnato, D. & Platt, R. (2019). Multiplexed genome engineering by Cas12a and CRISPR arrays encoded on single transcripts. *Nat. Methods*. 16, 887–893.
- Cramer G.R., Urano K., Delrot S., Pezzotti M. & Shinozaki. K. (2011). Effects of abiotic stress on plants: a systems biology perspective. *BMC Plant Biol.*, 11, 163-176.
- Deriano, L. & Roth, D.B. (2013). Modernizing the nonhomologous end-joining repertoire: alternative and classical NHEJ share the stage. *Annual Review of Genetics*, 47 (1), 433–455.
- Fedoroff, N.V., Battisti, D.S., Beachy, R.N., Cooper, P.J., Fischhoff, D.A., Hodges, C.N., Knauf, V.C., Lobell, D., Mazur, B.J. & Molden, D. (2010). Radically rethinking agriculture for the 21st century. *Science*, 327, 833-834.
- Gasiunas, G., Barrangou, R., Horvath, P. & Siksnys, V. (2012). Cas9–crRNA ribonucleoprotein complex mediates specific DNA cleavage for adaptive immunity in bacteria. *Proceedings of the National Academy of Sciences*, 109(39), 2579–2586,
- Gilmour, S.J., Zarka, D.G., Stockinger, E.J., Salazar, M.P., Houghton, J.M. & Thomashow M.F. (1998). Low temperature regulation of the *Arabidopsis* CBF family of AP2 transcriptional activators as an early step in cold induced *COR* gene expression. *The Plant Journal*, 16, 433– 442.
- Guo, X., Liu, D. & Chong, K. (2018). Cold signaling in plants: Insights into mechanisms and regulation. *J. Integr. Plant Biol.* 60, 745–756.
- Han, X., Chen, Z., Li, P., Xu, H., Liu, K., Zha, W., Li, S., Chen, J., Yang, G., Huang, J. & et al. (2022). Development of novel rice germplasm for salt-tolerance at seedling stage using CRISPR-Cas9. *Sustainability*, 14, 2621.
- Hesham, F.A. & Fahad, S. (2020). Melatonin application enhances biochar efficiency for drought tolerance in maize varieties: Modifications in physio-biochemical machinery. *Agron J.*, 1–22.
- Hu, H., Dai, M., Yao, J., Xiao, B., Li, X., Zhang, Q. & Xiong, L. (2006). Overexpressing a NAM, ATAF, and CUC (NAC) Transcription Factor Enhances Drought Resistance and Salt Tolerance in Rice. *Proceedings of the National Academy of Sciences*, 103(35), 12987– 12992.
- Illouz-Eliaz, N., Nissan, I., Nir, I., Ramon, U., Shohat, H. & Weiss, D. (2020). Mutations in the tomato gibberellin receptors suppress xylem proliferation and reduce water loss under water-deficit conditions. *J. Exp. Bot.*, 71, 3603–3612.
- Jia, Y.X., Ding, Y.L., Shi, Y.T., Zhang, X.Y., Gong, Z.Z. & Yang, S.H. (2016). The *cbfs* triple mutants reveal the essential functions of CBFs in cold acclimation and allow the definition of CBF regulons in *Arabidopsis*. *New Phytologist*, 212, 345– 353.

- Jinek, M., Chylinski, K., Fonfara, I., Hauer, M., Doudna, J.A. & Charpentier, E. (2012). A programmable dual-RNA guided DNA endonuclease in adaptive bacterial immunity. *Science*, 337, 6096, 816–821.
- Joung, J.K. & Sander, J.D. (2013). TALENs: a widely applicable technology for targeted genome editing. *Nature Reviews, Molecular Cell Biology*, 14, 1, 49–55,
- Kazuko, Y.S. & Shinozaki K. (2006). Transcriptional Regulatory Networks in Cellular Responses and Tolerance to Dehydration and Cold Stresses. *Annual Review of Plant Biology*, 57, 781-803.
- Kundzewicz, Z., Ulbrich, U., Brucher, T., Graczyk, D., Kruger, A. & Leckebusch G.C. (2005). Summer floods in central Europe-climate change track? *Nat. Hazard*, 36, 165-189.
- Lan, T., Zheng, Y., Su, Z., Yu, S., Song, H., Zheng, X., Lin, G. & Wu, W. (2019). OsSPL10, a SBP-Box gene, plays a dual role in salt tolerance and trichome formation in rice (*Oryza sativa* L.). *G3*, 9:4107–4114.
- Li, X., Xu, S., Fuhrmann-Aoyagi, M.B., Yuan, S., Iwama, T., Kobayashi, M. & Miura, K. (2022). CRISPR/Cas9 Technique for Temperature, Drought, and Salinity Stress Responses. *Curr. Issues Mol. Biol.*, 44, 2664–2682.
- Liao, S. Qin, X. Luo, L. Han, Y. Wang, X. Usman, B. Nawaz, G. Zhao, N. Liu, Y. & Li, R. (2019). CRISPR/Cas9-induced mutagenesis of semi-rolled leaf1, 2 confers curled leaf phenotype and drought tolerance by influencing protein expression patterns and ROS scavenging in rice (*Oryza sativa* L.). *Agronomy*, 9, 728.
- Liu, L., Zhang, J., Xu, J., Li, Y., Guo, L., Wang, Z., Zhang, X., Zhao, B., Guo, Y.D. & Zhang, N. (2020). CRISPR/Cas9 targeted mutagenesis of SILBD40, a lateral organ boundaries domain transcription factor, enhances drought tolerance in tomato. *Plant Sci.*, 301,110683.
- Liu, Q., Kasuga, M., Sakuma, Y., Abe, H. and Miura S., Yamaguchi-Shinozaki K. & Shinozaki K. (1998). Two transcription factors, DREB1 and DREB2, with an EREBP/AP2 DNA binding domain separate two cellular signal transduction pathways in drought and low temperature responsive gene expression, respectively, in *Arabidopsis*. *Plant Cell*, 10, 1391– 1406.
- Liu, S., Li, C., Wang, H., Wang, S., Yang, S., Liu, X., Yan, J., Li, B., Beatty, M. & Zastrow-Hayes, G. (2020). Mapping regulatory variants controlling gene expression in drought response and tolerance in maize. *Genome Biol.*, 21, 163.
- Liu, S., Li, C., Wang, H., Wang, S., Yang, S., Liu, X., Yan, J., Li, B., Beatty, M., Zastrow-Hayes, G. & et al. (2020). Mapping regulatory variants controlling gene expression in drought response and tolerance in maize. *Genome Biol.*, 21,163.
- Ma, X., Zhu, Q., Chen, Y. & Liu, Y.G. (2016). CRISPR/Cas9 platforms for genome editing in plants: developments and applications. *Molecular Plant*, 9 (7), 961–974.
- Marques S.J. & Arrabaca M.C. (2004). Contributions of soluble carbohydrates to the osmotic adjustment in the C<sub>4</sub> grass *setarias phacelata*: a comparison between rapidly and slowly imposed water stress. *Journal of Plant Physiology*, 161(5), 551-555.
- Mathivanan, S. (2021). Abiotic stress-induced molecular and physiological changes and adaptive mechanisms in plants. abiotic stress in plants, IntechOpen, doi:10.5772/intechopen.93367.
- Mian, A., Oomen, R.J., Isayenkov, S., Sentenac, H., Maathuis, F.J. & Very, A.A. (2011). Over-expression of a Na<sup>+</sup> and K<sup>+</sup>-permeable HKT transporter in barley improves salt tolerance. *Plant J.*, 68, 468–479.



- Miller, J.C., Tan, S., Qiao, G. & et al., 2011. A TALE nuclease architecture for efficient genome editing. *Nature Biotechnology*, 29 (2), 143–148.
- Munns, R. & Tester, M. (2008). Mechanisms of salinity tolerance. *Annu. Rev. Plant Biol.*, 59, 651.
- Mushtaq, M., Bhat, J.A., Mir, Z.A., Sakina, A., Ali, S. Singh, A.K., Tyagi, A., Salgotra, R.K., Dar, A.A. & Bhat, R. (2018). CRISPR/Cas approach: A new way of looking at plant-abiotic interactions. *J. Plant Physiol.*, 224, 156–162.
- Nawaz, G., Han, Y., Usman, B., Liu, F., Qin, B. & Li, R. (2019). Knockout of OsPRP1, a gene encoding proline-rich protein, confers enhanced cold sensitivity in rice (*Oryza sativa* L.) at the seedling stage. *Biotech*, 9, 254.
- Nunez-Munoz, L., Vargas-Hernandez, B., Hinojosa-Moya, J., Ruiz-Medrano, R. & Xoconostle-Cazares, B. (2021). Plant drought tolerance provided through genome editing of the trehalase gene. *Plant Signal. Behav.* 16, 1877005.
- Ogata, T., Ishizaki, T., Fujita, M. & Fujita, Y. (2020). CRISPR/Cas9-targeted mutagenesis of OsERA1 confers enhanced responses to abscisic acid and drought stress and increased primary root growth under nonstressed conditions in rice. *PLoS ONE*, 15, 0243376.
- Orvar, B.L., Sangwan, V., Omann, F. & Dhindsa, R.S. (2000). Early steps in cold sensing by plant cells: the role of actin cytoskeleton and membrane fluidity. *The Plant Journal*, 23, 785–794.
- Osakabe, Y. & Osakabe, K. (2015). Genome editing with engineered nucleases in plants. *Plant and Cell Physiology*, 56 (3), 389–400.
- Osakabe, Y. & Osakabe, K. (2017). Genome Editing to Improve Abiotic Stress Responses in Plants. In *Progress in Molecular Biology and Translational Science*; Elsevier: Amsterdam, The Netherlands, 149, 99–109.
- Osakabe, Y., Watanabe, T., Sugano, S. S., Ueta, R., Ishihara, R., Shinozaki, K. & et al. (2016). Optimization of CRISPR/Cas9 genome editing to modify abiotic stress responses in plants. *Sci. Rep.* 6, 26685. doi: 10.1038/srep26685.
- Park, J.J., Dempewolf, E., Zhang, W. & Wang, Z.Y. (2017). RNA-guided transcriptional activation via CRISPR/dCas9 mimics overexpression phenotypes in Arabidopsis. *PLoS ONE*, 12, e0179410.
- Piatek, A., Ali, Z., Baazim, H., Li, L., Abulfaraj, A. & Al-Shareef, S. (2015). RNA-guided transcriptional regulation in planta via synthetic dCas9-based transcription factors. *Plant Biotechnology*, 13, 578–589.
- Que, Z., Lu, Q., Liu, T., Li, S., Zou, J. & Chen, G. (2020). The rice annexin gene OsAnn5 is a positive regulator of cold stress tolerance at the seedling stage. *Res. Sq.*; in press.
- Rath, D., Amlinger, L., Rath, A. & Lundgren, M. (2015). The CRISPR-Cas immune system: biology, mechanisms and applications, *Biochimie*, 117, 119–128.
- Roca Paixao, J.F., Gillet, F.X., Ribeiro, T.P., Bournaud, C., Lourenco-Tessutti, I.T., Noriega, D.D., Melo, B.P., de Almeida-Engler, J. & Grossi-de-Sa, M.F. (2019). Improved drought stress tolerance in Arabidopsis by CRISPR/dCas9 fusion with a Histone Acetyl Transferase. *Sci. Rep.*, 9, 8080.
- Ruelland, E., Vaultier, M.N., Zachowski, A. & Hurry V. (2009). Cold signalling and cold acclimation in plants. *Advances in Botanical Research.*, 49, 35–150.
- Sanghera, G.S., Wani, S.H., Hussain, W. & Singh, N. (2011). Engineering cold stress tolerance in crop plants. *Curr. Genom.*, 12, 30.

- Shakespeare, S., Sivaji, M. & Sathish raj, R. (2022). Promises and Potentiality of Genome Editing in Crop Improvement. *Vijyan Varta*, 3 (7), 80-86.
- Shen, C., Que, Z., Xia, Y., Tang, N., Li, D., He, R. & Cao, M. (2017). Knock out of the annexin gene OsAnn3 via CRISPR/Cas9-mediated genome editing decreased cold tolerance in rice. *J. Plant Biol.*, 60, 539–547.
- Shi, J., Gao, H., Wang, H., Lafitte, H.R., Archibald, R.L., Yang, M., Hakimi, S.M., Mo, H., & Habben, J.E. (2017). ARGOS 8 variants generated by CRISPR-Cas9 improve maize grain yield under field drought stress conditions. *Plant Biotechnol. J.*, 15, 207–216.
- Siddiqui, K.S. & Cavicchioli, R. (2006). Cold-adapted enzymes. *Annual Review of Biochemistry*, 75, 403–433.
- Stockinger, E.J., Gilmour, S.J. & Thomashow, M.F. (1997). *Arabidopsis thaliana* CBF1 encodes an AP2 domain containing transcriptional activator that binds to the C-repeat/DRE, a cis-acting DNA regulatory element that stimulates transcription in response to low temperature and water deficit. *Proceedings of the National Academy of Sciences*, 94, 1035–1040.
- Suzuki, S., Ohta, K., Nakajima Y. & et al., 2020. Meganuclease-based artificial transcription factors, *ACS Synthetic Biology*, 9 (10), 2679–2691.
- Tran, M.T., Doan, D.T.H., Kim, J., Song, Y.J., Sung, Y.W., Das, S., Kim, E.J., Son, G.H., Kim, S.H. & Van Vu, T. (2021). CRISPR/Cas9-based precise excision of SlHyPRP1 domain (s) to obtain salt stress-tolerant tomato. *Plant Cell Rep.*, 40, 999–1011.
- Vishwakarma, K., Mishra, M., Patil, G., Mulkey, S., Ramawat, N., Pratap Singh, V., Deshmukh, R., Kumar Tripathi, D., Nguyen, H.T. & Sharma, S. (2019). Avenues of the membrane transport system in adaptation of plants to abiotic stresses. *Crit. Rev. Biotechnol.*, 39, 861–883.
- Volkov, V. (2015). Salinity tolerance in plants. Quantitative approach to ion transport starting from halophytes and stepping to genetic and protein engineering for manipulating ion fluxes. *Front. Plant Sci.*, 6, 873.
- Voytas, D.F. (2013). Plant genome engineering with sequence specific nucleases. *Annu. Rev. Plant Biol.* 64, 327–350.
- Wang, L., Zhao, R., Zheng, Y., Chen, L., Li, R., Ma, J. Hong, X., Ma, P., Sheng, J. & Shen, L. (2017). SIMAPK1/2/3 and antioxidant enzymes are associated with H<sub>2</sub>O<sub>2</sub>-induced chilling tolerance in tomato plants. *J. Agric. Food Chem.*, 65, 6812–6820.
- Wang, T., Xun, H., Wang, W., Ding, X., Tian, H., Hussain, S., Dong, Q., Li, Y., Cheng, Y., Wang, C. & et al. (2021). Mutation of GmAITSR genes by CRISPR/Cas9 genome editing results in enhanced salinity stress tolerance in soybean. *Front. Plant Sci.*, 12.
- Wang, W.C., Lin, T.C., Kieber, J. & Tsai, Y.C. (2019). Response Regulators 9 and 10 negatively regulate salinity tolerance in rice. *Plant Cell Physiol.*, 60, 2549–2563.
- Wang, Y., Cao, Y., Liang, X. & et al. (2022). A dirigent family protein confers variation of Casparian strip thickness and salt tolerance in maize. *Nat. Commun.*, 13, 2222.
- Wang, Y., Cheng, X., Shan, Q., Zhang, Y., Liu, J. & Gao, C. (2014). Simultaneous editing of three homoeoalleles in hexaploid bread wheat confers heritable resistance to powdery mildew. *Nat. Biotechnol.*, 32, 947–951.
- Wu, J., Yan, G., Duan, Z., Wang, Z., Kang, C., Guo, L. & et al. (2020). Roles of the *Brassica napus* DELLA protein BnaA6. RGA, in modulating drought tolerance by interacting with the ABA signaling component BnaA 10. ABF2. *Front. Plant Sci.*, 11. doi: 10.3389/fpls.2020.00577.

- Xiong, L., Schumaker, K.S., & Zhu J.K. (2002). Cell Signaling during cold, drought, and salt stress. *The Plant Cell*, 165-83.
- Yadav, S. Cold stress tolerance mechanisms in plants. A review. (2010). *Agron. Sustain. Dev.*, 30, 515–527.
- Yamaguchi & Shinozaki K. (1994). A novel cis-acting element in an *Arabidopsis* gene is involved in responsiveness to drought, low-temperature, or high-salt stress. *Plant Cell*, 6, 251– 264.
- Yang, W., Chen, S., Cheng, Y., Zhang, N., Ma, Y., Wang, W., Tian, H., Li, Y., Hussain, S., & Wang, S. (2020). Cell wall/vacuolar inhibitor of fructosidase 1 regulates ABA response and salt tolerance in *Arabidopsis*. *Plant Signal. Behav.*, 15, 1744293.
- Yu, J., Ge, H., Wang, X., Tang, R., Wang, Y., Zhao, F., Lan, W., Luan S. and Yang, L. (2017). Overexpression of pyrabactin resistance-like abscisic acid receptors enhances drought, osmotic, and cold tolerance in transgenic poplars. *Front Plant Sci.*, 8, 1752. <https://doi.org/10.3389/fpls.2017.01752>
- Yue, E. Cao, H. & Liu, B. (2020). OsmiR535, a potential genetic editing target for drought and salinity stress tolerance in *Oryza sativa*. *Plants*, 9, 1337.
- Yue, Y., Zhang, M., Zhang, J., Duan, L. & Li, Z. (2012). SOS1 gene overexpression increased salt tolerance in transgenic tobacco by maintaining a higher K<sup>+</sup>/Na<sup>+</sup> ratio. *J. Plant Physiol.*, 169, 255–261.
- Zargar, S.M., Nagar, P., Deshmukh, R., Nazir, M., Wani, A.A., Masoodi, K.Z., Agrawal, G.K. and Rakwal, R. (2017). Aquaporins as potential drought tolerance inducing proteins: Towards instigating stress tolerance. *J. Proteom.*, 169, 233–238.
- Zeng, Y., Wen, J., Zhao, W., Wang, Q. and Huang, W. (2020). Rational improvement of rice yield and cold tolerance by editing the three genes OsPIN5b, GS3, and OsMYB30 with the CRISPR–Cas9 system. *Front. Plant Sci.*, 10, 1663.
- Zhang, A., Liu, Y., Wang, F., Li, T., Chen, Z., Kong, D. Bi, J., Zhang, F., Luo, X. and Wang, J. (2019). Enhanced rice salinity tolerance via CRISPR/Cas9-targeted mutagenesis of the OsRR22 gene. *Mol. Breed.*, 39, 47.
- Zhang, A., Liu, Y., Wang, F., Li, T., Chen, Z., Kong, D., Bi, J., Zhang, F., Luo, X., Wang, J., et al. (2019). Enhanced rice salinity tolerance via CRISPR/Cas9-targeted mutagenesis of the OsRR22 gene. *Mol. Breed.*, 39, 47.
- Zhang, H. Zhang, J. Wei, P. Zhang, B. Gou, F. Feng, Z. Mao, Y. Yang, L. Zhang, H. Xu, N. et al. (2014). The CRISPR/Cas9 system produces specific and homozygous targeted gene editing in rice in one generation. *Plant Biotechnol. J.* 12, 797–807.
- Zhang, X., Fowler, S.G., Cheng, H.M., Lou, Y.G., Rhee, S.Y., Stockinger, E.J. and Thomashow M.F. (2004). Freezing sensitive tomato has a functional CBF cold response pathway, but a CBF regulon that differs from that of freezing tolerant *Arabidopsis*. *The Plant Journal*, 39, 905– 919.
- Zhao, C.Z., Zhang, Z.J, Xie, S.J, Si, T., Li, Y.Y. & Zhu, J.K. (2016). Mutational evidence for the critical role of CBF transcription factors in cold acclimation in *Arabidopsis*. *Plant Physiology.*, 171, 2744– 2759.
- Zhao, Y., Zhang, C., Liu, W., Gao, W., Liu, C., Song, G., Li, W.X., Mao, L., Chen, B. & Xu, Y. (2016). An alternative strategy for targeted gene replacement in plants using a dual-sgRNA/Cas9 design. *Sci. Rep.*, 6, 23890.
- Zhu, L., Chen, S., Alvarez, S., Asirvatham, V.S., Schachtman, D.P. & Wu Y. (2006). Cell wall proteome in the maize primary root elongation zone. I. Extraction and identification of water soluble and lightly ionically bound proteins. *Plant Physiol.*, 140, 311-325.