



# Applied Biotechnological Approaches for Reducing Yield Gap in Melon Grown Under Saline and Drought Stresses: an Overview

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## Abstract

Production of melon (*Cucumis melo* L.) is hampered by abiotic and biotic stress factors aggravated by climate change. To counter these challenges, plant breeders are employing biotechnological tools to generate high-yielding and stress-tolerant varieties to satisfy consumer and market demands. Currently, biotechnological tools are being used to complement conventional crop improvement and speed up the development of new varieties. This review highlights advances in biotechnological techniques for reducing the yield gap in melon crop production grown under saline and drought stress conditions. It also summarizes the current state of advanced biotechnological methods used for different objectives in melon crops grown under drought and salt stresses. In this review, we discussed and highlighted some difficulties that impeded the efficient obtention of enough melon yield productivity in previous years, and we also emphasized the greater contribution of biotechnological approaches to enhance global melon crop production. Further studies are required to thoroughly unravel the governing of drought and salt tolerance in melon species to develop quality and yield. In perspective, the use of high-throughput screening techniques and molecular markers is reported as a rapid and successful system to assess drought/salinity tolerance and high-yielding traits in numerous melon genotypes and produce new cultivars that contain the important and needed genes in a short period with an effective cost. Currently, biotechnological techniques such as MAS (marker-assisted selection), transcriptomics, genomics, proteomics, metabolomics and epigenomics, CRISPR/Cas9 (clustered regularly interspaced short palindromic repeats/cas9), SNPs (single-nucleotide polymorphism), GWAS (genome-wide association study), and GBS (genotyping-by-sequencing) have gained appreciation among breeders, for distinct purposes.

**Keywords** *Cucumis melo* · *Cucurbitaceae* · Biotechnology · Breeding · Drought · Salinity · Molecular markers

## 1 Introduction

Melon (*Cucumis melo* L.) is recognized for its economic worth as well as its nutritional and medicinal properties (Wen et al. 2022). Melon is an open-pollinated crop which belongs to the *Cucurbitaceae* family. It is generally grown in the Mediterranean and various regions of the world, and is affected by abiotic stress factors such as drought (Yavuz et al. 2021), temperature (Weng et al. 2021), and salinity (Lopez-Zaplana et al. 2022; Akrami and Arzani 2018; 2019).

Moreover, melon is one of the most desirable fruits and crops in terms of fruit structure and quality. One of the qualities of melon fruits includes the abundance of some key bioactive substances such as folic acid, vitamin C,  $\beta$ -carotene, and minerals including K and Mg (Can and Türkmen 2022; Zhang et al. 2022). Additionally, other present metabolites are volatiles associated with fruit aroma, pigments, organic acids, and carbohydrates responsible for sweetness and acidity. Melon, which has high economic importance, is globally grown on 1 million hectares of land and produces 28.5 M tons. China is the world's biggest melon producer with 13.8 M tons, followed by Turkey with 1.7 M tons and India with 1.3 M tons of production (FAOSTAT 2020). Moreover, the amount of melon produced in the world has increased, especially with the use of hybrid varieties (Cavalcante et al. 2020).

Improving yield from current arable lands will benefit global food security and climate change mitigation by

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closing yield gaps and minimizing agricultural expansion that is detrimental to protected land areas and forests. Identification of factors limiting present average production and production of high-yielding cultivars that can satisfy yield demands even under adverse environments are two potential solutions (Anderson et al. 2016; Suh et al. 2020; Shi et al. 2021; Tıraşçı and Erdoğan 2021). Environmental stress factors such as temperature, saline, and drought that threaten crop yield are indirectly engendered by CO<sub>2</sub> emitted into the atmosphere by environmental pollution, which creates greenhouse effects resulting in global climate change (Giordano et al. 2021). The intensification of the greenhouse effect and the formation of extreme temperatures and storms is an irreversible event (Liu et al. 2018a, b).

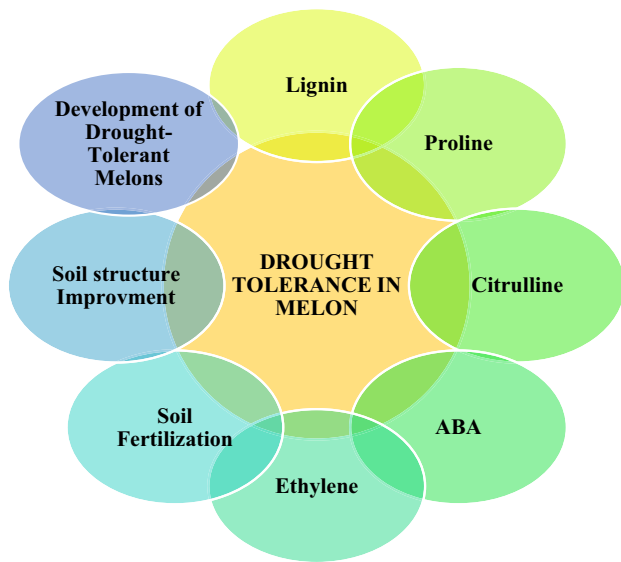
Constantly changing climatic conditions lead to changes in vegetative adaptation (Villalba-Bermell et al. 2021). Among the abiotic stresses, drought and salinity are interconnected and cause damage to the plant cell (Akhoundnejad and Daşgan 2019). Melon, as a moderately salinity-tolerant crop species, is cultivated in saline fields having different yield loss profiles depending on genotypes, environmental conditions, and severity of salt stress (Ariafar and Forouzan-deh 2017; Oliveira et al. 2019; Akrami and Arzani, 2019). Plants show different reactions to protect themselves from abiotic stress factors (Khan et al. 2015; Gong et al. 2020). Under stress conditions, plants develop escape, avoidance, and tolerance mechanisms (Chatterjee and Solankey 2015). Compared to other vegetables, the physiological response to drought in melon, which has high economic importance, has been less studied. Meanwhile, salt is one of the most pivotal factors affecting the production of melon (Akrami et al. 2019). Additionally, salinity is caused by the excessive accumulation of water-soluble salts caused by both environmental and anthropogenic factors (Gopalakrishnan et al. 2022). Irrigation with salt water, which is one of the causes of salinity, also reduces the efficiency. The highest salt concentration in water prevents the plant from taking water and prevents the accumulation of toxic ions (Na<sup>+</sup>) and the intake of nutrients like potassium (Marschner 2012; Taiz et al. 2017).

The most promising strategies to improve new cultivars with significantly improved genes tolerance to salt stress and water deficiency is through biotechnology (Nuccio et al. 2018; Suprasanna 2020). Biotechnological breeding is centered on altering the genetic structure of existing varieties to make them more suited to stress tolerance, productive, and cost-effective. This innovation increases the productivity and improves the quality of economically significant crops, as well as satisfies consumer demands and provides farmers with reliable varieties in a shorter time (Nyirahabimana et al. 2022). Other biotechnological studies are focusing on uncovering the natural defense systems employed by different crops to deal with stress, such as the complex regulatory

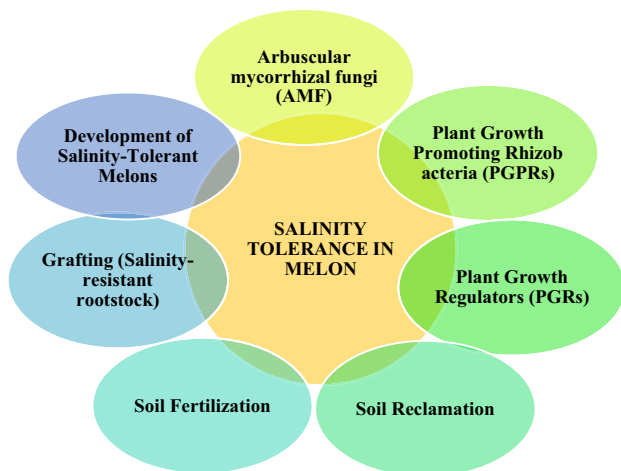
processes that include small RNAs, transcription factors, stress sensors, signaling, and defense pathways. Furthermore, plant breeders subsequently attempt to alter these natural mechanisms for tolerance or resistance to various stresses (Suprasanna 2020).

Severe droughts have been recorded all over the world, and they have been thoroughly attributed to global climate change, which has put a lot of pressure on agriculture and made the mission of reducing hunger and attaining food security even more challenging (Aduse Poku et al. 2020). Drought, which is one of the primary causes of yield loss and restricts plant growth, improvement, and yield, is among the leading abiotic stress adversities (Meddich et al. 2021; Astaraki et al. 2021) and reduces agricultural productivity by 50% in the world (Petkova et al. 2019; Fila et al. 2019; Anli et al. 2020). Moreover, drought is the situation where the amount of water in the soil decreases and there is not enough water for plant growth (Giordano et al. 2021). In addition to the increase in temperature, drought is also increasing due to the excessive use of natural resources (Jamalluddin et al. 2019). Plants have developed a mechanism that supports their growth by developing tolerance and adaptation under different stress conditions (Raza et al. 2019a, 2020). Since the water potential between leaves and soil decreases in drought conditions, plants try to decrease transpiration by their closing stomata to prevent loss of water and take more nutrients from the soil (Escalante-Magaña et al. 2019; Taiz et al. 2017).

The melon has a moderate sensitivity to salt towards flowering and a moderate saline tolerance during production. Melons grown in Brazil with 3–5 dS m<sup>-1</sup> saline irrigation water produce well. To make the amount of water required for plant production available, irrigation techniques are used (Melo et al. 2020; Terceiro Neto et al. 2021). The assessment of physiology and fruit production variations in melon plants (such as “Juazeiro” Piel de Sapo) under various water sustainable levels has been performed (Melo et al. 2020). Pre-germination treatments with plant bioactivators and regulators in melon seeds were evaluated for their effects on the development of seedlings that had been watered with biosaline water from fish-farming effluent. According to the study’s findings, salicylic and gibberellic acid seed pre-treatments reduce the impacts of water salinity and encourage growth modulations, resulting in more robust melon seedlings (Silva et al. 2022). Some of the plant mechanisms and management practices for drought tolerance in melon (Lodhi et al. 2013; Sarabi et al. 2017; Taiz et al. 2017; Akhoundnejad and Daşgan 2019; Escalante-Magaña et al. 2019; Fila et al. 2019; Kiran et al. 2019; Raza et al. 2019a, b; Giordano et al. 2021; Liu et al. 2021; Chevilly et al. 2021; Razi and Muneer 2021; Meddich et al. 2021) are highlighted in Fig. 1 as well as plant mechanisms and management



**Fig. 1** Plant mechanisms and management practices for drought tolerance in melon



**Fig. 2** Plant mechanisms and management practices for salinity tolerance in melon

practices for salinity tolerance in melon (Huang et al. 2012; Sarabi et al. 2017; Ilangumaran and Smith 2017; Yan et al. 2018; Comas et al., 2019; Abidalrazzaq Musluh Al Rubaye et al. 2021; Lin et al. 2021; Giordano et al. 2021; Oliveira et al. 2021; Gopalakrishnan et al. 2022) are mentioned in Fig. 2.

This review article emphasizes the role of available biotechnological tools used to assess drought and salinity tolerance in melon research as well as in current breeding efforts. We also discussed the prospect of high-throughput sequencing and gene editing technologies to support

ongoing efforts to increase yields despite the severity of abiotic stresses due to global climate change.

## 2 Research and Biotechnological Approaches for Salt and Drought Mitigation in Melon

In order to reach numerous breeding targets, scientists and plant breeders are under pressure to enhance available crops and improve novel crops that are disease and pest resistant, high-yielding, and tolerant to environmental stresses as well as more nutritious. It also includes meeting the demand of a growing global human population by 2050, as well as changing the current rate of crop production, which is now insufficient. Currently, technologies such as genotyping, genomic selection, marker-assisted selection, genome editing, and high-throughput phenotyping have accelerated the early selection and breeding of novel cultivars that can cope with global climate change and food demand (Tester and Langridge 2010; Hickey et al. 2019).

### 2.1 Biotechnological Approaches of Alleviation of Drought Stress in Melon

#### 2.1.1 Biochemical and Physiological Background

Furthermore, a vast number of studies have shown that phytohormones have a role in the drought stress response (Hossain et al. 2016; Xing et al. 2020). Plant development and productivity are significantly hampered by drought stress. Moreover, lipoxygenase (LOX), a key promoter of lipid peroxidation, is essential for direct and indirect abiotic stress responses (Liu et al. 2016; Xing et al. 2020). In response to osmotic stress, drought-tolerant plants store numerous organic osmolytes (compatible solutes). They are known to preserve cell turgor and absorb more water from the soil. Amino acids (as proline), small/polyol sugars (trehalose, mannitol), as well as tertiary sulfonium and quaternary ammonium compounds (such as dimethyl sulfoniopropionate, glycinebetaine) are three groups of compatible solutes. Compatible solutes can also operate as free radical scavengers, stabilizing proteins and/or membranes (Kusvuran et al. 2013). Furthermore, Chevilly et al. (2021) assessed melon cultivars at physiological and biochemical levels in the hopes of uncovering limiting factors for drought stress tolerance and defining specific traits and potential markers that would be targeted in breeding efforts. Authors discovered that the isoleucine, hydric potential, glycine, phenylalanine, serine, asparagine, and tryptophan, which are regulated by drought stress conditions, are the distinctive traits for drought tolerance.

Drought-stressed melon fruits usually grow soft, wrinkled, and discolored to brown. Furthermore, a lack of water causes premature ripening, resulting in smaller fruits. Plants respond to environmental stresses by undergoing developmental, physiological, and biochemical modifications, which include the activation of gene expression and the synthesis of a variety of proteins. Foliar enzyme activity, photosynthesis, mRNA accumulation, amino acid content, and carbohydrates all fluctuate when melon crops encounter drought stress conditions (Rojas et al. 2002). For instance, Kusvuran (2012) reported that the osmotic effect can be crucial in drought tolerance of melon crops during the early stages of growth. Drought stress reduces numerous physiological parameters like plant growth rate, stomatal conductance, leaf water potential, and osmotic potential. However, in certain resistance genotypes, these changes happen at a slower rate. Similarly, citrulline, a non-essential amino acid and an effective hydroxyl radical scavenger, has been identified as a key biochemical biomarker for determining drought tolerance in young melon genotypes. Thus, citrulline levels rise during drought stress and can be two times greater in drought-tolerant melons than in sensitive ones. Its presence is also linked to total amino acids, osmotic potential, plant dry weight, and proline, especially in tolerant genotypes (Kusvuran et al. 2013).

Moreover, stomata, which manage the flow of water and carbon dioxide between the plant and its environment, are another morphological indicators for drought tolerance. The overall efficiency of water utilization is determined by stomata control. Stomata density and stomatal opening modulation can influence the rate of transpiration. Water stress tolerance could be achieved by reducing the frequency and size of stomata. Stomata density plays an important role in drought resistance in melon genotypes during drought. Numerous reports suggest that drought-tolerant melon genotypes have low stomata density in the leaf. This characteristic is relevant for screening melon germplasm for drought resistance during the early stages of plant development (Kusvuran et al. 2009). Owing to Motallebi-Azar et al. (2019), in melon, dehydrin proteins have a crucial role in the mechanism of drought tolerance and could be a potential marker for selecting drought-tolerant melon cultivars. By testing four Iranian and local varieties as well as one commercial variety, the authors observed that the level of expression of dehydrin proteins in different variations was variable and depended on the level of drought stress imposed. Nevertheless, under extreme drought stress, dehydrin (45 and 50 kDa) proteins demonstrated high expression levels in all cultivars. Dehydrin protein quantity was higher in tolerant genotypes than in susceptible and moderate drought cultivars, as indicated by the reduced loss in leaves water content and fresh weight.

## 2.1.2 Melon germplasm Characterization and Conservation

Plant-breeding programs are primarily focused on developing high-yielding varieties under normal conditions and preserving that yield and production under abiotic stress. Naroumi Rad et al. (2017) highlighted the importance of several morphological and physiological features in evaluating melon germplasm for the preservation of genetic resources and melon breeding. The same authors characterized 36 different melon accessions grown in warm and dry territories in Karaj and found a high degree of diversity in the following morphological and physiological features: fruit weight, cavity diameter, single plant yield, and fruit length. Furthermore, fruit size changeability had considerable sorting potential. In their findings, they distinguished three different clusters that could serve as foundation parents for future breeding efforts capitalizing on fruit size and yield under drought stress. Likewise, Astaraki et al. (2022) used in their field research the largest melon germplasm collection, which included 30 genotypes from countries such as Afghanistan, France, Iran, Japan, Turkey, the USA, and Uzbekistan, with the greater part of genotypes (19) originating from Iran. The yield stability of all those diverse commercial melon genotypes was tested under drought stress. The authors concluded that yield stability was an essential factor to consider while evaluating melon genotype. After screening, the vast number of the highly drought-tolerant genotypes originated from Iran, and they are Mamaghani (Iran), Nahavandi (Iran), Shadegan (Iran), Crenshaw (USA), and Suski-eSabz (Iran). These types are exceptional genotypes that may be able to withstand drought stress. However, the total soluble solids (TSS) of Iranian melon genotypes were not acceptable, which could be a new breeding target for plant breeders.

Similarly, Akhoundnejad and Dasgan (2020) investigated drought tolerance and sensitivity in five melon genotypes when they were exposed to water deficits. Drought treatments, as expected, induced considerable variations in the assessed morphological and physiological indicators, with significant relationships between photosynthesis, yield, transpiration, and stomatal closure. According to the findings, some melon genotypes showed great promise under drought stress conditions. The CU179 and CU316 genotypes performed better and were judged more tolerant to stress scenarios. Additionally, in Egypt, Ibrahim and Ramadan (2013) conducted genotypic correlation and path analyses utilizing different agro-morphological traits and yield traits of 13 sweet melon genotypes under drought stress conditions. The efficiency of selecting for total yield per plant in sweet melon under drought conditions should be done using variables such as fruit weight and length, according to the findings of correlation and path analyses. In brief, the findings from several studies stated above will serve as the foundation

for future breeding efforts to develop new drought-tolerant lines and cultivars with high potential fruit yields.

### 2.1.3 Genomic Studies Expression

Breeders use genetic maps to facilitate more effective breeding using marker-assisted selection (MAS). The latest melon consensus genetic map has localized and detailed QTLs affecting yield-related features such as fruit weight, fruit number, and fruit yield (Diaz et al. 2011). This integrated genetic includes a large variety of molecular markers such as SNPs, SSRs, AFLPs, RAPDs, RFLPs, InDels, and IMAs, as well as several other important morphological features. The map covered 1150 cM and had an average marker density of one unique locus every 0.72 cM. Moreover, stress defense genes are important tools for breeders to evaluate and employ in genetic engineering to mitigate the negative effects of abiotic stresses (Aduse Poku et al. 2020).

Plants adjust their gene expression in response to environmental threats like drought, making them better suited to undue conditions (Rojas et al. 2002). Progress in molecular genetics has demonstrated that several genes are engaged in the activation of abiotic stress-related responses. Free radical scavengers, embryogenesis abundant (LEA) proteins, osmoprotectants, late chaperones, and heat shock proteins are among the first group of genes involved in direct defense of key proteins and membranes. Membrane transporters and ion channels, which are involved in the ions' and water's intake, make up the second group. The third category includes regulatory proteins such as kinases and transcription factors that regulate stress-related gene transcription. Those transcription factors are members of the following key transcription factor families: bHLH, MYB, bZIP, AP2/EREBP, and NAC (Hossain et al. 2016). Because it is well established that the root system is a critical part of the plant that perceives and responds to signals of water stress, Rojas et al. (2002) conducted a differential gene expression assessment in melon roots under drought stress conditions. A dozen differently expressed partial cDNAs were reamplified and cloned using reverse transcription PCR (RT-PCR). Following that, one of the clones revealed a 28–amino acid fragment of maize cell wall invertase. In sucrose metabolism, cell wall invertase catalyzes the irreversible conversion of sucrose into glucose and fructose. It also plays a role in stress response, sugar signaling, and other pleiotropic functions (Nishanth et al. 2018).

A comprehensive evaluation of the molecular mechanisms regulating the tolerance of numerous abiotic stresses, including drought stress, is needed to guarantee high yield and quality crop productivity, as well as to help with the development of crop varieties that can reduce the severity of abiotic stress on productivity (Shimira and Taşkın 2022). A number of melon drought-responsive genes and

transcriptional factors have been identified and reported in the literature as shown in Table 1. Additionally, microRNA (miRNAs) which are small RNAs that control mRNAs at both transcriptional and posttranscriptional levels constitute another important regulator of plant stress responses, and they are known for their impact for genes knock-in/out to enhance stress tolerance in agricultural crops. This is also why Sanz-Carbonell et al. (2019) carried out deep-sequencing and computational-based research in melon to understand miRNA-mediated response to abiotic stress. Under stress conditions, the expression of 24 known miRNAs was considerably negatively and/or positively regulated (downregulated and/or upregulated) and/or during at least one stress condition. Furthermore, the findings reveal that miRNAs that are downregulated in response to stress have as targets genes that are believed to be associated with the plant's stress response, whereas miRNAs that are upregulated have as targets genes that are associated with development. It appears that miR398 and miR408 stand out from other miRNAs in coordinating responses to several stresses such as drought, cold, and salinity. Briefly, miRNA-mediated regulation is a critical, complex, and dynamic mechanism in melon's ability to respond effectively to abiotic stresses (Sanz-Carbonell et al. 2019, 2020). These findings might provide a good platform for future melon breeding efforts, particularly in the production of drought-tolerant melon cultivars that could help boost yields and close yield gaps.

## 2.2 Current Biotechnological Techniques on Salt Stress in Melon Crops

### 2.2.1 Biochemical and Physiological Background

Salinity is a critical and primary environmental factor affecting and limiting plant production, especially in the regions of arids and semi-arids with insufficient precipitation and high salt concentrations in the soils. Saline stress paves the way for morphological, biochemical, and the physiological response changes that occur in plants. Salinity is pertinent to many conditions, including unbalanced nutrition, chloroplast and cell membrane distortion, and plant metabolism changes (Sarabi et al. 2017). Salinity has a number of detrimental impacts on crops, including altered cell metabolism, osmotic stress, nutritional disruptions, ion toxicity, and lower photosynthetic efficiency, all of which reduce plant viability and production. Overall, soil salinization is a major abiotic stressor that has an impact on the environment and agriculture productivity. Saline stress in plants disrupts osmotic balance and ion equilibrium, resulting in oxidation, metabolic inhibition and growth, and eventual plant death or loss (Zhang et al. 2021).

The most prevalent abiotic stress is salinity, which causes physiological and biochemical changes in the plant (Fu et al.

**Table 1** Gene related to abiotic stresses tolerance in melon

N°	Variety	Gene/family	Function and/or mechanism of action	Reference
1	Melon ( <i>Cucumis melo</i> L.)	<i>CmCAD</i> genes ( <i>CmCAD1</i> , 2, 3, and 5)	<i>CmCAD</i> genes are involved in lignin synthesis and contributes to drought tolerance. Positively, are regulated by ABA, H <sub>2</sub> O <sub>2</sub> and MeJA in drought stress conditions. Additionally, ABA and H <sub>2</sub> O <sub>2</sub> are involved in the positive regulations to <i>CmCAD1</i> , 2, 3, and 5, whereas JA is involved in the positive regulations to <i>CmCAD2</i> , 3, and 5	(Liu et al. 2021)
2	Oriental melon ( <i>Cucumis melo</i> L.)	<i>CmCAD2</i> and <i>CmCAD3</i>	<i>CmCAD2</i> and <i>CmCAD3</i> genes by synthesize lignin and are helping oriental melon to cope with drought stress	(Liu et al. 2020)
3	Melon ( <i>Cucumis melo</i> L.)	<i>CmMlo1</i> gene	<i>CmMlo1</i> gene has a key role in abiotic stresses tolerance in melon, and it is mainly expressed in melon cotyledon and flower	(Cheng et al. 2012)
4	Melon ( <i>Cucumis melo</i> L.)	Lipoxygenases (LOXs) gene known as <i>CmLOX08</i>	<i>CmLOX08</i> gene is key player in abiotic stresses responses including drought, salt, and wounds	(Wang et al. 2019)
5	Oriental melon ( <i>Cucumis melo</i> var. <i>makuwa</i> Makino)	<i>CmLOX10</i> gene	<i>CmLOX10</i> gene is crucial in the regulation of drought tolerance in oriental melon seedlings. It also promotes JA accumulation and stomatal closure	(Xing et al. 2020)
6	Oriental melon (“CaiHong7”)	<i>CmCADs</i> genes	<i>CmCADs</i> genes are crucial to stress responses and signaling pathway. It significantly promotes lignin deposition in stems and roots, and stem sections under abiotic stress	(Liu et al. 2018a, b)
7	Melon ( <i>Cucumis melo</i> L.)	<i>CmNCED3</i> and, <i>AtNCED3</i> genes of <i>NCED</i> subfamily within <i>CCD</i> Genes family	<i>CmNCED3</i> and <i>AtNCED3</i> plays a crucial role in environmental stress responses (drought, salt, and low temperature stresses) since they are highly expressed under abiotic stress	(Cheng et al. 2022)

2018). Soil salinity is caused by carrying natural rocks to water by breaking them down, irrigation with salt water, too much chemical fertilization, etc. (Zhu 2001). Sodium caused by salinity causes a decrease in fruit weight and potassium amount in the leaves (Tedeschi et al. 2017; Akrami et al. 2019). Sodium accumulation disrupts the Na<sup>+</sup>/K<sup>+</sup> ratio in plants and causes damage to cells (Deinlein et al. 2014). Potassium is thought to have a reducing effect on sodium in plant parts, but its effect on melon, which is moderately sensitive to salinity, has not yet been explained (Gao et al. 2020). Additionally, salinity raises two different categories of stress in plants: ionic and osmotic. A small amount of water and a high level of salinity in the soil cause osmotic stress, and harmful ions around the plant root zone cause ionic stress (Okçu et al. 2005). Salt stress causes premature aging of leaves (Naseer et al. 2022). Since there is a decrease in stomatal conductivity and limitations occur in photosynthesis, a decrease in viability and yield occurs in the plant (Marschner 2011; Munns and Tester 2008). In addition, salt stress, especially in melon, is understood by the Na amount

increased in roots and leaves (Lopez-Zaplana et al. 2022). In salinity problems, water intake decreases in plants due to osmotic stress. Competition occurs between potassium and calcium, and nutritional problems arise (Munns and Tester 2008; Sharma et al. 2012; Acosta-Motos et al. 2017). Generally, in salty conditions, the vegetative parts of the plants, especially the leaves, turn a dark green color and shrinkage occurs (Mer et al. 2000). Some of the management practices used for salinity tolerance in melon are listed in Table 2.

Currently, Sarabi and Ghashghaie (2022) carried out a study about the use of HCA, PCA, and OPLSDA to evaluate the biochemical and physiological reactions of three distinct melon genotypes at different concentrations of NaCl for 15 and 30 days of experiment in a greenhouse. The study of salt tolerance-related features is important not only for understanding salinity tolerance mechanisms, but also for incorporating them into salinity tolerance breeding programs. Generally, field salt stress increased leaf TChl, MDA, Pro, Car, TSC, Chla, Chlb, and H<sub>2</sub>O<sub>2</sub> and caused the depletion of leaf RWC and MSI as well as yield. It has been shown

**Table 2** Biotechnological approaches used to improve abiotic stress tolerance in melon plants

No:	Main objective of the study	Applied methods	Findings	References
1	The genome-wide investigation was carried out to discover <i>CCD</i> gene members in six <i>Cucurbitaceae</i> species, including melon, based on <i>CCD</i> genes in response to abiotic stress in melon	qRT-PCR analysis	After salt treatment, expression of CmNCED3 increased dramatically while expression of CmCCD4 and CmCCD8 was downregulated	(Cheng et al. 2022)
2	Analysis of <i>CmMlo1</i> gene expression in melon and molecular cloning	RT-PCR	The <i>CmMlo1</i> is primarily expressed flower and cotyledon in melon. And the results showed <i>CmMlo1</i> is involved to abiotic stress including saline	(Cheng et al. 2012)
3	Determination of genes that respond early to saline stress and reveal several new ESTs in the roots of melon ( <i>Cucumis melo</i> L.) seedlings	ESTs, RT-PCR	Saline stress activated a significant ration of the ESTs	(Wei et al. 2013)
4	Comparative analysis of saline stress-induced gene expression in two melon ( <i>Cucumis melo</i> L.) cultivars	ESTs, qRT-PCR,	A <i>NAC</i> gene (JZ477011) was heterologously expressed in yeast for functional characterization and has been increased the susceptibility of yeast cells to high salinity and impeded their growth	(Wei et al. 2014)
5	Transcriptome comparison and physiological analysis of two melon ( <i>Cucumis melo</i> L.) cultivars in response to saline stress	qRT-PCR, RNA-seq	Genes encoding transcription factors ( <i>MYB</i> , <i>NAC</i> and <i>WRKY</i> ) have been examined. The <i>NAC1</i> and <i>NAC2</i> reacted directly to salinity stress in all varieties, normally with an up-regulated trend	(Wang et al. 2016)
6	Genotypic differences in biochemical and physiological responses to salinity stress in melon ( <i>Cucumis melo</i> L.) plants: prospects for selection of local salt-tolerant species	Dye binding technique	The increase of SOD activity under salt stress was notable. And the landrace genotypes showed some promising behaviours with appropriate tolerance to salt stress	(Sarabi et al. 2017)
7	Comparative adaptation responses of melon ( <i>Cucumis melo</i> L.) genotypes to salinity stress	qRT-PCR	When genotypes exposed to 75 mM NaCl, the expression of <i>TCPI5</i> and <i>WRKY24</i> levels increased more, whereas <i>CmADH2</i> and <i>Dof3</i> elevated under 50 mM NaCl conditions	(Erdinc et al. 2021)

that there was a dynamic interaction between biomarkers for photosynthetic pigment (Chla), sugar osmolytes (TSC), and lipid peroxidation (MDA). In addition, authors reported that the cell wall integrity and cell viability under salinity stress in melon have been preserved and that yield has radically decreased (Akrami and Arzani 2018; Erdinc 2018). Mostly, salinity causes an excessive accumulation of reactive oxygen species (ROS), which could result in lipid peroxidation, protein oxidation, damage to DNA, enzyme inactivation, and interaction with other requisite plant cell components. To decrease ROS toxicity, plants possess distinct kinds of non-enzymatic and enzymatic antioxidative systems (Kusvuran et al. 2021).

### 2.2.2 Salinity Tolerance Germplasm Characterization and Conservation

Salts absorbed in soil solution get into close contact with roots and influence plant growth. The effects of salinity stress on plants are more complicated than pictured by the authors. The deleterious effects of salinity stress on higher plants can be divided into short-term or mild effects (osmotic stress) and long-term or severe salinity stress (ion toxicity) (Munns and Tester 2008; Arzani and Ashraf 2016). In addition to the primary effects, salinity stress has a cascade of secondary effects such as oxidative stress and nutritional imbalance (Arzani 2008). Plants have evolved various adaptive mechanisms to counteract the potential harmful effects of toxic salt ions (Arzani and Ashraf 2016). Osmotic adjustment, ion exclusion, ion sequestration, and ion homeostasis are the most significant mechanisms. Several plant features, at proteomic and metabolomic levels, are involved in salinity tolerance. Plant growth genes are linked to signals, hormones, transcription factors, and molecules, and they are likely to be shared by other stimuli (Giordano et al. 2021; Zahra et al. 2022). Recently, based on the efficient use of melon germplasm resources, the analysis of the genetic relevance and diversity of melons with varying degrees of salt tolerance has been performed to ensure the theory of using melon germplasm resources. Due to the different salt tolerance levels, SRAP (sequence-related amplified polymorphism) markers with 27 varieties of melon have been used. The results have been reported that the salt-tolerant melon was distributed among three groups: salt sensitive melon (first group), medium salt-tolerant melon (second group), and salt-tolerant melon (third group) (Gao et al. 2019). Further studies provide the required information for using melon germplasm resources based on saline tolerance (Zhu et al. 2010; Malek et al. 2012; Sarabi et al. 2017; Akrami and Arzani 2018; Zhao et al. 2018; Xiong et al. 2018; Akrami and Arzani 2019; Ibrarullah et al. 2019; da Silva et al. 2019; da Silva et al. 2021).

### 2.2.3 Biotechnological Approaches for Alleviation of Salinity in Melon

Appropriately, discovering new ways to produce plants that are more resilient to effects caused by salt stress remains the highest priority objective. Salt-tolerant rootstock markedly declined the salt stress damaging effects in plant through the depletion intake of Na and Cl, which intensifies micro-nutrients K and Ca intake (Kuşvuran et al. 2021). The 27 EST markers have been examined with real-time PCR. And the results proved that salt stress influences the increase of a proportion of the ESTs (Wei et al. 2013). Recently, the analogy of two melon cultivars (BXC and YL) transcriptome study has been reported in which 1171 genes were salt stress responsive in BXC, and 1487 were determined as saline stress sensitive in YL, and RNA-Seq identified 12 genes which indicated the reliability of the latter (Wang et al. 2016).

### 2.2.4 Genomic Studies Expression in Salt Tolerance in Melon Crop

Progress in molecular genetics has demonstrated that several genes are engaged in the activation of abiotic stress-related responses. Free radical scavengers, osmoprotectants, heat shock proteins, and chaperones are among the first groups of genes involved in the direct defense of key proteins and membranes. Membrane transporters and ion channels, which are involved in the ions' and water's intake, make up the second group. Regulatory proteins such as transcription factors and kinases that regulate stress-related gene transcription have been obtained in the third category. Those transcription components are associated with the following key transcription factor families: bHLH, MYB, bZIP, AP2/EREBP, and NAC (Hossain et al. 2016). Physiological and biotechnological approaches have become prevalent in many laboratories for identifying drought and saline-tolerant cultivars. Moreover, to screen for salinity tolerance in various crops, a DNA-based molecular marker approach has been devised. Molecular markers such as RAPD (random amplified polymorphic DNA), RFLP (restriction fragment length polymorphism), SSRs (simple sequence repeats), AFLP (amplified fragment length polymorphism), EST-SSRs (expressed sequence tags and simple sequence repeats), SRAP (sequence-related amplified polymorphism), and ILPs (intron length polymorphism) have been shown to be useful in susceptible and rapid screening of germplasm for saline tolerance. Nonetheless, progress in high-throughput sequencing technology has made SNPs (single-nucleotide polymorphism) a marker of preference in salt tolerance research. Determining specific genes associated with saline conditions stress tolerance is crucial, and it opens up new possibilities for marker-assisted selection breeding programs and gives an immense understanding on salt tolerance in plants (Datir 2018).



Additionally, genome editing tools such as clustered regulatory interspaced short palindromic repeats (CRISPR) and CRISPR-associated nuclease 9 (Cas9) systems (CRISPR/Cas9) have recently been applied to incorporate focused to characterize candidate genes and genome mutagenesis in different important agricultural crops (Rani et al. 2016; Khatoia et al. 2017). This genome editing technique can be used to analyse the genetics of abiotic stress tolerance in horticultural crops like melon (Bhatta and Malla 2020). Even though melon research on the metabolome and proteome is still in its early stages, these omics techniques can be combined with genomic and transcriptome studies to identify and describe novel genes related to abiotic stress factors' signaling biosynthesis pathways (Khurana and Checker 2011). Besides, improved biotechnological research in melon can reveal genetic and epigenetic mechanisms of gene expression, which are influenced by histone post-translational modifications, DNA methylation, and the RNAi (small non-coding RNAs) pathways. Furthermore, the epigenetic system is involved in many features of plant life that comprise agronomically significant characteristics and abiotic stress responses (Schmitz and Zhang 2011). Moreover, the further QTLs and linkage mapping studies are needed to uncover genetic basis of single and paired spikelets in the advanced melons cultivars to accelerate modern and advanced breeding to increase yield productivity. Additionally, as it has been reported and mentioned in several studies performed in cucurbits by using various high-throughput technologies, for instance, GBS in cucumber (Nyirahabimana et al. 2022), MAS in melon (Nyirahabimana and Solmaz 2021), a genome-wide study in melon under saline conditions (Wei et al. 2016), and gene modification is an effective approach for germplasm of watermelon such as GAWS (Joshi et al. 2021; Gong et al. 2022).

### 3 Conclusions and Future Perspectives

High-throughput biotechnological methods such as transcriptomic analysis, genome editing, RNA interference, epigenomics, and virus-induced gene silencing tools are recommended to expedite the progress of functional genome for advanced breeding programs to increase and fill the gap in melon crop production. Classical breeding techniques require a lot of time, but these methods have helped to improve superior melon cultivars for several traits, including salinity tolerance. Nonetheless, abiotic stress factors like salt, drought, and heat during melon cultivation are the primary restraints for melon production and yield around the world. Furthermore, emerging genomic and biotechnological methods like functional genomics, marker-assisted breeding, genetic engineering, marker-assisted selection, and others have been used to speed up breeding programs.

Nevertheless, their full potential has yet to be realized in various crop productions, including melon. Biotechnological techniques, including genome editing approaches, can introduce mutations in the plant genome. Production of genome-edited melon plant varieties usually starts with the selection of genes of interest and the construction of gene pools. Further studies are required to improve, develop, and increase the melon production to satisfy the consumers preference and fulfill the gap obtained in the melon production all over the world.

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**Data Availability** Data sharing is not applicable to this article as no datasets were generated during the current study.

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