agronomy

MDPI

Review

MicroRNA and cDNA-Microarray as Potential Targets against Abiotic Stress Response in Plants: Advances and Prospects

Tariq Pervaiz [1,2], Muhammad Waqas Amjid [3], Ashraf El-kereamy [2], Shi-Hui Niu [1,*] and Harry X. Wu [1,4,5,*]

[1] Beijing Advanced Innovation Center for Tree Breeding by Molecular Design, National Engineering Laboratory for Tree Breeding, College of Biological Sciences and Technology, Beijing Forestry University, Beijing 100083, China; tariqzoqi2009@gmail.com
[2] Department of Botany and Plant Sciences, University of California Riverside, Riverside, CA 22963, USA; ashrafe@ucr.edu
[3] State Key Laboratory of Crop Genetics and Germplasm Enhancement, Cotton Germplasm Enhancement and Application Engineering Research Center (Ministry of Education), Nanjing Agricultural University, Nanjing 210095, China; waqasamjid@hotmail.com
[4] Umeå Plant Science Centre, Department of Forest Genetics and Plant Physiology, Swedish University of Agricultural Sciences, Linnaeus väg 6, SE-901 83 Umeå, Sweden
[5] CSIRO National Research Collection Australia, Black Mountain Laboratory, Canberra, ACT 2601, Australia
* Correspondence: arrennew@bjfu.edu.cn (S.-H.N.); harry.wu@slu.se (H.X.W.)

Abstract: Abiotic stresses, such as temperature (heat and cold), salinity, and drought negatively affect plant productivity; hence, the molecular responses of abiotic stresses need to be investigated. Numerous molecular and genetic engineering studies have made substantial contributions and revealed that abiotic stresses are the key factors associated with production losses in plants. In response to abiotic stresses, altered expression patterns of miRNAs have been reported, and, as a result, cDNA-microarray and microRNA (miRNA) have been used to identify genes and their expression patterns against environmental adversities in plants. MicroRNA plays a significant role in environmental stresses, plant growth and development, and regulation of various biological and metabolic activities. MicroRNAs have been studied for over a decade to identify those susceptible to environmental stimuli, characterize expression patterns, and recognize their involvement in stress responses and tolerance. Recent findings have been reported that plants assign miRNAs as critical post-transcriptional regulators of gene expression in a sequence-specific manner to adapt to multiple abiotic stresses during their growth and developmental cycle. In this study, we reviewed the current status and described the application of cDNA-microarray and miRNA to understand the abiotic stress responses and different approaches used in plants to survive against different stresses. Despite the accessibility to suitable miRNAs, there is a lack of simple ways to identify miRNA and the application of cDNA-microarray. The elucidation of miRNA responses to abiotic stresses may lead to developing technologies for the early detection of plant environmental stressors. The miRNAs and cDNA-microarrays are powerful tools to enhance abiotic stress tolerance in plants through multiple advanced sequencing and bioinformatics techniques, including miRNA-regulated network, miRNA target prediction, miRNA identification, expression profile, features (disease or stress, biomarkers) association, tools based on machine learning algorithms, NGS, and tools specific for plants. Such technologies were established to identify miRNA and their target gene network prediction, emphasizing current achievements, impediments, and future perspectives. Furthermore, there is also a need to identify and classify new functional genes that may play a role in stress resistance, since many plant genes constitute an unexplained fraction.

Keywords: abiotic stress tolerance; drought stress; salinity stress; cold stress; miRNA target gene expression; adaptation

Citation: Pervaiz, T.; Amjid, M.W.; El-kereamy, A.; Niu, S.-H.; Wu, H.X. MicroRNA and cDNA-Microarray as Potential Targets against Abiotic Stress Response in Plants: Advances and Prospects. *Agronomy* **2022**, *12*, 11. https://doi.org/10.3390/agronomy12010011

Academic Editor: Alfonso Albacete

Received: 17 November 2021
Accepted: 15 December 2021
Published: 22 December 2021

1. Introduction

Plants are subjected to a wide range of abiotic stresses that are primarily hostile to plant growth, leading to plant death worldwide. Abiotic stresses have an extensive impact on various physiological, molecular, and metabolic responses. Much progress has been made in unravelling the complex stress response mechanisms, particularly in identifying stress-responsive genes with the help of biotechnological tools [1,2]. MicroRNAs (miRNAs), play a critical role in post-transcriptional regulation through base-pairing with other miRNA targets, including transcription factors (TFs) [1,3]. Understanding the role of miRNAs in abiotic stresses may be helpful in the development of innovative ways for improving plant responses against abiotic stresses. MicroRNAs are involved in multiple cellular and metabolic pathways under abiotic stresses, such as flowering, morphogenesis, signal transduction [4–6], and gene feedback regulation [7]. MicroRNAs are a group of single-stranded non-protein-coding short length RNA of approximately 18–25 nucleotides in length with a highly conserved class [8–10]. MicroRNAs are formed by antecedence with distinctive stem-loop assemblies [11]. In the plants, miRNAs are important regulators of gene expression at various stages of plant development; for instance, 959 founding members representing 178 miRNA families were identified in rapeseed (*Brassica napus*), earth mosses (*Physcomitrella patens*), arabidopsis (*Arabidopsis thaliana*), maize (*Zea mays*), black cottonwood (*Populus trichocarpa*), barrel clover (*Medicago truncatula*), rice (*Oryza sativa*), soybean (*Glycine max*), sorghum (*Sorghum bicolor*), and sugar cane (*Saccharum officinarum*) [12,13] (Tables 1 and 2). Usually, intronic miRNAs are coordinately expressed in host plant miRNAs, suggesting that they are also initiated from mutual transcripts. Host gene expression by situ analysis was used to probe the temporal and spatial localization of intronic miRNAs. These non-coding small RNAs are proposed to perform crucial roles in plant adaptation and immunity to adverse environmental conditions [14,15].

Table 1. Examples of miRNAs identified in model plants under drought, cold and salinity stresses.

Stress Condition	Plant Species	Inducible Genes	Known Responsive miRNAs	Functions	References
Drought stress	*Arabidopsis thaliana*	Rd29A (At5g52310) *CCAAT-binding transcription factors*	miR164, miR169, miR389, miR393, miR396, miR397, miR402	Pathogen immune response Drought tolerance Oxidative stress tolerance Pathogen immunity response Syncytium formation response to parasitic nematodes	[16–19]
	Medicago truncatula	*CCAAT Binding Factor (CBF)* *Growth Regulating Factor (GRF)* *Cu/Zn superoxide dismutases (CSD1, CSD2)* *TIR-NBS-LRR domain protein*	miR169, miR396 miR398, miR2118	Drought tolerance Syncytium formation response to parasitic nematodes Oxidative stress tolerance Photoperiod-sensitive male sterility	[16,20]
	Oryza sativa	SalT (LOC_Os01g24710) *TIR1* OsLEA3 (LOC_Os05g46480)	miR393 miR402	Salt/cold tolerance	[6,17,18,21]
Cold stress	*Arabidopsis thaliana*	*Rd29A* (At5g52310) *CBF3* (At4g25480)	*miR165*, *miR172*, *miR169*, *miR396*, *miR397*, *miR402*	Drought/cold tolerance Drought tolerance Heat stress tolerance	[16,17]
	Oryza Sativa	*OsWRKY71* (LOC_Os02g08440) *OsMAPK2*(LOC_Os03g17700) Os05g47550, Os03g42280 Os01g73250, Os12g16350 Os03g19380	*miR319*, *miR389*, *miR393*, miR1320, miR1435 miR1884b, CHY1 CP12-2	Drought/salt tolerance Cold tolerance Pathogen immunity response	[17,21–23]

Table 1. *Cont.*

Stress Condition	Plant Species	Inducible Genes	Known Responsive miRNAs	Functions	References
Salinity stress	*Arabidopsis thaliana*	*Rd29A* (At5g52310) *COR15A* (At2g42540)	*miR389*, *miR393*,	Oxidative stress tolerance Heat stress tolerance	[24]
	Populus trichocarpa	Dihydropyrimidinase	miR162, miR164, miR166, miR167, miR168, miR172, miR395, miR396	Pathogen immune response Drought tolerance Drought/cold tolerance Sulfate-deficiency response	[25–27]
	Glycine max		miR1507a, miR395	Sulfate-deficiency response	[28]
	Oryza sativa	*SalT* (LOC_Os01g24710) *OsLEA3* (LOC_Os05g46480)	miR156, miR158, miR159, miR397, miR398, miR482.2, miR530a, miR1445	Drought tolerance Pathogen immune response Heat stress tolerance	[22,29–31]
	Zea mays		*miR402*	Seed germination and seedling growth of Arabidopsis under stress	[18]

Table 2. Microarray analysis of genes involved in the drought, salinity and cold stress responses in Arabidopsis.

Phenotype of Mutants	Genes	Function	AGI Code	Coded Proteins	Microarrays	
Increased tolerance to drought	*AtPARP2*	DNA repair	At2g31320	Poly (ADPribose) polymerase	24K Affymetrix	[32–34]
Hypersensitive to drought stress	*AHK1/ ATHK1*	positive regulator of drought and salt stress responses	At2g17820	Histidine kinase	22K Agilent	[32,35,36]
Increased tolerance to drought stress	*AREB1/ ABF2*	regulate the ABRE-dependent expression	At1g45249	bZIP TF	22K Agilent	[33,37,38]
Increased tolerance to salt stress	*AtbZIP60*	encodes a predicted protein of 295 aa	At1g42990	bZIP TF	44K Agilent	[37,39]
Increased tolerance to drought stress	*AtMYB60*	regulates stomatal movements and plant drought tolerance	At1g08810	MYB TF	7K cDNA	[40]
Increased sensitivity to drought stress	*AtMYB41*	control of primary metabolism and negative regulation	At4g28110	MYB TF	24K Affymetrix	[41,42]
Increased tolerance to drought and salt stress	*AHK2*	positive regulators for cytokinin signaling	At5g35750	Histidine kinase	Agilent	[35,36]
Increased tolerance to drought and salt stress	*AHK3*	perception of cytokinin, downstream signal transduction	At1g27320	Histidine kinase	22K Agilent	[35,36]
Increased tolerance to drought and freezing stress	*DREB1A/ CBF3*	stress-inducible transcription factor	ERF/AP2 TF	ERF/AP2 TF	1.3K cDNA	[43]
Increased tolerance to drought stress	*DREB2A*	heat shock-stress responses.	At5g05410	ERF/AP2 TF	22K Agilent 7K cDNA	[44]
Hypersensitive to salt	*HOS10*	coordinating factor for responses to abiotic stress and for growth and development.	At1g35515	MYB TF	24K Affymetrix	[32,45]
Increased tolerance to drought stress	*ZFHD1*	mediates all the protein-protein interactions	At1g69600	Zinc finger HD TF	22K Agilent	[36,39]

Numerous miRNAs/target gene expression modules are responsive to abiotic stresses in arabidopsis; therefore, altering the molecular profile of certain expression modules might help plants adapt to abiotic stresses [46,47]. To date, miRNAs have become an important field of intense study in recent years. Functional analysis of conserved miRNAs revealed their association with numerous developmental and biological processes. They

regulate diverse metabolic events, including meristem boundary formation, organ separation and auxin signaling, the transition from the vegetative to the reproductive stage (juvenile-to-adult), and stress tolerance (Figure 1). The first reported miRNA in *Arabidopsis thaliana* to regulate the auxin signaling pathway was miR398, and miR398 was the first-ever reported miRNA related to stress tolerance. At the same time, the expression of miR398 was down-regulated under various oxidative activities and environmental stresses (Figure 1) [48,49], which further validate the substantial involvement of miRNAs in adverse environmental conditions [15]. MicroRNAs are significantly hardboard during plant development by negative gene expressions at the post-transcriptional level [50,51], and hence are considered as a popular molecular tool in modern biotechnology to study signal transduction, environmental extremes, response to stresses, protein degradation, biogenesis, and pathogen incursion [50,52,53]. Recently, several miRNAs have been mutually recognized by experimental and computational tactics in many crops [54]. In contrast, hundreds of identified miRNAs are documented as conserved across several species, suggesting that miRNAs might be used to develop abiotic stress tolerance in plants through genetic modifications [52,55].

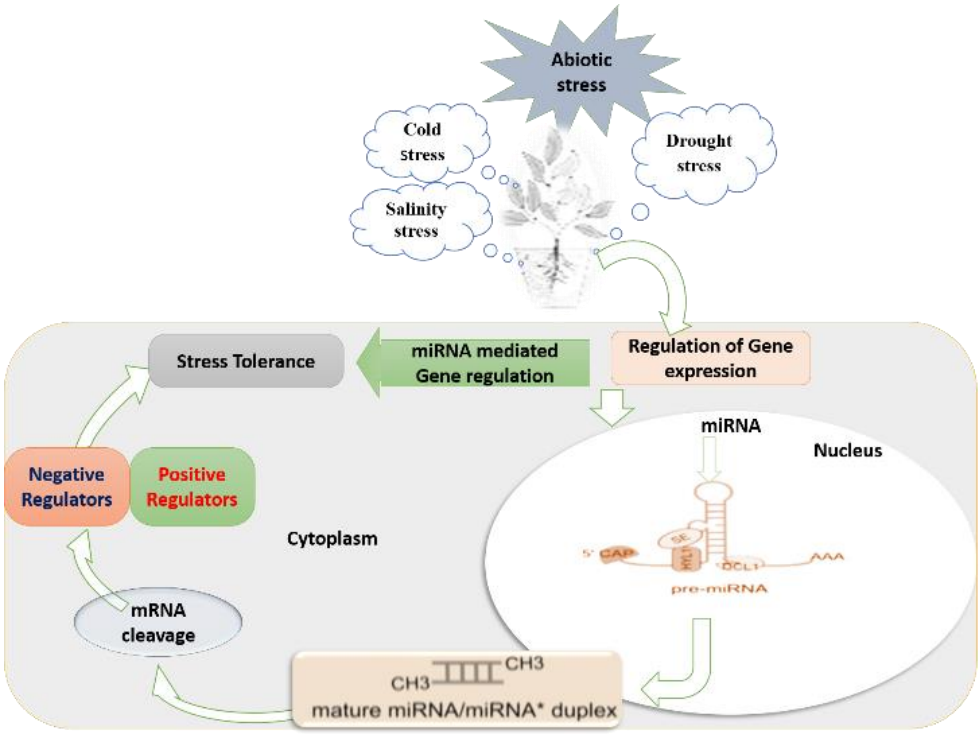

Figure 1. Schematic summary of miRNA-mediated regulatory mechanisms under abiotic stress in plant cells, with the particular formation process of miRNAs and miRNA mediated gene regulation: (1) miRNA gene is transcribed to a long sequence of primary miRNA (pri-miRNA). Primary miRNAs (pri-miRNAs) are transcribed from nuclear-encoded MIR genes by RNA polymerase II (Pol II), leading to precursor transcripts with a characteristic hairpin structure. (2) The pri-miRNA is cleaved to a stem-loop intermediate called miRNA precursor or pre-miRNA.

The second important function of miRNAs is in post-transcriptional regulation by targeting mRNAs for repressing or cleavage translation [16]. Many detrimental environmental factors adversely affect the plant's metabolic activities which, as a result, inhibit plant growth and development. However, it is quite challenging to differentiate and quantify the impact of various stresses on the plants through visual identification of hazardous factors, such as ozone, wound, and drought. Therefore, the development of sensitive and reliable techniques for diagnostics based on determining altering genes expression in DNA microarray is required [56]. Thus, the use of high-throughput sequencing (HTS)

and genome tilling miRNA are focused on discovering the function of epigenetic mechanisms in ecological adaptation and genome idiomatic expressions. However, epigenomics, expression-pattern, and functional characterization urge us to elucidate the communal regulatory pathways by miRNAs that control abiotic stress resistance in plants [57]. Small RNA cloning and high-throughput deep sequencing technologies can obtain the expression profiles of both known and unknown miRNAs. The study of post-transcriptional regulation is also crucial in improving stress tolerance and suggesting next-generation targeting for classical breeding and genetic improvement.

DNA microarrays are a commonly developed tool in functional genomics. Analysis of the microarray expression profiles is a positive approach to improve in-depth understanding of genes involved in regulatory networks and signal transduction associated with resistance against multiple abiotic stresses [58,59]. With the continued progress of genome sequencing, DNA-microarray technology has become the pioneer in biotechnology and has bridged the gap between functional genomics and sequencing data. Microarrays are classified into two main classes according to the nature of immobilized probes: (1) DNA microarrays created with DNA-fragments which are normally produced by employing PCR techniques [60–62] and spotted cDNA-microarrays (most commonly used) and (2) oligonucleotide microarrays produced with longer (up to 120-mer) or shorter (10 to 40-mer) oligonucleotides premeditatedly corresponding to explicit coding targets. These cDNA-microarrays have certain advantages, particularly for regulating gene expression patterns. However, oligonucleotide-microarrays are restricted to low sequence complication array elements. The hybridization specificity for a compound probe is amended with arrays containing DNA fragments that are significantly longer than oligonucleotides [61,63]. The spotted cDNA-microarray was the earliest and widely used technology, which comprised several PCR-amplified probes of cDNA-fragments dropped, cross-linked, and dried in a matrix pattern of spots on a treated glass surface. The targets for these samples are preferentially identified cDNA solutions derived from reverse-transcribed mRNAs obtained from two cell samples populations [64,65]. There are two modifications to the DNA array series that may contain cDNAs that are immobilized to a firm base, such as oligonucleotides or glass/nylon membranes, that are perceived on glass slides (20 to 80-mer) [63]. The most hotly debated topics are the data normalization techniques, the purpose of which is to reduce the sample variations resulting from the technical features of microarray processing that may obscure biological differences in a specific experiment [66]. The review presents a perspective analysis and bridges the gap between previous and recent advancements in MicroRNAs and cDNA-Microarray as potent targets to cope with abiotic adversities in plants.

2. MicroRNAs and Microarray Target Prediction against Abiotic Stress

Perusing plant stress responses is an inclusive concern, which has been threatened by global warming and other abiotic factors. Currently, numerous miRNAs related to stress-responses have been identified as being triggered under high salinity, low temperature, and drought [58,67,68] (Tables 1–3, Figure 2). The stress-induced miRNAs depend upon the type of stress, tissues or organs, and plant genotype. Stress-sensitive miRNAs can either be negative regulators by downregulation or positive regulators by upregulation of the accumulation of positive regulators [57]. MicroRNA regulates gene modulation in a sequence-specific mode and plays a significant role against stress. Understanding and recognizing abiotic stress-associated microRNAs can help to establish schemes and improve tolerance against extreme stress [69,70]. Various advancements in miRNA identification—for example, deep sequencing, cloning, and prediction by bioinformatics methods, including miRNA-regulated network, miRNA target prediction, miRNA identification, expression profile, features (disease or stress, biomarker) association, tools based on machine learning algorithms, NGS, and tools specific for plants—have been developed to study the expression patterns of miRNA against stress [70–72]. High-throughput sequencing (HTS) evaluated the miRNA landscape of Arabidopsis entire seedlings subjected to heat, drought, and

salinity stress, and 121, 123, and 118 miRNAs with a larger than 2-fold changed abundance, respectively, were discovered [46]. cDNA-microarray includes 3628 distinctive sequences retrieved from the Yukon ecotype of *Thellungiella salsuginea*, earlier stress-induced cDNA libraries, and reported transcript profiles in response to simulated drought, cold, and salinity [73]. Many stress-inducible genes are responsible for low temperature and dehydration; their sequences have been used to prepare cDNA-microarray with descriptive exposure of the *T. salsuginea* genome developed with stress-associated gene expression [41,73,74]. In addition, microarray revealed a larger number of stress-related genes (1886) as differentially regulated in *RGA1* mutants [75]. Using full-length cDNA or Gene Chips array transcription profiling experiments on *A. thaliana* reveals an extensive alteration occurrence in transcription against salinity, cold, and drought stress [74,76] (Table 2).

Table 3. miRNAs regulated by drought stress, salinity stress, and cold stress in plants.

Stress Condition	Plant Species	miRNA	Key Functions	Response	References
Drought stress	*Medicago truncatula*	miR398a,b miR408 miR399k miR2089 miR2111a-f,h-s miR2111g miR4414a	Oxidative stress tolerance Salt/drought/cold/oxidative osmotic-stress responses Phosphate-deficiency response	Up-regulated	[20,77–80]
		miR398b,c miR2111u,v miR5274b miR1510a-3p, 5p miR1510a	Heat stress tolerance Drought responsive Oxidative-stress tolerance triggering phasiRNA production from numerous NB-LRRs	Down-regulated	[77,79,80]
	Glycine max	miR5554a-c	Drought responsive		[79]
Salinity stress	*Glycine max*	miR169d miR395a miR395b,c miR1510a-5p miR1520d,e,l,n,q	Drought tolerance Sulfate-deficiency response triggering phasiRNA production from numerous NB-LRRs	Up-regulated	[20,81,82]
		gma-miR159b,c gma-miR169b,c gma-miR1520c	Pathogen immune response Drought/Salt tolerance	Down-regulated	[82]
	Phaseolus vulgaris	pvu-miR159.2	Plant–nematode interaction		
Cold stress	*Phaseolus vulgaris*	pvu-miR2118	regulate the expression of genes encoding the TIR-NBS-LRR resistance protein	Up-regulated	[31]

Cold- or drought-inducing genes were clustered based on the RNA gel blot and microarray analyses. The clusters were (1) cold-specific, (2) cold-inducible, and (3) drought-specific inducible genes. Recently, microRNAs have appeared as gene expression regulators that have also been associated with stress responses. However, the association between stress responses and miRNA expression is just beginning to be unfolded and documented. Fourteen stress-inducible miRNAs were established using microarray, in which the results of three main environmental stresses in Arabidopsis were plotted. Of them, 10 were cold regulated and had high salinity, while four were detected for drought miRNAs [83,84] (Tables 1 and 2). Seki M., et al. [43] reported 20 genes related with cold and drought-inducible genes, five which were drought-specific, and four novel genes, including *FL5-2D23*, *FL5-3J4*, *FL2-56*, and *FL6-55*, and two genes that were cold-specific inducible, including a novel (*FL5-90*) gene. Additionally, in rice, two siRNAs were previously reported as miR441 and miR446 [70,85,86]. They were testified to be down-regulated due to water deficiency; miR169g is the individual gene tempted by the scarcity of water which belongs to the miR169 family (Table 1). Moreover, the miRNAs responsive to abiotic stress inducements were comprised of 21 miRNAs belonging to 11 miRNA families which were up-regulated by UV-B stress in Arabidopsis [51,87,88].

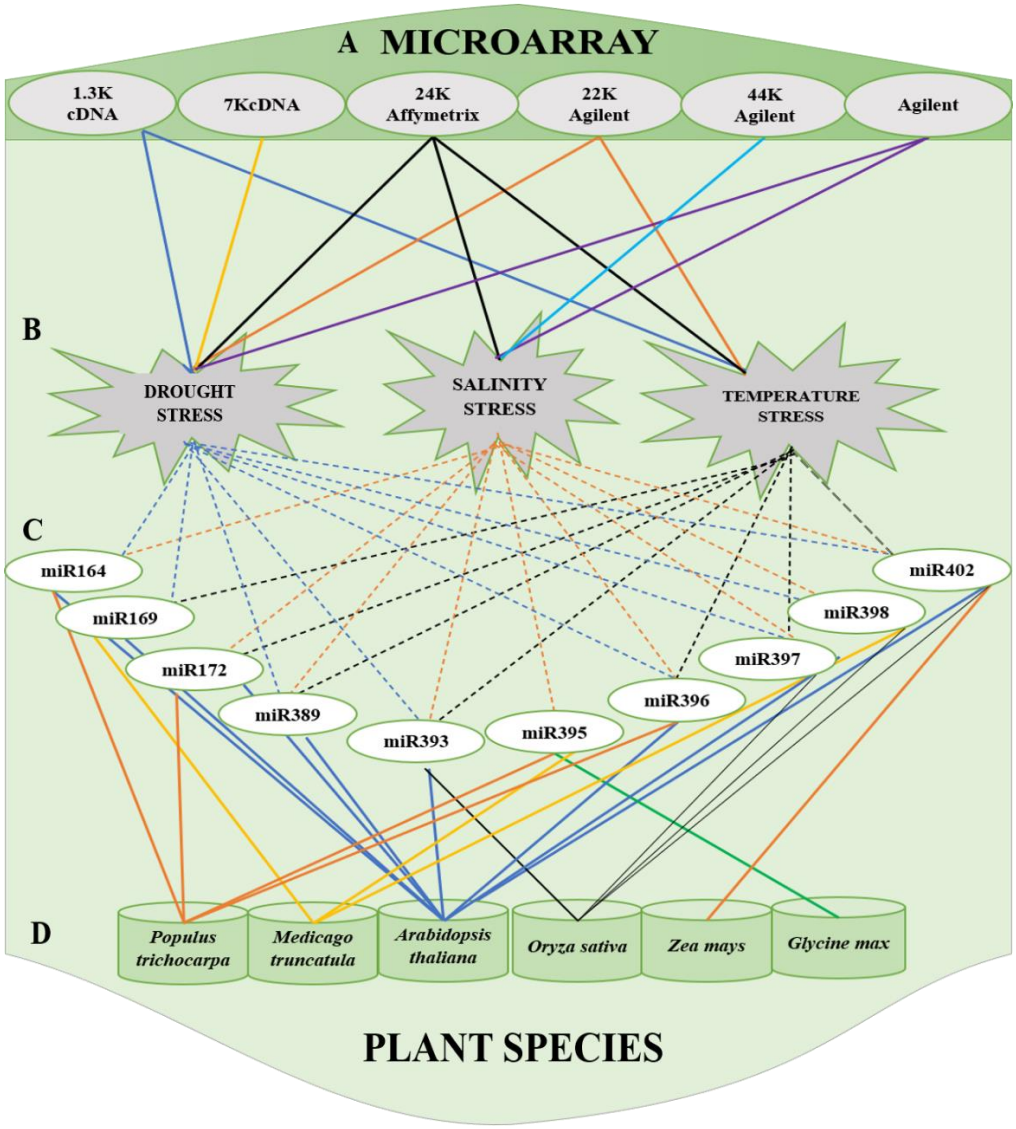

Figure 2. Summary of commonly used (**A**) microarrays (cDNA, Affymetrix, and Agilent) to stress and (**B**) miRNAs, categorized based on the stress, that respond to drought stress, salinity and temperature stress and (**C**) miRNAs reported in (**D**) plant species: *Populus trichocarpa*, *Medicago truncatula*, *Arabidopsis thaliana*, *Oryza sativa*, *Zea mays* and *Glycine max*.

High-throughput sequencing (HTS) microarray techniques have been employed for gene expression profiling under environmental stresses [42,89–91]. Several members of stress-regulated gene families were reported, such as *bZIP* to drought, *AP2* family to drought and cold, *MYB* to dehydration, *NAC* and *bHLH* to drought, ABA, and salinity, and *zinc finger* to drought and cold [92–94]. In addition, up-to-date, numerous drought-sensitive genes have been acknowledged in populous and pine [95,96].

3. Drought Responsive miRNAs and cDNA-Microarray

Drought stress is the foremost ecological factor that profoundly influences plant growth and development. Drought or soil water scarcity and perturbations is a main abiotic stress condition that causes yield reduction or complete crop loss [69]. It may be enduring in climatic zones with low or random water accessibility, due to meteorological changes during plant growth [97,98]. Therefore, preliminary physiological modifications in drought stress lead to radical gene expression variations [99]. A transcriptomic study in *Pinus taeda* was conducted in order to understand how plants were treated for mild drought

and recuperation cycles [100]. To understand the role of microRNA, an oligonucleotide microarray was employed to control a rice microRNA expression profile against drought stress. Furthermore, it was confirmed that mir169g was stimulated by drought along with the mir169 family, and the introduction of mir169g was more prominent in roots than in shoots [16,93]. Among the miR169 family, only miR169g in *Oryza sativa* was regulated by drought [16]. Many genes associated with drought stress responses have been identified (Table 3) through cloning and characterization of cDNAs [101]. The examination of gene regulation through the drought stress response illuminated the roles of genes involved against abiotic stresses [67]. Moreover, microRNAs induced in drought was identified, and *mir169g* was reported as the only family member of mir169 which was induced under drought condition. The presence of *mir169g* was more pronounced in plant roots than in shoots. Several microRNAs in rice were modified against stress conditions on the microarray. RNA-seq analysis revealed two adjacent Dehydration-responsive elements (*DREs*) upstream of the *MIR169g*. *Mir169g* was substantially up-regulated and mir169 was the only family member caused via drought. The expression of *mir169g* might be directly synchronized by the *CBF/DREBs* [16,41].

Water uptake mechanisms are improved under stress, and the crop cells can confer drought avoidance to retain water and regulate the water deficit. The molecular response of higher plant mechanisms to water stress was analyzed by identifying various genes that are sensitive to drought stress at the transcriptional levels [102]. Comprehensive study on transcriptome analysis has presented important evidence on gene expression and pathways expressed differently in cotton cultivars, which are useful in developing drought tolerance [15,42]. MicroRNAs are known to significantly regulate the function against stress, but miRNAs associated with drought have not been recognized (Figure 2). Moreover, it is unclear that miRNAs could contribute to drought lenience capabilities in some plants (such as cowpeas) [103,104].

Expression microarrays provided novel insights into the physiological and metabolic pathways of dehydration tolerance, which led to the detection of candidate genes that might be helpful to speed up the breeding of tolerant varieties [99,100], and exhibited a photosynthetic acclimatization trend in response to moderate drought. Because of the novelty of the technology, performing DNA-microarray experiments remains a challenge [105,106]. *PHENOPSIS* was developed as an automated controlled drought screen to measure various Arabidopsis accessions efficiency and identify resistant ecotypes [107]. cDNA-microarrays have been designed for aquaporins (AQPs) to determine the expression patterns of 35 Arabidopsis *AQPs* in roots, flowers, and leaves, however, no leaf specific *AQPs* were identified. Plasma membrane intrinsic protein (PIP) transcripts were reported, usually down-regulated under moderate drought in the leaves, apart from *AtPIP2;5-6* and *AtPIP1*; 4, which were expressed constitutively and were unaffected by drought stress [108]. Liu, et al. [84] reported seven drought regulated miRNAs by microarray analysis in *Arabidopsis thaliana* (miR167, miR165, miR31, miR156, miR168, miR171, and miR396) and confirmed this by spotting their expression patterns in their promoter sequences and analyzing the cis-elements. Moreover, an additional subset of c.150 gene expression was discovered during recovery from the stress. Identifying co-regulated gene groups has made it possible to identify common sequence patterns between promoters of certain genes and to detect transcription factors that control their expression [30,67,76] (Tables 1 and 2).

The plant stress-responsive pathways are not linear, but are dynamically integrated circuits consisting of several passages involving various tissues, cellular compartments, cofactors, and signaling molecules to organize a precise response to particular signals [109,110]. Microarray research showed that transgenic drought resistance was associated with several stress tolerant pathway genes, such as *DREB1A/CBF3, RD29A,* and *COR15A*, and was up-regulated. Protein phosphorylation/dephosphorylation is the main signaling event, which is being stimulated by osmotic stress. Arabidopsis 2-Oligo Microarray (Agilent) was used to analyze transcription profiles of the *SRK2C* gene, and protein kinase activated by osmotic stress (Table 1, Figure 2) [111].

4. miRNAs and cDNA-Microarray Associated with Cold Stress

Cold stress (frost and chilling) decreases crop yields worldwide through tissue degradation and delayed growth. Most temperate plants have evolved cold resistance through cold-acclimatization [112]. Signaling pathways were being used in response to winter stress. The functional genes transform reactions, and reposts suggest that the signaling pathways for leaf senescence and plant defense responses may overlap [113]. The most characteristic region of cold-stress responsive genes includes transcription factors, such as *CBF/DREB* and stress-inducible candidate genes, identified as *KIN* (cold-induced), *COR* (cold-regulated), and *LTI* genes (induced by low temperature) or *RD* (dehydration) [114]. Several *HSPs* (heat shock proteins) are also reported for their functions against cold stress. *HSPs*, which perform as molecular chaperons, play an important regulatory function in protecting from stress by restoring normal protein conformation and thus maintaining cellular homeostasis in plants [115]. The number of the miRNA target genes in expression is intricate during stress and plant growth. These miRNAs are co-regulated by both developmental signals and ecological factors (Table 3). The cold-responsive miRNAs were detected by microarray analysis in *Arabidopsis thaliana* (miR165, miR31, miR156, miR168, miR171, miR396) and recommended by identifying their expression patterns in their promoter sequences and evaluating the cis-components (Table 3, Figure 1) [116,117]. Furthermore, high-intensity light (HL) responsive genes were assessed with the drought-inducible genes reported with a similar microarray system, which exposed an impenetrable intersection between drought and HL-induced genes. Moreover, 10 genes were identified as being involved in the regulation by HL, drought, salinity, and cold stress (Tables 1 and 2). These genes are comprised of *ERD10*, *RD29A*, *KIN1*, *LEA14*, *COR15a*, and *ERD7*, and most of them are considered to be concerned in the defense of cellular components [78,118,119]. Along with the HL-inducible genes, some are also identified and encouraged by other stresses (heat, drought, and cold), including *AtGolS*, *LEA*, *RAB*, *RD*, *COR*, *ERD*, *HSP*, *KIN*, lipid-transfer proteins, and *fibrillins* [76,120,121].

DNA microarrays almost in all genes of the unicellular *Synechocystis sp PCC6803* were used to investigate the gene expression sequential software [122]. A cDNA-microarray was used to test the profile expression in cold stress, and 328 temperature-regulated transcripts were reported. *OsMYB3R-2* was studied further and was shown to be a dominant regulator against stress [123]. In this study, there was an attempt to use a 3.1K cDNA-microarray to express the cold-regulated transcripts in the *Capsicum annuum*. Several TFs, including the *EREBP* (*CaEREBP-C1* to *C4*) family of four genes, a protein of the ring domain, a *bZIP* protein (CaBZ1), RVA1, a WRKY (CaWRKY1), and HSF1 protein have been observed among the cold stress-regulated genes. These genes included *CaBZ1*, *CaEREBP-C3*, *NtPRp27*, the *SAR8.2* protein precursor, putative trans-activator factor, malate hydrogenase, putative protein of auxin-repressed, xyloglu-canendo-1, 4-D-gucanase precursor, LEA protein 5 (*LEA5*), homologous *DNAJ* protein, *PR10* and Stns *LTP* [124,125]. cDNA microarray z1300 full-length cDNAs were used in Arabidopsis to identify cold stress-inducing genes and target genes of *DREB1A/CBF3*. Six genes were documented based on microarray and, in RNA gel blot analyses, it was observed that a novel *DREB1A* controls cold- and drought-inducible genes [43,126]. Furthermore, microarray with full-length cDNA was performed by 1300 full-length cDNAs and cDNA microarray to discover cold-induced genes. Previous reposts exhibited the target genes of *DREB1A/CBF3* and stress-inducible gene expressions were controlled by transcription factors [76]; in contrast, stress-sensitive genes' expressions were reported as specific to the growth stage [42]. Full-length cDNA microarray is convenient for analyzing the Arabidopsis gene expression patterns under cold stress, and can also be used to identify the functional genes of stress-related TFs that are likely to act as DNA elements by merging the genomic sequence data with the expression data [76,127]. Additionally, cold stress is also induced by the increase in the proline content in plants (osmoprotectant). Microarray and RNA gel blot research found that the proline can induce the expression of several genes with the proline-responsive elements in their promoters (PRE, ACTCAT) [120,127,128]. Microarray analysis was carried out to detect the cold-inducible

AP2 gene family transcription factor *RAV1* [129], which could control plant growth under stress. *RAV1* is down-regulated by epibrassinolide, and transgenic Arabidopsis overexpressing *RAV1* exhibits a rosette leaf and adjacent root growth retardation, although the early-flowering phenotype showed antisense to RAV1 plants [130,131].

5. miRNAs and cDNA-Microarray Response to Salinity Stress

Salt intrusion from saline soils and irrigation water is one of the most severe and harmful risks to reduce agricultural production and adverse effects on cultivated land and the geographical distribution of plant species [70,132,133], coupled with oxidative stress [134]. The most imperative cations in saline soils are calcium, potassium, magnesium, and sodium, and the main anions in saline soils are chloride, bicarbonate, sulfate, nitrate, and carbonates. Other electrolytes causative to salinity are borane, molybdenum, strontium, silicon dioxide, aluminum cation, and barium ion [135,136]. Higher concentrations of sodium chloride (NaCl) typically affect plant development, metabolism, and physiology at various metabolic phases (ion toxicity, nutrient imbalance, and oxidative stress) [70,137]. Despite such advances in scientific research, it remains unclear about the underlying molecular mechanism of salinity responses in plants. However, based on the combination of microarray and inhibition subtractive hybridization (SSH), changes in the transcriptome profile caused by salt induction were studied and evaluated [138]. Investigation of complete transcriptomics suggests that these processes, such as the synthesis of osmolytes and ion carriers and the regulation of transcription and translation mechanisms, have distinctive reactions under salinity stress. In particular, the introduction of transcripts of specific TFs, ribosomal genes, RNA-binding proteins, and translation initiation and elongation factors has been testified [139,140].

Using cDNA microarray in *Synechocystis*, 19 genes were reported to be instantaneously regulated under salinity stress. The salt- and osmo-regulated genes, and some putative sensor molecules, have been implicated during salinity stress signaling [35]. Several differentially regulated miRNAs have been reported against salinity stress. In *A. thaliana*, several microRNAs are regulated against salinity stress, such as miR156, miR158, miR159, miR165, miR167, miR168, miR169, miR171, miR319, miR393, miR394, miR396, and miR397 (Table 3, Figure 2) [84]. In *Populus trichocarpa*, miR1445, miR1447, miR1446a-e, miR530a, and miR171l-n were down-regulated (Table 3) [141]. Arenas-Huertero et al. [31] reported, in *Proteus vulgaris*, the production of miRS1 and miR159.2 expression in response to salinity. Furthermore, miR169g and family members of miR169n were induced in saline-rich conditions [142]. However, there is a need to discover and annotate novel functional genes which have a probable function against salinity stress. Subsequently, a large number of genes in plants still have unknown functions [143]. Recent studies revealed that specific down-regulation of the bacterial-type *phosphoenolpyruvate carboxylase* (*PEPC*) gene *Atppc4* by artificial microRNA enhanced the salinity tolerance in *A. thaliana*. The increased salinity tolerance might be linked to enhanced PEPC activity [10,144]. Transcript control for salinity-tolerant rice with microarrays, like 1728 cDNAs from salinity-stressed roots libraries, was studied in response to high salinity (Table 3) [144–146].

A tiling path microarray was used to examine the high-throughput expression profiling patterns under various environmental stresses for all of the known miRNAs [16,70] (Tables 1 and 4). The analysis revealed that the effects of miRNAs under low-temperature, drought, and high salinity with miRNA chips represent, approximately, all of the reported miRNAs cloned or recognized in *A. thaliana* (L.). High salinity stress agitates homeostasis in water potential. Extreme changes in water homeostasis and ions lead to molecular breakdown, stunted growth, and even the death of cells or whole plants [16,147].

Table 4. Software and tools used for the detection of plant miRNA and cDNA microarray data analysis.

Software and Tools	Function	Website	Reference	Accessed
Software and tools used for detection of plant miRNA and data analysis				
MiPred	Random forest (RF)-based miRNA predictor, which can distinguish between real and pseudo-miRNA precursors	http://server.malab.cn/MiPred/	[72]	5 November 2021
miBridge	Algorithm and database	http://sitemaker.umich.edu/mibridge/home	[148]	5 November 2021
miRTar	A novel rule-based model learning method for cell line specific microRNA target prediction	http://miRTar.mbc.nctu.edu.tw	[72]	5 November 2021
PolymiRTS	Linking polymorphisms in microRNAs and their target sites	http://compbio.uthsc.edu/miRSNP	[149]	25 November 2021
miRGator	microRNA portal for deep sequencing, expression profiling and mRNA targeting	http://mirgator.kobic.re.kr	[150]	10 November 2021
Bowtie	Aligns efficiently, and short-read aligners	http://bowtie-bio.sourceforge.net	[72]	5 November 2021
miRBase	Provides handy and useful ID conversion tools	http://www.mirbase.org/	[72]	25 November 2021
miRDB	miRNA target databases	http://www.mirdb.org	[151]	25 November 2021
mirDIP	Integrative database of microRNA target predictions	http://ophid.utoronto.ca/mirDIP	[152]	25 November 2021
miRanda	Predict or collect miRNA targets	http://34.236.212.39/microrna/home.do	[72]	25 November 2021
RNAhybrid	microRNA target prediction	https://bibiserv.cebitec.uni-bielefeld.de/rnahybrid	[72]	8 November 2021
miTALOS	Analyzes tissue specific microRNA function.	http://mips.helmholtz-muenchen.de/mitalos	[153]	5 November 2021
RNA22	microRNA target predictions	https://cm.jefferson.edu/rna22	[154]	5 November 2021
psRNATarget	Small RNA target analysis server	http://plantgrn.noble.org/psRNATarget/	[155]	5 November 2021
miRandola	Curated knowledge base of non-invasive biomarkers	http://mirandola.iit.cnr.it/	[155]	5 November 2021
ChIPBase	Decoding transcriptional regulatory networks of non-coding RNAs and protein-coding genes from ChIP-seq data	http://rna.sysu.edu.cn/chipbase/	[155,156]	1 October 2021
MirGeneDB	Curated miRNA gene database	http://mirgenedb.org/	[157]	28 November 2021
TarHunter	Predicting conserved microRNA targets and target mimics in plants	http://tarhunter.genetics.ac.cn	[158]	28 November 2021
TissueAtlas	Tissue specificity miRNA database	https://ccb-web.cs.uni-saarland.de/tissueatlas/	[72]	28 November 2021
miRNAme Converter	miRNA ID converter	http://163.172.134.150/miRNAmeConverter-shiny	[159]	28 November 2021

Table 4. *Cont.*

Software and Tools	Function	Website	Reference	Accessed
Software and tools used for detection of plant microarray and data analysis				
Array Designer	Design primers and probes for oligo and cDNA expression microarrays.	http://www.premierbiosoft.com/dnamicroarray/index.html	[160]	1 November 2021
Stanford Microarray Database SMD	Stores raw and normalized data from microarray experiments	http://smd-www.stanford.edu//download/	[161]	1 November 2021
eArray	Designing Agilent arrays	http://earray.chem.agilent.com/earray/login.do	[160]	1 November 2021
Significance Analysis of Microarrays	Adjustments for multiple testing, statistical analysis for discrete, quantitative, and time series data, gene set enrichment analysis	http://www-stat.stanford.edu/~tibs/SAM/	[162]	5 November 2021
Visual OMP	Design software for RNA, DNA, single or multiple probe design, microarrays, Taq Manassays, genotyping, single and multiplex PCR, secondary structure simulation, sequencing, genotyping.	http://www.dnasoftware.com/Products/VisualOMP	[160]	5 November 2021
caArray	Open-source, web and programmatically accessible microarray data management system that supports the annotation of microarray	http://caarray.nci.nih.gov/		5 November 2021
Gene Expression Model Selector	Diagnostic models and biomarker discovery	http://www.gems-system.org/	[163]	18 November 2021
Gene index	Gene Index Project is to use the available EST and gene sequences, along with the reference genomes, to provide an inventory of likely genes and variants.	http://compbio.dfci.harvard.edu/tgi/plant.html	[160]	5 November 2021
Genesis	Java package of tools to simultaneously visualize and analyze a whole set of gene expression experiments	http://genome.tugraz.at/genesisclient/genesisclient_description.shtml		18 November 2021
RMA Express	Standalone GUI program for Windows, OS X and Linux to compute gene expression summary values for Affymetrix	http://rmaexpress.bmbolstad.com http://www.r-project.org http://www.bioconductor.org		18 November 2021
dCHIP	Model-based expression analysis for Affymetrix gene expression arrays	http://www.dchip.org	[164]	18 November 2021
TM4	Microarray Data Manager (MADAM), TIGR Spotfinder, Microarray Data Analysis System (MIDAS), and Multi experiment Viewer (MeV)	http://www.tm4.org/	[164]	18 November 2021

Table 4. *Cont.*

Software and Tools	Function	Website	Reference	Accessed
Able Image Analyser	Software for image analysis. It enables dimensional measurements: distance, area, angle in digital images	http://able.mulabs.com	[160]	18 November 2021
ImaGene	Unique, robust, room-temperature preservation solutions for nucleic acids, biospecimens and bioreagents for in the living ectors	http://www.biodiscovery.com/index/imagene	[160]	13 November 2021
Spotfinder	Custom-designed cDNA array, the chips are scanned using a microarray scanner	http://www.tm4.org/spotfinder.html	[164]	18 November 2021
SNOMAD	Web-based tool and has various normalization options for two-channel and single-channel experiments	http://pevsnerlab.kennedykrieger.org/snomadinput.html	[164]	18 November 2021
Multiexperimet Viewer	Cloud-based application supporting analysis, visualization, and stratification of large genomic data	http://www.tm4.org/mev.html		18 November 2021
Onto-Express and Pathway-Express	Automatically translates DE gene transcripts from microarray experiments into functional profiles characterizing the impact of the condition studied	http://vortex.cs.wayne.edu/projects.htm	[164]	13 November 2021
DAVID/EASE	Database for annotation, visualization and integrated discovery (DAVID) is an online tool for annotation and functional analysis. Expression analysis systematic sxplorer (EASE)	http://david.abcc.ncifcrf.gov	[164]	13 November 2021

Oligo-DNA microarrays were developed in common wheat, and these microarrays were designed to include approximately 32,000 distinctive genes characterized by several expressed sequence tags (ESTs). To classify the salinity-stress responsive genes, the expression profiles of transcripts that responded to stress were examined using microarrays. It was concluded that 5996 genes were verified by more than a 2-fold change in expression. These genes were categorized into twelve groups based on gene expression patterns [165]. Transcription-regulator activity, DNA binding, and the genes' assigned transcription factor functions were preferentially classified as immediate response genes. In wheat, candidate genes were identified as involved in salinity-stress tolerance [165,166]. These genes are active in the regulation of transcription [112,143] and the signal transduction that is engaged in metabolic pathways [167] or acting as ion transporters [168]. cDNA library in yeast (*Saccharomyces cerevisiae*) was examined using a synthetic medium augmented with excessive salt concentrations (900 mM). A few clones showed comparatively improved growth. The notorious clones bore the *Guanyl transferase* (OsMPG1) mannose-1-phosphate gene [133]. Extreme salinity stress was significantly linked with the transcription factors of four tomato genes from the family of *zinc finger*. There has been prior evidence of the relationship between *zinc finger* transcription factors and plant salinity tolerance [169,170]. Overexpression of *OSISAP1* in transgenic tobacco resulted in tolerance to salinity, dehydration, and cold stress in the new sprouts [171].

A microarray containing 384 genes associated with stress responses was used in *Medicago truncatula* genotypes (*Jemalong A17* and *108-R*) to compare rooting gene expression during salt stress. The homolog of flora *TFIIIA*-related TF, *MtZpt2*-1, and *COLD-REGULATEDA1* genes were known to regulate the previous genes and were acknowledged in *Jemalong A17* stress-tolerant genotypes. Two *MtZpt2* Transcription factors (*MtZpt2-1* and *MtZpt2-2*) have shown increased expression in the roots compared to *108-R* [172]. Salinity stress is attributed to diverse stresses that persuade overlapping patterns in gene expression. For example, in an investigation of 8100 *A. thaliana* genes, approximately 2400 genes were reported to have a widespread expression in exposure to salt, oxidative and cold stress [92]. In addition, 23 genes were reported against NaCl stress. This also accounted for a small percentage of DEGs, including encoding transcription factors *WOX2* and *BZIP3*, calcium-binding protein *CML42*, ubiquitin-protein ligase *UBC17*, and *IDA-like 5* protein [92]. Most prominently, synthesized *isiA* encoded a novel chlorophyll (*Chl*)-binding protein [173] (Table 3).

6. Potential Role of Bioinformatics in the Prediction of miRNA and cDNA Microarray

Next-generation sequencing methods are crucial in gene expression profiling, epigenomics, genomics, and transcriptomics. These tools can sequence multiple DNA molecules within a short period. The recent introduction of innovative "-omics" technologies, such as metabolomics, proteomics, and genomics allows for analyzing and identifying the genetic elements that contribute to system complexity [72,90,174,175]. Bioinformatics tools developed for miRNA prediction include miRNA target prediction, analysis, and structure prediction. For example, miRanda, RNAhybrid, RNA22, and TarHunter detect miRNA expression and perform analysis based on miRNA-Seq data (Table 4). Existing plant miRNA prediction tools lack a cross-species conservation filter and eTM prediction function. TarHunter features a strict cross-species conservation filter and the capability of predicting eTMs [158]. Despite ongoing progress, bioinformatics prediction of microRNA targets remains difficult, since current tools have a lack of accuracy and sensitivity. [72,176]. Microarrays are an effective method for determining the quantity of RNA in a sample. Since microarray data have computational complexity and contain hundreds of genes, statistical and bioinformatics methods are required for data interpretation [160]. These specialized tools provide statistical analysis, sample comparisons, and functional interpretation of data generated in a series following visualization and normalization in a microarray study, such as Array Designer, eArray, Visual OMP, caArray, and dCHIP (Table 4). The software, including Able Image Analyser, Gene pix pro-6.0, and GeneChip operating software, are used for analyzing images in order to obtain the intensity at each spot and quantify the expression for each transcript. Additionally, this also provides different types of discoveries by comparing gene expression data with already reported biological information, such as protein–protein interactions, pathway analysis, transcription factor binding sites, and network analysis tools, including Array Designer, eArray, Significance Analysis of Microarrays, Gene Expression, and Model Selector (Table 4) [164].

7. Conclusions and Future Perspectives

MicroRNAs (miRNAs) have been considered a potential target in genetic engineering against abiotic stresses in plants. Thus, miRNAs can also be utilized in the initial monitoring and transmission of abiotic stresses, and to elucidate the genetic and physiological responses against stress in plants. This review summarized current developments and the history of miRNAs and microarray with diverse functions in several stress responses, predominantly abiotic stresses. Many traditional approaches have identified significant numbers of miRNAs in plants from various organisms. Microarray-based genomic technologies for ecological studies have received great attention, particularly in plants, to disclose the role of stress-responsive loci in plants. DNA microarrays provide a novel insight into the cell and provide a solution for several problems from the viewpoint of analytical calculation, despite the inconceivable amount of work done in

the last two decades to reduce the different sources of uncertainty on the subsequent measurements. The review will provide valuable insight to plant researchers, especially plant breeders and stress physiologists, to design a comprehensive strategy to cope with environmental stresses.

The elucidation of miRNA responses to abiotic stresses may lead to the development of technologies for the early detection of plants' environmental stressors. MicroRNAs and cDNA-microarrays are powerful targets for engineering abiotic stress tolerance in transgenic plants. The field of bioinformatics is developing rapidly, and it is inevitable to progress in plant genomics and breeding without integrating the latest bioinformatics tools. Multiple advanced sequencing and bioinformatics tools were established to identify miRNAs and their target gene network and prediction. As the understanding of the function of miRNAs under stress deepens, the potential use of miRNA mediated genes to enhance plant tolerance will also increase. In the future, the large-scale microarrays might be substituted with small biosensors which contain a unique or a small number of novel microbes deposited on an electronic platform. We would like to conclude by illustrating the existing gap between the detection of stress-regulated miRNAs and microarray to validate their role. In conclusion, we recommend the utilization of miRNAs for the identification and classification of new functional genes conferring a significant functional role in stress tolerance and to exploit the unexplained fraction of genes further.

Author Contributions: T.P. and M.W.A.: have made substantial contributions to formulate, Drafting and retrieve data, A.E.-k.; revised and improved the technical language S.-H.N.; Revised and improved the MS, H.X.W.; Final approval and revised for publication. All authors have read and agreed to the published version of the manuscript.

Funding: This work is funded by the National Natural Science Foundation of China (31870651).

Institutional Review Board Statement: Not applicable.

Informed Consent Statement: Not applicable.

Data Availability Statement: Not applicable.

Conflicts of Interest: The authors declare no conflict of interest.

References

1. Pervaiz, T.; Liu, S.-W.; Uddin, S.; Amjid, M.W.; Niu, S.-H.; Wu, H.X. The Transcriptional Landscape and Hub Genes Associated with Physiological Responses to Drought Stress in Pinus tabuliformis. *Int. J. Mol. Sci.* **2021**, *22*, 9604. [CrossRef]
2. Raza, A. Eco-physiological and biochemical responses of rapeseed (Brassica napus L.) to abiotic stresses: Consequences and mitigation strategies. *J. Plant Growth Regul.* **2021**, *40*, 1368–1388. [CrossRef]
3. Li, C.; Zhang, B. MicroRNAs in control of plant development. *J. Cell. Physiol.* **2016**, *231*, 303–313. [CrossRef]
4. Latef, A.A.H.A.; Hashem, A.; Rasool, S.; Abd_Allah, E.F.; Alqarawi, A.; Egamberdieva, D.; Jan, S.; Anjum, N.A.; Ahmad, P. Arbuscular mycorrhizal symbiosis and abiotic stress in plants: A review. *J. Plant Biol.* **2016**, *59*, 407–426. [CrossRef]
5. Vishwakarma, K.; Upadhyay, N.; Kumar, N.; Yadav, G.; Singh, J.; Mishra, R.K.; Kumar, V.; Verma, R.; Upadhyay, R.; Pandey, M. Abscisic acid signaling and abiotic stress tolerance in plants: A review on current knowledge and future prospects. *Front. Plant Sci.* **2017**, *8*, 161. [CrossRef] [PubMed]
6. Meng, Y.; Ma, X.; Chen, D.; Wu, P.; Chen, M. MicroRNA-mediated signaling involved in plant root development. *Biochem. Biophys. Res. Commun.* **2010**, *393*, 345–349. [CrossRef] [PubMed]
7. Begara-Morales, J.C.; Chaki, M.; Valderrama, R.; Mata-Pérez, C.; Padilla, M.N.; Barroso, J.B. The function of S-nitrosothiols during abiotic stress in plants. *J. Exp. Bot.* **2019**, *70*, 4429–4439. [CrossRef]
8. Dunn, L.E.; Ivens, A.; Netherton, C.L.; Chapman, D.A.; Beard, P.M. Identification of a functional small non-coding RNA encoded by African swine fever virus. *J. Virol.* **2020**, *94*, 865147. [CrossRef] [PubMed]
9. Borges, F.; Martienssen, R.A. The expanding world of small RNAs in plants. *Nat. Rev. Mol. Cell Biol.* **2015**, *16*, 727–741. [CrossRef]
10. Wang, C.; Han, J.; Liu, C.; Kibet, K.N.; Kayesh, E.; Shangguan, L.; Li, X.; Fang, J. Identification of microRNAs from Amur grape (Vitis amurensis Rupr.) by deep sequencing and analysis of microRNA variations with bioinformatics. *BMC Genom.* **2012**, *13*, 122. [CrossRef]
11. Bartel, D.P. MicroRNAs: Genomics, biogenesis, mechanism, and function. *Cell* **2004**, *116*, 281–297. [CrossRef]
12. Islam, W.; Adnan, M.; Huang, Z.; Lu, G.-D.; Chen, H.Y. Small RNAS from seed to mature plant. *Crit. Rev. Plant Sci.* **2019**, *38*, 117–139. [CrossRef]

13. Wang, Y.; Wang, Q.; Gao, L.; Zhu, B.; Ju, Z.; Luo, Y.; Zuo, J. Parsing the regulatory network between small RNAs and target genes in ethylene pathway in tomato. *Front. Plant Sci.* **2017**, *8*, 527. [CrossRef]
14. Slaby, O.; Laga, R.; Sedlacek, O. Therapeutic targeting of non-coding RNAs in cancer. *Biochem. J.* **2017**, *474*, 4219–4251. [CrossRef]
15. Nejat, N.; Mantri, N. Emerging roles of long non-coding RNAs in plant response to biotic and abiotic stresses. *Crit. Rev. Biotechnol.* **2018**, *38*, 93–105. [CrossRef] [PubMed]
16. Zhao, B.; Liang, R.; Ge, L.; Li, W.; Xiao, H.; Lin, H.; Ruan, K.; Jin, Y. Identification of drought-induced microRNAs in rice. *Biochem. Biophys. Res. Commun.* **2007**, *354*, 585–590. [CrossRef]
17. Sunkar, R.; Zhu, J.-K. Novel and stress-regulated microRNAs and other small RNAs from Arabidopsis. *Plant Cell* **2004**, *16*, 2001–2019. [CrossRef] [PubMed]
18. Wang, Y.; Long, L.-H. Identification and isolation of the coldresistance related miRNAs in Pisum sativum Linn. *J. Liaoning Norm. Univ.* **2010**, *2*, 027.
19. Ebert, M.S.; Neilson, J.R.; Sharp, P.A. MicroRNA sponges: Competitive inhibitors of small RNAs in mammalian cells. *Nat. Methods* **2007**, *4*, 721–726. [CrossRef]
20. Sunkar, R.; Chinnusamy, V.; Zhu, J.; Zhu, J.-K. Small RNAs as big players in plant abiotic stress responses and nutrient deprivation. *Trends Plant Sci.* **2007**, *12*, 301–309. [CrossRef]
21. Raffaele, S.; Mongrand, S.; Gamas, P.; Niebel, A.; Ott, T. Genome-wide annotation of remorins, a plant-specific protein family: Evolutionary and functional perspectives. *Plant Physiol.* **2007**, *145*, 593–600. [CrossRef]
22. Zhou, X.; Jeker, L.T.; Fife, B.T.; Zhu, S.; Anderson, M.S.; McManus, M.T.; Bluestone, J.A. Selective miRNA disruption in T reg cells leads to uncontrolled autoimmunity. *J. Exp. Med.* **2008**, *205*, 1983–1991. [CrossRef]
23. Rabbani, M.A.; Maruyama, K.; Abe, H.; Khan, M.A.; Katsura, K.; Ito, Y.; Yoshiwara, K.; Seki, M.; Shinozaki, K.; Yamaguchi-Shinozaki, K. Monitoring expression profiles of rice genes under cold, drought, and high-salinity stresses and abscisic acid application using cDNA microarray and RNA gel-blot analyses. *Plant Physiol.* **2003**, *133*, 1755–1767. [CrossRef] [PubMed]
24. Moons, A.; Prinsen, E.; Bauw, G.; Van Montagu, M. Antagonistic effects of abscisic acid and jasmonates on salt stress-inducible transcripts in rice roots. *Plant Cell* **1997**, *9*, 2243–2259. [PubMed]
25. Boualem, A.; Laporte, P.; Jovanovic, M.; Laffont, C.; Plet, J.; Combier, J.P.; Niebel, A.; Crespi, M.; Frugier, F. MicroRNA166 controls root and nodule development in Medicago truncatula. *Plant J.* **2008**, *54*, 876–887. [CrossRef] [PubMed]
26. Yang, F.; Yu, D. Overexpression of Arabidopsis MiR396 enhances drought tolerance in transgenic tobacco plants. *Acta Bot. Yunnanica* **2009**, *31*, 421–426. [CrossRef]
27. Subramanian, S.; Fu, Y.; Sunkar, R.; Barbazuk, W.B.; Zhu, J.-K.; Yu, O. Novel and nodulation-regulated microRNAs in soybean roots. *BMC Genom.* **2008**, *9*, 1–14. [CrossRef]
28. Zeng, H.Q.; Zhu, Y.Y.; Huang, S.Q.; Yang, Z.M. Analysis of phosphorus-deficient responsive miRNAs and cis-elements from soybean (Glycine max L.). *J. Plant Physiol.* **2010**, *167*, 1289–1297. [CrossRef] [PubMed]
29. Cui, H.; Zhai, J.; Ma, C. miRLocator: Machine learning-based prediction of mature microRNAs within plant pre-miRNA sequences. *PLoS ONE* **2015**, *10*, e0142753. [CrossRef]
30. Yu, Y.; Wu, G.; Yuan, H.; Cheng, L.; Zhao, D.; Huang, W.; Zhang, S.; Zhang, L.; Chen, H.; Zhang, J.; et al. Identification and characterization of miRNAs and targets in flax (Linum usitatissimum) under saline, alkaline, and saline-alkaline stresses. *BMC Plant Biol.* **2016**, *16*, 124. [CrossRef] [PubMed]
31. Arenas-Huertero, C.; Pérez, B.; Rabanal, F.; Blanco-Melo, D.; De la Rosa, C.; Estrada-Navarrete, G.; Sanchez, F.; Covarrubias, A.A.; Reyes, J.L. Conserved and novel miRNAs in the legume Phaseolus vulgaris in response to stress. *Plant Mol. Biol.* **2009**, *70*, 385–401. [CrossRef] [PubMed]
32. Gu, Z.; Pan, W.; Chen, W.; Lian, Q.; Wu, Q.; Lv, Z.; Cheng, X.; Ge, X. New perspectives on the plant PARP family: Arabidopsis PARP3 is inactive, and PARP1 exhibits predominant poly (ADP-ribose) polymerase activity in response to DNA damage. *BMC Plant Biol.* **2019**, *19*, 364. [CrossRef]
33. Rasheed, S.; Bashir, K.; Matsui, A.; Tanaka, M.; Seki, M. Transcriptomic Analysis of Soil-Grown Arabidopsis thaliana Roots and Shoots in Response to a Drought Stress. *Front. Plant Sci.* **2016**, *7*, 180. [CrossRef] [PubMed]
34. Vanderauwera, S.; De Block, M.; Van de Steene, N.; Van De Cotte, B.; Metzlaff, M.; Van Breusegem, F. Silencing of poly (ADP-ribose) polymerase in plants alters abiotic stress signal transduction. *Proc. Natl. Acad. Sci. USA* **2007**, *104*, 15150–15155. [CrossRef] [PubMed]
35. Marin, K.; Suzuki, I.; Yamaguchi, K.; Ribbeck, K.; Yamamoto, H.; Kanesaki, Y.; Hagemann, M.; Murata, N. Identification of histidine kinases that act as sensors in the perception of salt stress in Synechocystis sp. PCC 6803. *Proc. Natl. Acad. Sci. USA* **2003**, *100*, 9061–9066. [CrossRef]
36. Tran, L.-S.P.; Urao, T.; Qin, F.; Maruyama, K.; Kakimoto, T.; Shinozaki, K.; Yamaguchi-Shinozaki, K. Functional analysis of AHK1/ATHK1 and cytokinin receptor histidine kinases in response to abscisic acid, drought, and salt stress in Arabidopsis. *Proc. Natl. Acad. Sci. USA* **2007**, *104*, 20623–20628. [CrossRef] [PubMed]
37. Seki, M.; Narusaka, M.; Ishida, J.; Nanjo, T.; Fujita, M.; Oono, Y.; Kamiya, A.; Nakajima, M.; Enju, A.; Sakurai, T. Monitoring the expression profiles of 7000 Arabidopsis genes under drought, cold and high-salinity stresses using a full-length cDNA microarray. *Plant J.* **2002**, *31*, 279–292. [CrossRef]

38. Fujita, Y.; Fujita, M.; Satoh, R.; Maruyama, K.; Parvez, M.M.; Seki, M.; Hiratsu, K.; Ohme-Takagi, M.; Shinozaki, K.; Yamaguchi-Shinozaki, K. AREB1 is a transcription activator of novel ABRE-dependent ABA signaling that enhances drought stress tolerance in Arabidopsis. *Plant Cell* **2005**, *17*, 3470–3488. [CrossRef]
39. Fujita, M.; Mizukado, S.; Fujita, Y.; Ichikawa, T.; Nakazawa, M.; Seki, M.; Matsui, M.; Yamaguchi-Shinozaki, K.; Shinozaki, K. Identification of stress-tolerance-related transcription-factor genes via mini-scale Full-length cDNA Over-eXpressor (FOX) gene hunting system. *Biochem. Biophys. Res. Commun.* **2007**, *364*, 250–257. [CrossRef]
40. Cominelli, E.; Galbiati, M.; Vavasseur, A.; Conti, L.; Sala, T.; Vuylsteke, M.; Leonhardt, N.; Dellaporta, S.L.; Tonelli, C. A guard-cell-specific MYB transcription factor regulates stomatal movements and plant drought tolerance. *Curr. Biol.* **2005**, *15*, 1196–1200. [CrossRef]
41. Wang, R.; Okamoto, M.; Xing, X.; Crawford, N.M. Microarray analysis of the nitrate response in Arabidopsis roots and shoots reveals over 1,000 rapidly responding genes and new linkages to glucose, trehalose-6-phosphate, iron, and sulfate metabolism. *Plant Physiol.* **2003**, *132*, 556–567. [CrossRef] [PubMed]
42. Padmalatha, K.V.; Dhandapani, G.; Kanakachari, M.; Kumar, S.; Dass, A.; Patil, D.P.; Rajamani, V.; Kumar, K.; Pathak, R.; Rawat, B. Genome-wide transcriptomic analysis of cotton under drought stress reveal significant down-regulation of genes and pathways involved in fibre elongation and up-regulation of defense responsive genes. *Plant Mol. Biol.* **2012**, *78*, 223–246. [CrossRef]
43. Seki, M.; Narusaka, M.; Abe, H.; Kasuga, M.; Yamaguchi-Shinozaki, K.; Carninci, P.; Hayashizaki, Y.; Shinozaki, K. Monitoring the expression pattern of 1300 Arabidopsis genes under drought and cold stresses by using a full-length cDNA microarray. *Plant Cell* **2001**, *13*, 61–72. [CrossRef] [PubMed]
44. Sakuma, Y.; Maruyama, K.; Osakabe, Y.; Qin, F.; Seki, M.; Shinozaki, K.; Yamaguchi-Shinozaki, K. Functional analysis of an Arabidopsis transcription factor, DREB2A, involved in drought-responsive gene expression. *Plant Cell* **2006**, *18*, 1292–1309. [CrossRef]
45. Zhu, J.; Verslues, P.E.; Zheng, X.; Lee, B.-H.; Zhan, X.; Manabe, Y.; Sokolchik, I.; Zhu, Y.; Dong, C.-H.; Zhu, J.-K. HOS10 encodes an R2R3-type MYB transcription factor essential for cold acclimation in plants. *Proc. Natl. Acad. Sci. USA* **2005**, *102*, 9966–9971. [CrossRef] [PubMed]
46. Pegler, J.L.; Oultram, J.M.J.; Grof, C.P.L.; Eamens, A.L. Profiling the Abiotic Stress Responsive microRNA Landscape of Arabidopsis thaliana. *Plants* **2019**, *8*, 58. [CrossRef]
47. Sharif, R.; Raza, A.; Chen, P.; Li, Y.; El-Ballat, E.M.; Rauf, A.; Hano, C.; El-Esawi, M.A. HD-ZIP gene family: Potential roles in improving plant growth and regulating stress-responsive mechanisms in plants. *Genes* **2021**, *12*, 1256. [CrossRef]
48. De la Rosa, C.; Covarrubias, A.A.; Reyes, J.L. A dicistronic precursor encoding miR398 and the legume-specific miR2119 coregulates CSD1 and ADH1 mRNAs in response to water deficit. *Plant Cell Environ.* **2019**, *42*, 133–144. [CrossRef]
49. Lu, Q.; Guo, F.; Xu, Q.; Cang, J. LncRNA improves cold resistance of winter wheat by interacting with miR398. *Funct. Plant Biol.* **2020**, *47*, 544–557. [CrossRef]
50. Dykes, I.M.; Emanueli, C. Transcriptional and post-transcriptional gene regulation by long non-coding RNA. *Genom. Proteom. Bioinform.* **2017**, *15*, 177–186. [CrossRef]
51. Jeong, D.-H.; Green, P.J. The role of rice microRNAs in abiotic stress responses. *J. Plant Biol.* **2013**, *56*, 187–197. [CrossRef]
52. Behbahani, G.D.; Ghahhari, N.M.; Javidi, M.A.; Molan, A.F.; Feizi, N.; Babashah, S. MicroRNA-mediated post-transcriptional regulation of epithelial to mesenchymal transition in cancer. *Pathol. Oncol. Res.* **2017**, *23*, 1–12. [CrossRef]
53. Haider, M.S.; Jogaiah, S.; Pervaiz, T.; Yanxue, Z.; Khan, N.; Fang, J. Physiological and transcriptional variations inducing complex adaptive mechanisms in grapevine by salt stress. *Environ. Exp. Bot.* **2019**, *162*, 455–467. [CrossRef]
54. Yu, H.; Song, C.; Jia, Q.; Wang, C.; Li, F.; Nicholas, K.K.; Zhang, X.; Fang, J. Computational identification of microRNAs in apple expressed sequence tags and validation of their precise sequences by miR-RACE. *Physiol. Plant.* **2011**, *141*, 56–70. [CrossRef] [PubMed]
55. Michlewski, G.; Cáceres, J.F. Post-transcriptional control of miRNA biogenesis. *Rna* **2019**, *25*, 1–16. [CrossRef]
56. González, A.; Ramos, J.; De Paz, J.F.; Corchado, J.M. Obtaining relevant genes by analysis of expression arrays with a multi-agent system. In *Proceedings of the 9th International Conference on Practical Applications of Computational Biology and Bioinformatics*; Springer: Singapore, 2015; pp. 137–146.
57. Wani, S.H.; Kumar, V.; Khare, T.; Tripathi, P.; Shah, T.; Ramakrishna, C.; Aglawe, S.; Mangrauthia, S.K. miRNA applications for engineering abiotic stress tolerance in plants. *Plant Cell* **2020**, *75*, 1081. [CrossRef]
58. Ghorbani, R.; Alemzadeh, A.; Razi, H. Microarray analysis of transcriptional responses to salt and drought stress in Arabidopsis thaliana. *Heliyon* **2019**, *5*, e02614. [CrossRef] [PubMed]
59. Raza, A.; Su, W.; Hussain, M.A.; Mehmood, S.S.; Zhang, X.; Cheng, Y.; Zou, X.; Lv, Y. Integrated Analysis of Metabolome and Transcriptome Reveals Insights for Cold Tolerance in Rapeseed (Brassica napus L.). *Front. Plant Sci.* **2021**, *12*, 12. [CrossRef]
60. Chun, J.Y. Detection of Target Nucleic Acid Sequences Using Dual-Labeled Immobilized Probes on Solid Phase. European Patent EP2630262A2, 10 May 2017.
61. Jiménez Meneses, P. Study of Substrate Modulation and Bioreceptor Anchoring for the Development of High Performance Microarrays. Ph.D. Thesis, Universitat Politècnica de València, Valencia, Spain, 2020.
62. Raza, A. Metabolomics: A systems biology approach for enhancing heat stress tolerance in plants. *Plant Cell Rep.* **2020**. [CrossRef]
63. Viemann, D.; Schulze-Osthoff, K.; Roth, J. Potentials and pitfalls of DNA array analysis of the endothelial stress response. *Biochim. Biophys. Acta (BBA)-Mol. Cell Res.* **2005**, *1746*, 73–84. [CrossRef] [PubMed]

64. Sasik, R.; Woelk, C.; Corbeil, J. Microarray truths and consequences. *J. Mol. Endocrinol.* **2004**, *33*, 1–9. [CrossRef] [PubMed]
65. Fredonnet, J.; Foncy, J.; Cau, J.-C.; Séverac, C.; François, J.M.; Trévisiol, E. Automated and multiplexed soft lithography for the production of low-density DNA microarrays. *Microarrays* **2016**, *5*, 25. [CrossRef] [PubMed]
66. Jaksik, R.; Iwanaszko, M.; Rzeszowska-Wolny, J.; Kimmel, M. Microarray experiments and factors which affect their reliability. *Biol. Direct.* **2015**, *10*, 46. [CrossRef] [PubMed]
67. Shinozaki, K.; Yamaguchi-Shinozaki, K. Gene networks involved in drought stress response and tolerance. *J. Exp. Bot.* **2007**, *58*, 221–227. [CrossRef]
68. Jain, M. Emerging role of metabolic pathways in abiotic stress tolerance. *J. Plant Biochem. Physiol.* **2013**, *1*, 10–4172. [CrossRef]
69. Barrera-Figueroa, B.E.; Wu, Z.; Liu, R. Abiotic stress-associated microRNAs in plants: Discovery, expression analysis, and evolution. *Front. Biol.* **2013**, *8*, 189–197. [CrossRef]
70. Lotfi, A.; Pervaiz, T.; Jiu, S.; Faghihi, F.; Jahanbakhshian, Z.; Khorzoghi, E.G.; Fang, J. Role of microRNAs and their target genes in salinity response in plants. *Plant Growth Regul.* **2017**, *82*, 377–390. [CrossRef]
71. Li, X.; Wang, X.; Zhang, S.; Liu, D.; Duan, Y.; Dong, W. Identification of soybean microRNAs involved in soybean cyst nematode infection by deep sequencing. *PLoS ONE* **2012**, *7*, e39650. [CrossRef]
72. Chen, L.; Heikkinen, L.; Wang, C.; Yang, Y.; Sun, H.; Wong, G. Trends in the development of miRNA bioinformatics tools. *Brief Bioinform.* **2019**, *20*, 1836–1852. [CrossRef]
73. Wong, C.E.; Li, Y.; Labbe, A.; Guevara, D.; Nuin, P.; Whitty, B.; Diaz, C.; Golding, G.B.; Gray, G.R.; Weretilnyk, E.A. Transcriptional profiling implicates novel interactions between abiotic stress and hormonal responses in Thellungiella, a close relative of Arabidopsis. *Plant Physiol.* **2006**, *140*, 1437–1450. [CrossRef]
74. Liu, Y.; Ji, X.; Zheng, L.; Nie, X.; Wang, Y. Microarray analysis of transcriptional responses to abscisic acid and salt stress in Arabidopsis thaliana. *Int. J. Mol. Sci.* **2013**, *14*, 9979–9998. [CrossRef] [PubMed]
75. Jangam, A.P.; Pathak, R.R.; Raghuram, N. Microarray Analysis of Rice d1 (RGA1) Mutant Reveals the Potential Role of G-Protein Alpha Subunit in Regulating Multiple Abiotic Stresses Such as Drought, Salinity, Heat, and Cold. *Front. Plant Sci.* **2016**, *7*, 11. [CrossRef] [PubMed]
76. Seki, M.; Narusaka, M.; Kamiya, A.; Ishida, J.; Satou, M.; Sakurai, T.; Nakajima, M.; Enju, A.; Akiyama, K.; Oono, Y. Functional annotation of a full-length Arabidopsis cDNA collection. *Science* **2002**, *296*, 141–145. [CrossRef] [PubMed]
77. Trindade, I.; Capitão, C.; Dalmay, T.; Fevereiro, M.P.; Dos Santos, D.M. miR398 and miR408 are up-regulated in response to water deficit in Medicago truncatula. *Planta* **2010**, *231*, 705–716. [CrossRef]
78. Fang, Z.; Zhang, X.; Gao, J.; Wang, P.; Xu, X.; Liu, Z.; Shen, S.; Feng, B. A buckwheat (Fagopyrum esculentum) DRE-binding transcription factor gene, FeDREB1, enhances freezing and drought tolerance of transgenic Arabidopsis. *Plant Mol. Biol. Report.* **2015**, *33*, 1510–1525. [CrossRef]
79. Wang, T.; Chen, L.; Zhao, M.; Tian, Q.; Zhang, W.-H. Identification of drought-responsive microRNAs in Medicago truncatula by genome-wide high-throughput sequencing. *BMC Genom.* **2011**, *12*, 1–11. [CrossRef]
80. Mantri, N.; Basker, N.; Ford, R.; Pang, E.; Pardeshi, V. The role of micro-ribonucleic acids in legumes with a focus on abiotic stress response. *Plant Genome* **2013**, *6*. [CrossRef]
81. Li, H.; Dong, Y.; Yin, H.; Wang, N.; Yang, J.; Liu, X.; Wang, Y.; Wu, J.; Li, X. Characterization of the stress associated microRNAs in Glycine max by deep sequencing. *BMC Plant Biol.* **2011**, *11*, 1–12. [CrossRef]
82. Dong, Z.; Shi, L.; Wang, Y.; Chen, L.; Cai, Z.; Wang, Y.; Jin, J.; Li, X. Identification and dynamic regulation of microRNAs involved in salt stress responses in functional soybean nodules by high-throughput sequencing. *Int. J. Mol. Sci.* **2013**, *14*, 2717–2738. [CrossRef]
83. Zhang, B. MicroRNA: A new target for improving plant tolerance to abiotic stress. *J. Exp. Bot.* **2015**, *66*, 1749–1761. [CrossRef]
84. Liu, H.-H.; Tian, X.; Li, Y.-J.; Wu, C.-A.; Zheng, C.-C. Microarray-based analysis of stress-regulated microRNAs in Arabidopsis thaliana. *Rna* **2008**, *14*, 836–843. [CrossRef] [PubMed]
85. Meyers, B.C.; Axtell, M.J.; Bartel, B.; Bartel, D.P.; Baulcombe, D.; Bowman, J.L.; Cao, X.; Carrington, J.C.; Chen, X.; Green, P.J. Criteria for annotation of plant MicroRNAs. *Plant Cell* **2008**, *20*, 3186–3190. [CrossRef] [PubMed]
86. Ta, K.N.; Sabot, F.; Adam, H.; Vigouroux, Y.; De Mita, S.; Ghesquière, A.; Do, N.V.; Gantet, P.; Jouannic, S. miR2118-triggered phased siRNAs are differentially expressed during the panicle development of wild and domesticated African rice species. *Rice* **2016**, *9*, 10. [CrossRef] [PubMed]
87. Yan, H.; Kikuchi, S.; Neumann, P.; Zhang, W.; Wu, Y.; Chen, F.; Jiang, J. Genome-wide mapping of cytosine methylation revealed dynamic DNA methylation patterns associated with genes and centromeres in rice. *Plant J.* **2010**, *63*, 353–365. [CrossRef]
88. Zhou, S.; Wei, S.; Boone, B.; Levy, S. Microarray analysis of genes affected by salt stress in tomato. *Afr. J. Environ. Sci. Technol.* **2007**, *1*, 14–26.
89. Cohen, D.; Bogeat-Triboulot, M.-B.; Tisserant, E.; Balzergue, S.; Martin-Magniette, M.-L.; Lelandais, G.; Ningre, N.; Renou, J.-P.; Tamby, J.-P.; Le Thiec, D. Comparative transcriptomics of drought responses in Populus: A meta-analysis of genome-wide expression profiling in mature leaves and root apices across two genotypes. *BMC Genom.* **2010**, *11*, 630. [CrossRef]
90. Pervaiz, T.; Lotfi, A.; Haider, M.S.; Haifang, J.; Fang, J. High Throughput Sequencing Advances and Future Challenges. *J. Plant Biochem. Physiol.* **2017**, *5*, 188. [CrossRef]
91. Raza, A.; Tabassum, J.; Kudapa, H.; Varshney, R.K. Can omics deliver temperature resilient ready-to-grow crps? *Crit. Rev. Biotechnol.* **2021**, *41*, 1–24. [CrossRef]

92. Liu, M.; Shi, J.; Lu, C. Identification of stress-responsive genes in Ammopiptanthus mongolicususing ESTs generated from cold-and drought-stressed seedlings. *BMC Plant Biol.* **2013**, *13*, 88. [CrossRef]
93. Mittal, S.; Banduni, P.; Mallikarjuna, M.G.; Rao, A.R.; Jain, P.A.; Dash, P.K.; Thirunavukkarasu, N. Structural, Functional, and Evolutionary Characterization of Major Drought Transcription Factors Families in Maize. *Front. Chem.* **2018**, *6*, 177. [CrossRef]
94. Pervaiz, T.; Songtao, J.; Faghihi, F.; Haider, M.S.; Fang, J. Naturally occurring anthocyanin, structure, functions and biosynthetic pathway in fruit plants. *J. Plant Biochem. Physiol.* **2017**, *5*, 1–9. [CrossRef]
95. Street, N.R.; Skogström, O.; Sjödin, A.; Tucker, J.; Rodríguez-Acosta, M.; Nilsson, P.; Jansson, S.; Taylor, G. The genetics and genomics of the drought response in Populus. *Plant J.* **2006**, *48*, 321–341. [CrossRef]
96. Lorenz, W.W.; Sun, F.; Liang, C.; Kolychev, D.; Wang, H.; Zhao, X.; Cordonnier-Pratt, M.-M.; Pratt, L.H.; Dean, J.F. Water stress-responsive genes in loblolly pine (Pinus taeda) roots identified by analyses of expressed sequence tag libraries. *Tree Physiol.* **2006**, *26*, 1–16. [CrossRef] [PubMed]
97. Rosegrant, M.W.; Cline, S.A. Global food security: Challenges and policies. *Science* **2003**, *302*, 1917–1919. [CrossRef] [PubMed]
98. Du, M.; Ding, G.; Cai, Q. The transcriptomic responses of Pinus massoniana to drought stress. *Forests* **2018**, *9*, 326. [CrossRef]
99. Kathiresan, A.; Lafitte, H.; Chen, J.; Mansueto, L.; Bruskiewich, R.; Bennett, J. Gene expression microarrays and their application in drought stress research. *Field Crops Res.* **2006**, *97*, 101–110. [CrossRef]
100. Vásquez-Robinet, C.; Watkinson, J.I.; Sioson, A.A.; Ramakrishnan, N.; Heath, L.S.; Grene, R. Differential expression of heat shock protein genes in preconditioning for photosynthetic acclimation in water-stressed loblolly pine. *Plant Physiol. Biochem.* **2010**, *48*, 256–264. [CrossRef]
101. Contour-Ansel, D.; Torres-Franklin, M.L.; Cruz De Carvalho, M.H.; D'Arcy-Lameta, A.; Zuily-Fodil, Y. Glutathione reductase in leaves of cowpea: Cloning of two cDNAs, expression and enzymatic activity under progressive drought stress, desiccation and abscisic acid treatment. *Ann. Bot.* **2006**, *98*, 1279–1287. [CrossRef] [PubMed]
102. Hasegawa, P.M.; Bressan, R.A.; Zhu, J.-K.; Bohnert, H.J. Plant cellular and molecular responses to high salinity. *Annu. Rev. Plant Biol.* **2000**, *51*, 463–499. [CrossRef] [PubMed]
103. Barrera-Figueroa, B.E.; Gao, L.; Diop, N.N.; Wu, Z.; Ehlers, J.D.; Roberts, P.A.; Close, T.J.; Zhu, J.-K.; Liu, R. Identification and comparative analysis of drought-associated microRNAs in two cowpea genotypes. *BMC Plant Biol.* **2011**, *11*, 127. [CrossRef] [PubMed]
104. Han, M.; Lu, X.; Yu, J.; Chen, X.; Wang, X.; Malik, W.A.; Wang, J.; Wang, D.; Wang, S.; Guo, L.; et al. Transcriptome Analysis Reveals Cotton (Gossypium hirsutum) Genes That Are Differentially Expressed in Cadmium Stress Tolerance. *Int. J. Mol. Sci.* **2019**, *20*, 1479. [CrossRef] [PubMed]
105. Harb, A.; Krishnan, A.; Ambavaram, M.M.; Pereira, A. Molecular and physiological analysis of drought stress in Arabidopsis reveals early responses leading to acclimation in plant growth. *Plant Physiol.* **2010**, *154*, 1254–1271. [CrossRef]
106. Muyal, J.P.; Singh, S.K.; Fehrenbach, H. DNA-microarray technology: Comparison of methodological factors of recent technique towards gene expression profiling. *Crit. Rev. Biotechnol.* **2008**, *28*, 239–251. [CrossRef] [PubMed]
107. Granier, C.; Aguirrezabal, L.; Chenu, K.; Cookson, S.J.; Dauzat, M.; Hamard, P.; Thioux, J.J.; Rolland, G.; Bouchier-Combaud, S.; Lebaudy, A. PHENOPSIS, an automated platform for reproducible phenotyping of plant responses to soil water deficit in Arabidopsis thaliana permitted the identification of an accession with low sensitivity to soil water deficit. *New Phytol.* **2006**, *169*, 623–635. [CrossRef]
108. Alexandersson, E.; Fraysse, L.; Sjövall-Larsen, S.; Gustavsson, S.; Fellert, M.; Karlsson, M.; Johanson, U.; Kjellbom, P. Whole gene family expression and drought stress regulation of aquaporins. *Plant Mol. Biol.* **2005**, *59*, 469–484. [CrossRef]
109. Dombrowski, J.E. Salt stress activation of wound-related genes in tomato plants. *Plant Physiol.* **2003**, *132*, 2098–2107. [CrossRef]
110. Vishwakarma, K.; Mishra, M.; Patil, G.; Mulkey, S.; Ramawat, N.; Pratap Singh, V.; Deshmukh, R.; Kumar Tripathi, D.; Nguyen, H.T.; Sharma, S. Avenues of the membrane transport system in adaptation of plants to abiotic stresses. *Crit. Rev. Biotechnol.* **2019**, *39*, 861–883. [CrossRef]
111. Umezawa, T.; Yoshida, R.; Maruyama, K.; Yamaguchi-Shinozaki, K.; Shinozaki, K. SRK2C, a SNF1-related protein kinase 2, improves drought tolerance by controlling stress-responsive gene expression in Arabidopsis thaliana. *Proc. Natl. Acad. Sci. USA* **2004**, *101*, 17306–17311. [CrossRef]
112. Chinnusamy, V.; Zhu, J.; Zhu, J.-K. Cold stress regulation of gene expression in plants. *Trends Plant Sci.* **2007**, *12*, 444–451. [CrossRef]
113. Xue-Xuan, X.; Hong-Bo, S.; Yuan-Yuan, M.; Gang, X.; Jun-Na, S.; Dong-Gang, G.; Cheng-Jiang, R. Biotechnological implications from abscisic acid (ABA) roles in cold stress and leaf senescence as an important signal for improving plant sustainable survival under abiotic-stressed conditions. *Crit. Rev. Biotechnol.* **2010**, *30*, 222–230. [CrossRef] [PubMed]
114. Benedict, C.; Geisler, M.; Trygg, J.; Huner, N.; Hurry, V. Consensus by democracy. Using meta-analyses of microarray and genomic data to model the cold acclimation signaling pathway in Arabidopsis. *Plant Physiol.* **2006**, *141*, 1219–1232. [CrossRef] [PubMed]
115. Wang, Z.-L.; Li, P.-H.; Fredricksen, M.; Gong, Z.-Z.; Kim, C.; Zhang, C.; Bohnert, H.J.; Zhu, J.-K.; Bressan, R.A.; Hasegawa, P.M. Expressed sequence tags from Thellungiella halophila, a new model to study plant salt-tolerance. *Plant Sci.* **2004**, *166*, 609–616. [CrossRef]
116. Ciarmiello, L.F.; Woodrow, P.; Fuggi, A.; Pontecorvo, G.; Carillo, P. *Plant Genes for Abiotic Stress. Abiotic Stress in Plants—Mechanisms and Adaptations*. 2011, pp. 283–308. Available online: https://www.intechopen.com/chapters/18407 (accessed on 22 December 2020).

117. Kurikesu, I.; Anuja, T.; Gangaprasad, A.; Nair, A.J. Regulation of micrornas during biotic and abiotic stress. *Bull. Pure Appl. Sci. -Bot.* **2018**, *37*, 49–55. [CrossRef]
118. Kimura, M.; Yamamoto, Y.Y.; Seki, M.; Sakurai, T.; Sato, M.; Abe, T.; Yoshida, S.; Manabe, K.; Shinozaki, K.; Matsui, M. Identification of Arabidopsis genes regulated by high light-stress using cDNA microarray. *Photochem. Photobiol.* **2003**, *77*, 226–233.
119. Albert, E. Genetic and Genomic Determinants of Response to Water Deficit in Tomato (Solanum lycopersicum) and Impact on Fruit Quality. Ph.D. Thesis, Université d'Avignon, Avignon, France, 2017.
120. Satoh, R.; Nakashima, K.; Seki, M.; Shinozaki, K.; Yamaguchi-Shinozaki, K. ACTCAT, a novel cis-acting element for proline-and hypoosmolarity-responsive expression of the ProDH gene encoding proline dehydrogenase in Arabidopsis. *Plant Physiol.* **2002**, *130*, 709–719. [CrossRef]
121. Guo, M.; Liu, J.H.; Ma, X.; Luo, D.X.; Gong, Z.H.; Lu, M.H. The Plant Heat Stress Transcription Factors (HSFs): Structure, Regulation, and Function in Response to Abiotic Stresses. *Front. Plant Sci.* **2016**, *7*, 114. [CrossRef] [PubMed]
122. Hihara, Y.; Kamei, A.; Kanehisa, M.; Kaplan, A.; Ikeuchi, M. DNA microarray analysis of cyanobacterial gene expression during acclimation to high light. *Plant Cell* **2001**, *13*, 793–806. [CrossRef]
123. Dai, X.; Xu, Y.; Ma, Q.; Xu, W.; Wang, T.; Xue, Y.; Chong, K. Overexpression of an R1R2R3 MYB gene, OsMYB3R-2, increases tolerance to freezing, drought, and salt stress in transgenic Arabidopsis. *Plant Physiol.* **2007**, *143*, 1739–1751. [CrossRef] [PubMed]
124. Hwang, E.-W.; Kim, K.-A.; Park, S.-C.; Jeong, M.-J.; Byun, M.-O.; Kwon, H.-B. Expression profiles of hot pepper (Capsicum annuum) genes under cold stress conditions. *J. Biosci.* **2005**, *30*, 657–667. [CrossRef]
125. da Silva, J.A.T.; Yücel, M. Revealing response of plants to biotic and abiotic stresses with microarray technology. *Genes Genomes Genom.* **2008**, *2*, 14–48.
126. Ravikumar, G.; Manimaran, P.; Voleti, S.R.; Subrahmanyam, D.; Sundaram, R.M.; Bansal, K.C.; Viraktamath, B.C.; Balachandran, S.M. Stress-inducible expression of AtDREB1A transcription factor greatly improves drought stress tolerance in transgenic indica rice. *Transgenic Res.* **2014**, *23*, 421–439. [CrossRef]
127. Leviatan, N.; Alkan, N.; Leshkowitz, D.; Fluhr, R. Genome-wide survey of cold stress regulated alternative splicing in Arabidopsis thaliana with tiling microarray. *PLoS ONE* **2013**, *8*, e66511. [CrossRef]
128. Oono, Y.; Seki, M.; Nanjo, T.; Narusaka, M.; Fujita, M.; Satoh, R.; Satou, M.; Sakurai, T.; Ishida, J.; Akiyama, K. Monitoring expression profiles of Arabidopsis gene expression during rehydration process after dehydration using ca. 7000 full-length cDNA microarray. *Plant J.* **2003**, *34*, 868–887. [CrossRef]
129. Maruyama, K.; Sakuma, Y.; Kasuga, M.; Ito, Y.; Seki, M.; Goda, H.; Shimada, Y.; Yoshida, S.; Shinozaki, K.; Yamaguchi-Shinozaki, K. Identification of cold-inducible downstream genes of the Arabidopsis DREB1A/CBF3 transcriptional factor using two microarray systems. *Plant J.* **2004**, *38*, 982–993. [CrossRef]
130. Hu, H.; Dai, M.; Yao, J.; Xiao, B.; Li, X.; Zhang, Q.; Xiong, L. Overexpressing a NAM, ATAF, and CUC (NAC) transcription factor enhances drought resistance and salt tolerance in rice. *Proc. Natl. Acad. Sci. USA* **2006**, *103*, 12987–12992. [CrossRef] [PubMed]
131. Song, X.; Li, Y.; Hou, X. Genome-wide analysis of the AP2/ERF transcription factor superfamily in Chinese cabbage (Brassica rapa ssp. pekinensis). *BMC Genom.* **2013**, *14*, 573. [CrossRef] [PubMed]
132. Lata, R.; Chowdhury, S.; Gond, S.K.; White, J.F., Jr. Induction of abiotic stress tolerance in plants by endophytic microbes. *Lett. Appl. Microbiol.* **2018**, *66*, 268–276. [CrossRef]
133. Kumar, R.; Mustafiz, A.; Sahoo, K.K.; Sharma, V.; Samanta, S.; Sopory, S.K.; Pareek, A.; Singla-Pareek, S.L. Functional screening of cDNA library from a salt tolerant rice genotype Pokkali identifies mannose-1-phosphate guanyl transferase gene (OsMPG1) as a key member of salinity stress response. *Plant Mol. Biol.* **2012**, *79*, 555–568. [CrossRef]
134. Miller, G.; Suzuki, N.; Ciftci-Yilmaz, S.; Mittler, R. Reactive oxygen species homeostasis and signalling during drought and salinity stresses. *Plant Cell Environ.* **2010**, *33*, 453–467. [CrossRef]
135. Hu, Y.; Burucs, Z.; von Tucher, S.; Schmidhalter, U. Short-term effects of drought and salinity on mineral nutrient distribution along growing leaves of maize seedlings. *Environ. Exp. Bot.* **2007**, *60*, 268–275. [CrossRef]
136. Mangrauthia, S.K.; Agarwal, S.; Sailaja, B.; Madhav, M.S.; Voleti, S. MicroRNAs and their role in salt stress response in plants. In *Salt Stress in Plants*; Springer: Berlin/Heidelberg, Germany, 2013; pp. 15–46.
137. Vinocur, B.; Altman, A. Recent advances in engineering plant tolerance to abiotic stress: Achievements and limitations. *Curr. Opin. Biotechnol.* **2005**, *16*, 123–132. [CrossRef]
138. Ouyang, B.; Yang, T.; Li, H.; Zhang, L.; Zhang, Y.; Zhang, J.; Fei, Z.; Ye, Z. Identification of early salt stress response genes in tomato root by suppression subtractive hybridization and microarray analysis. *J. Exp. Bot.* **2007**, *58*, 507–520. [CrossRef] [PubMed]
139. Sahi, C.; Singh, A.; Kumar, K.; Blumwald, E.; Grover, A. Salt stress response in rice: Genetics, molecular biology, and comparative genomics. *Funct. Integr. Genom.* **2006**, *6*, 263–284. [CrossRef] [PubMed]
140. Zhu, Y.N.; Shi, D.Q.; Ruan, M.B.; Zhang, L.L.; Meng, Z.H.; Liu, J.; Yang, W.C. Transcriptome analysis reveals crosstalk of responsive genes to multiple abiotic stresses in cotton (Gossypium hirsutum L.). *PLoS ONE* **2013**, *8*, e80218.
141. Chan, Z.; Bigelow, P.J.; Loescher, W.; Grumet, R. Comparison of salt stress resistance genes in transgenic Arabidopsis thaliana indicates that extent of transcriptomic change may not predict secondary phenotypic or fitness effects. *Plant Biotechnol. J.* **2012**, *10*, 284–300. [CrossRef] [PubMed]
142. Khraiwesh, B.; Zhu, J.-K.; Zhu, J. Role of miRNAs and siRNAs in biotic and abiotic stress responses of plants. *Biochim. Biophys. Acta (BBA)-Gene Regul. Mech.* **2012**, *1819*, 137–148. [CrossRef]

143. Kumari, S.; Singh, P.; Singla-Pareek, S.L.; Pareek, A. Heterologous expression of a salinity and developmentally regulated rice cyclophilin gene (OsCyp2) in E. coli and S. cerevisiae confers tolerance towards multiple abiotic stresses. *Mol. Biotechnol.* **2009**, *42*, 195–204. [CrossRef]
144. Wu, T.; Yang, C.; Ding, B.; Feng, Z.; Wang, Q.; He, J.; Tong, J.; Xiao, L.; Jiang, L.; Wan, J. Microarray-based gene expression analysis of strong seed dormancy in rice cv. N22 and less dormant mutant derivatives. *Plant Physiol. Biochem.* **2016**, *99*, 27–38. [CrossRef] [PubMed]
145. Kawasaki, S.; Borchert, C.; Deyholos, M.; Wang, H.; Brazille, S.; Kawai, K.; Galbraith, D.; Bohnert, H.J. Gene expression profiles during the initial phase of salt stress in rice. *Plant Cell* **2001**, *13*, 889–905. [CrossRef] [PubMed]
146. Kong, W.; Zhong, H.; Gong, Z.; Fang, X.; Sun, T.; Deng, X.; Li, Y. Meta-analysis of salt stress transcriptome responses in different rice genotypes at the seedling stage. *Plants* **2019**, *8*, 64. [CrossRef] [PubMed]
147. Zhu, J.K. Salt and drought stress signal transduction in plants. *Annu. Rev. Plant Biol.* **2002**, *53*, 247–273. [CrossRef]
148. Lee, I.; Ajay, S.S.; Yook, J.I.; Kim, H.S.; Hong, S.H.; Kim, N.H.; Dhanasekaran, S.M.; Chinnaiyan, A.M.; Athey, B.D. New class of microRNA targets containing simultaneous 5′-UTR and 3′-UTR interaction sites. *Genome Res.* **2009**, *19*, 1175–1183. [CrossRef]
149. Bhattacharya, A.; Ziebarth, J.D.; Cui, Y. PolymiRTS Database 3.0: Linking polymorphisms in microRNAs and their target sites with human diseases and biological pathways. *Nucleic Acids Res.* **2014**, *42*, D86–D91. [CrossRef]
150. Cho, S.; Jang, I.; Jun, Y.; Yoon, S.; Ko, M.; Kwon, Y.; Choi, I.; Chang, H.; Ryu, D.; Lee, B.; et al. MiRGator v3.0: A microRNA portal for deep sequencing, expression profiling and mRNA targeting. *Nucleic Acids Res.* **2013**, *41*, D257. [CrossRef]
151. Wang, X. Improving microRNA target prediction by modeling with unambiguously identified microRNA-target pairs from CLIP-ligation studies. *Bioinformatics* **2016**, *32*, 1316–1322. [CrossRef] [PubMed]
152. Tokar, T.; Pastrello, C.; Rossos, A.E.M.; Abovsky, M.; Hauschild, A.C.; Tsay, M.; Lu, R.; Jurisica, I. mirDIP 4.1-integrative database of human microRNA target predictions. *Nucleic Acids Res.* **2018**, *46*, D360–D370. [CrossRef]
153. Preusse, M.; Theis, F.J.; Mueller, N.S. miTALOS v2: Analyzing Tissue Specific microRNA Function. *PLoS ONE* **2016**, *11*, e0151771. [CrossRef] [PubMed]
154. Loher, P.; Rigoutsos, I. Interactive exploration of RNA22 microRNA target predictions. *Bioinformatics* **2012**, *28*, 3322–3323. [CrossRef] [PubMed]
155. Dai, X.; Zhuang, Z.; Zhao, P.X. psRNATarget: A plant small RNA target analysis server (2017 release). *Nucleic Acids Res.* **2018**, *46*, W49–W54. [CrossRef]
156. Zhou, K.R.; Liu, S.; Sun, W.J.; Zheng, L.L.; Zhou, H.; Yang, J.H.; Qu, L.H. ChIPBase v2.0: Decoding transcriptional regulatory networks of non-coding RNAs and protein-coding genes from ChIP-seq data. *Nucleic Acids Res.* **2017**, *45*, D43–D50. [CrossRef] [PubMed]
157. Fromm, B.; Billipp, T.; Peck, L.E.; Johansen, M.; Tarver, J.E.; King, B.L.; Newcomb, J.M.; Sempere, L.F.; Flatmark, K.; Hovig, E.; et al. A Uniform System for the Annotation of Vertebrate microRNA Genes and the Evolution of the Human microRNAome. *Annu. Rev. Genet.* **2015**, *49*, 213–242. [CrossRef] [PubMed]
158. Ma, X.; Liu, C.; Gu, L.; Mo, B.; Cao, X.; Chen, X. TarHunter, a tool for predicting conserved microRNA targets and target mimics in plants. *Bioinformatics* **2018**, *34*, 1574–1576. [CrossRef]
159. Haunsberger, S.J.; Connolly, N.M.; Prehn, J.H. miRNAmeConverter: An R/bioconductor package for translating mature miRNA names to different miRBase versions. *Bioinformatics* **2017**, *33*, 592–593. [CrossRef] [PubMed]
160. Page, G.P.; Coulibaly, I. Bioinformatic tools for inferring functional information from plant microarray data: Tools for the first steps. *Int. J. Plant Genom.* **2008**, *2008*, 147563. [CrossRef] [PubMed]
161. Demeter, J.; Beauheim, C.; Gollub, J.; Hernandez-Boussard, T.; Jin, H.; Maier, D.; Matese, J.C.; Nitzberg, M.; Wymore, F.; Zachariah, Z.K.; et al. The Stanford Microarray Database: Implementation of new analysis tools and open source release of software. *Nucleic Acids Res.* **2007**, *35*, D766–D770. [CrossRef]
162. Tusher, V.G.; Tibshirani, R.; Chu, G. Significance analysis of microarrays applied to the ionizing radiation response. *Proc. Natl. Acad. Sci. USA* **2001**, *98*, 5116–5121. [CrossRef]
163. Alonso-Betanzos, A.; Bolón-Canedo, V.; Morán-Fernández, L.; Sánchez-Maroño, N. A Review of Microarray Datasets: Where to Find Them and Specific Characteristics. *Methods Mol. Biol.* **2019**, *1986*, 65–85.
164. Mehta, J.P.; Rani, S. Software and tools for microarray data analysis. *Methods Mol. Biol.* **2011**, *784*, 41–53.
165. Kawaura, K.; Mochida, K.; Ogihara, Y. Genome-wide analysis for identification of salt-responsive genes in common wheat. *Funct. Integr. Genom.* **2008**, *8*, 277–286. [CrossRef]
166. Fernandez, P.; Di Rienzo, J.; Fernandez, L.; Hopp, H.E.; Paniego, N.; Heinz, R.A. Transcriptomic identification of candidate genes involved in sunflower responses to chilling and salt stresses based on cDNA microarray analysis. *BMC Plant Biol.* **2008**, *8*, 11. [CrossRef]
167. Singla-Pareek, S.L.; Yadav, S.K.; Pareek, A.; Reddy, M.K.; Sopory, S.K. Enhancing salt tolerance in a crop plant by overexpression of glyoxalase II. *Transgenic Res.* **2008**, *17*, 171–180. [CrossRef] [PubMed]
168. Uddin, M.I.; Qi, Y.; Yamada, S.; Shibuya, I.; Deng, X.P.; Kwak, S.S.; Kaminaka, H.; Tanaka, K. Overexpression of a new rice vacuolar antiporter regulating protein OsARP improves salt tolerance in tobacco. *Plant Cell Physiol.* **2008**, *49*, 880–890. [CrossRef] [PubMed]
169. Sakamoto, K.; Göransson, O.; Hardie, D.G.; Alessi, D.R. Activity of LKB1 and AMPK-related kinases in skeletal muscle: Effects of contraction, phenformin, and AICAR. *Am. J. Physiol. Endocrinol. Metab.* **2004**, *287*, E310–E317. [CrossRef]

170. Hichri, I.; Muhovski, Y.; Žižková, E.; Dobrev, P.I.; Gharbi, E.; Franco-Zorrilla, J.M.; Lopez-Vidriero, I.; Solano, R.; Clippe, A.; Errachid, A. The Solanum lycopersicum WRKY3 transcription factor SlWRKY3 is involved in salt stress tolerance in tomato. *Front. Plant Sci.* **2017**, *8*, 1343. [CrossRef] [PubMed]
171. Mukhopadhyay, S.; Mandal, S.K.; Bhaduri, S.; Armstrong, W.H. Manganese clusters with relevance to photosystem II. *Chem. Rev.* **2004**, *104*, 3981–4026. [CrossRef]
172. De Lorenzo, L.; Merchan, F.; Blanchet, S.; Megías, M.; Frugier, F.; Crespi, M.; Sousa, C. Differential expression of the TFIIIA regulatory pathway in response to salt stress between Medicago truncatula genotypes. *Plant Physiol.* **2007**, *145*, 1521–1532. [CrossRef] [PubMed]
173. Havaux, M.; Guedeney, G.; Hagemann, M.; Yeremenko, N.; Matthijs, H.C.; Jeanjean, R. The chlorophyll-binding protein IsiA is inducible by high light and protects the cyanobacterium Synechocystis PCC6803 from photooxidative stress. *FEBS Lett.* **2005**, *579*, 2289–2293. [CrossRef]
174. Upadhyay, J.; Joshi, R.; Singh, B.; Bohra, A.; Vijayan, R.; Bhatt, M.; Bisht, S.S.; Wani, S.H. Application of Bioinformatics in Understanding of Plant Stress Tolerance. *Plant Bioinform.* **2017**, 347–374.
175. Raza, A.; Razzaq, A.; Mehmood, S.S.; Hussain, M.A.; Wei, S.; He, H.; Zaman, Q.U.; Xuekun, Z.; Yong, C.; Hasanuzzaman, M. Omics: The way forward to enhance abiotic stress tolerance in Brassica napus L. *GM Crops Food* **2021**, *12*, 251–281. [CrossRef] [PubMed]
176. Quillet, A.; Saad, C.; Ferry, G.; Anouar, Y.; Vergne, N.; Lecroq, T.; Dubessy, C. Improving Bioinformatics Prediction of microRNA Targets by Ranks Aggregation. *Front. Genet.* **2019**, *10*, 1330. [CrossRef]