

Table S1. Molecular approaches to develop resilient plants to abiotic stresses (drought, heat and salinity).

Molecular Approach	Species	Results	Reference
QTL Mapping/GWAS salt	<i>Glycine max</i>	Identified seven QTLs colocalized or positioned adjacent to known QTLs and/or potential candidate genes associated with drought stress.	Dhungana et al. 2021
		Identified 23 QTLs related to drought tolerance. Among them, seven QTLs were related to plant height, and five QTL were related to seed weight.	Ren et al. 2020
		Examined the germinating seed drought-tolerance phenotypes and genotypes of a panel of 259 released Chinese soybean cultivars. Based on 4616 SNPs, conducted a mixed-linear model GWAS that identified a total of 15 SNPs associated with at least one drought-tolerance index.	Liu et al. 2020
		Mapped 45 unique SNPs that tagged 44 loci associated with canopy wilting. Several new soybean accessions were identified with canopy wilting superior to those of check genotypes.	Steketee et al. 2020
		Ten novel QTLs were identified for salt tolerance. Two novel loci, qST6, and qST10, participate in defense mechanisms against ion toxicity and the physiological damage induced by salt stress and together exert an additive effect on salt tolerance.	Cho et al. 2021a
		Identified two QTLs, a major QTL on chromosome 3, and a minor QTL on chromosome 19. A Single nucleotide polymorphism (SNP) markers associated with salt tolerance was also found.	Lopez et al. 2018
	<i>Triticum aestivum</i>	Identified 40 additive QTLs under terminal heat stress. 23 QTLs for chlorophyll fluorescence and 17 for chlorophyll content	Bhusal et al. 2018
		27 additive QTLs and five pairs of epistatic effects. Six QTLs (QGY-2B, QGY-2D, QPro-5B, QWSC-4A, QFv/Fm-6A and QCMS-4B) were related to both traits, heat tolerant and high-performance	Hassan et al. 2018
		<i>Triticum aestivum</i> Validation of one QTL (6A target) in the field conditions mapped in a previous GWAS. Developed near-isogenic lines, this locus 6A contributed to yield compounds under drought and heat stress in field conditions.	Schmidt et al. 2020
	<i>Triticum turgidum</i> L. ssp. durum	Uses GWAS to identify QTLs for yield under heat and drought stresses.	Sukumaran et al. 2018

	<i>Zea mays</i> L.	Detected 65 QTLs: 41 associated with salt tolerance and 24 related to normal growth. Salt tolerance-related QTL clustered on chromosomes 1, 3, 7, and 9, among which 13 major effect QTL on chromosome 1 individually explained more than 21% of the phenotypic variation.	Luo et al. 2019
		Five QTLs on chromosomes 2, 5 and 6 were mapped. Two major QTLs on chromosome 5 associated with alkaline tolerance at the maize seedling stage were mapped to marker intervals of dCap-SLAF31521 and dCap-SLAF31535 and phi024 and dCap-SLAF31521, respectively.	Zhang et al. 2018
	non-cultivated tomato	Meta quantitative trait loci (MQTL) revealed 13 MQTL associated with heat tolerance traits (pollen viability, number of pollen and number of flowers).	Ayenon et al. 2019
	Tomato species (<i>Solanum</i> sp.)	Identified 69 plasticity QTLs (pQTLs) involved in heat response between 2 populations and 837 genes differentially expressed in ovary of 6 genotypes.	Bineau et al. 2021
		Association mapping on a wide tomato germplasm collection (81 landraces) found 1800 polymorphic SNs and 35 QTLs associated to agronomical traits under heat stress.	Ruggieri et al. 2019
		Multi-environmental QTL analysis found 22 QTLs linked to reproductive traits and temperatures.	Gonzalo et al. 2020
	<i>Oryza sativa</i> L.	Identified 653 QTLs for drought tolerance from 27 genetic maps. 70 meta-QTLs were identified and 453 QTLs were mapped into the meta-QTL. Five meta-QTLs included traits that respond to drought. Proteins responsive to drought stress were identified, such as abscisic acid-insensitive protein 5, G-box binding factor 4, protein kinase PINOID, histidine kinase 2, aquaporin PIP 1-2.	Selamat and Nadarajah., 2021
		Used a panel of 180 Vietnamese rice landraces genotyped with 21,623 single-nucleotide polymorphism markers to perform GWAS for different drought response and recovery traits. Identified 14 QTLs for leaf relative water content, 9 for slope of relative water content, 12 for drought sensitivity score, 3 for recovery ability and 1 for relative crop growth rate.	Hoang et al. 2019
		Temperature values were used to perform GWA analysis using a 45K SNP map. A QTL for canopy temperature under drought was detected on chromosome 3. The candidate genes underlying the QTL point towards differences in the regulation of guard cell solute intake for stomatal opening as the possible source of temperature variation.	Melandri et al. 2020

		Identified 935 QTLs for salinity tolerance at the seedling and reproductive stages, of which 63 meta-QTLs indicate the most important genomic regions for salt tolerance in rice.	Singh et al. 2021
		Identified 14 QTLs in an F4 population for physiological traits (chlorophyll a, chlorophyll b, and carotenoid) and agronomic traits (plant height, filled grain number, grain yield, and spikelet fertility percentage). Both physiological and agronomic traits were involved in salinity tolerance at the reproductive stage.	Ahmadizadeh et al. 2021
		A total of 23 QTLs were identified for four germination traits and 46 loci were identified for several morphological and physiological parameters at the seedling stage. Among them, nine and 33 loci with the ACC9 alleles increased salt tolerance at the germination and seedling stages.	Nakhla et al. 2021
		From 54 QTLs for reproductive stage under heat stress, five minor QTLs, four for spikelet fertility under heat stress and two for stress tolerance index spikelet fertility, of which one QTL was mapped for both the traits were identified.	Ravikiran et al. 2020
		Genotyping-by-sequencing to generate SNP. 10 QTL regions for vegetative stage heat stress tolerance with 1,037 potential transcripts included transcription factors, chaperone proteins, proteases, protein kinases, phospholipases, and proteins related to disease resistance and defense and novel hypothetical proteins.	Kilasi et al. 2018
	<i>Cicer arietinum</i> L.	13 stable QTLs for 7 traits, four of them for multiple including heat stress tolerance.	Kushwah et al. 2021
		In the QTLs regions were identified 32 candidate genes (HSP, HSTF) involving in flowering time regulation and pollen-specific genes.	Jha et al. 2021
	<i>Cucumis sativus</i> L.	Overexpression of CsCaM3 (Calmodulin) gene in cucumber regulates the high temperature-responsive genes resulting in protection of the plants against oxidative and photosynthesis system damage and improves heat tolerance.	Yu et al. 2018
	<i>Agrostis stolonifera</i>	Transgenic <i>A. stolonifera</i> plants overexpressing (Osa-miR393a) from <i>O. sativa</i> increased abiotic stress tolerance (Drought, heat and salt). Expression of miR393 target gene (AsAFB2 and AsTIR1) was reduced in transgenic plants.	Zhao et al. 2019
	<i>Musa acuminata</i>	Overexpression of a heat shock protein (HSc70) in transgenic plants enhanced yield.	Trapero-Mozos et al. 2018
		Overexpression of WRKY106 from <i>Zea mays</i> improves tolerance to heat and drought	Wang et al. 2018

Genetic engineering	<i>Zea mays</i>	stress in <i>A. thaliana</i> .	
		BASIC LEUCINE ZIPPER60, bZIP60-mutant plant, impaired the normal the increasing in expression of a group of heat shock protein genes in response to high temperature.	Li et al. 2020
		Calcium-dependent protein kinases (CDPKs). Maize plants overexpressing ZmCDPK7 gene increase thermotolerance while knockout plants showed the opposite response.	Zhao et al. 2020b
	<i>Triticum aestivum</i>	Constitutive overexpression of the spliced form of TabZIP60 gene from <i>T. aestivum</i> enhanced heat tolerance in <i>Arabidopsis</i> .	Geng et al. 2018
		Overexpression of <i>TaHsfA6f</i> gene from wheat in <i>Arabidopsis</i> enhanced tolerance to heat, salt and drought stresses.	Bi et al. 2020
	<i>Brassica campestris</i>	Constitutive overexpression of a heat stress transcription factor <i>BcHsfA1</i> from <i>Brassica campestris</i> increased heat tolerance in transgenic tobacco seedling.	Zhu et al. 2018
	<i>Gossypium hirsutum</i>	Overexpression of AsHSP70 from <i>Agave sisalana</i> increased heat tolerance in transgenic cotton.	Batcho et al. 2021
	<i>Solanum lycopersicum</i> L.	BRASSINAZOLE RESISTANT 1 (BZR1) is regulator of brassinosteroid response. CRISPR-bzr1 mutant decreased tomato plants growth by reducing Respiratory Burst Oxidase Homolog 1 (RBOH1) and H ₂ O ₂ . Silencing of RBOH1 annulled the BZR1-mediated heat tolerance and its overexpression increase H ₂ O ₂ producing resulting in thermo-tolerance.	Yin et al. 2018
		SIMAPK3 a Mitogen-activated protein kinases gene from tomato was engendering CRISPR/Cas9-mediated slmapk3 mutant lines were more tolerance to heat stress by decreasing reactive oxygen species (ROS) formation, increasing transcription of antioxidant enzymes, heat stress transcription factors, and heat shock proteins.	Yu et al. 2019
		Overexpression of TPSP (trehalose-6-phosphate synthase/phosphatase) gene from <i>E. coli</i> into tomato plants improved germinating of transgenic seed lines under heat stress.	Lyu et al. 2018
		The gene for glycinebetaine synthesis: Betaine aldehyde dehydrogenase (BADH) and choline oxidase (COD) were engineered into tomato plants showing the involvement of glycinebetaine thermo-tolerance.	Zhang et al. 2020
		SICIPK24M-overexpression lines displayed enhanced tolerance to high salinity. Transgenic plants retained higher contents of Na ⁺ and K ⁺ in the roots compared to the wild-type tomato under salt stress.	Cho et al. 2021b

<i>Glycine max</i>	Identified 38 CrRLK1L (<i>Catharanthus roseus</i> kinase 1L receptors) genes. Five genes up-regulated in response to drought and salt stress. GmCrRLK1L20 up-regulated under drought and salinity stresses. Overexpression of GmCrRLK1L20 gene in hairy roots improved both drought tolerance and salt stresses and enhanced the expression of six stress-responsive genes.	Wang et al. 2021
	Constructed lines overexpressing GmDREB1. GmDREB1 improved drought resistance in fields and greenhouses. Protein interaction verification, showed that GmDREB1 interacts with GmERF008 (Glyma.04G041200) and GmERF106 (Glyma.10G194200) to form a dimer. GmDREB1 overexpression promoted the expression of melatonin biosynthesis-related genes and stress tolerance gene.	Chen et al. 2022
	GmLecRlk gene conferred soybean salt tolerance when it was overexpressed alone in soybean hairy root. GmLecRlk improves the salt tolerance of soybean by upregulating GmERF3, GmbHLH30, and GmDREB2 and downregulating GmGH3.6, GmPUB8, and GmLAMP1.	Zhang et al. 2022
	GmMYB68-overexpression lines showed enhanced resistance to salt and alkali stresses and their osmotic adjustment and photosynthetic rates were also stronger than that of GmMYB68-RNAi and wild type plants. The overexpression of GmMYB68 increased grain number and 100-grain weights under salt stress.	He et al. 2019
	Overexpression of <i>GmHsp90A2</i> gene in transgenic soybean increase heat stress tolerance while CRISPR/Cas9-knockout mutant reduced it.	Huang et al. 2019
<i>Oryza sativa L</i>	Isolated a novel HMG (High mobility group) gene, OsHMGB707, localized in the quantitative trait loci (QTL) interval of rice drought tolerance. OsHMGB707 was up-regulated by dehydration and high salt treatment. Its overexpression significantly enhanced drought tolerance in transgenic plants, its knockdown (RNAi) did not affect the drought tolerance of the transgenic plants.	Xu et al. 2021
	Rice variety ADT 43 engineered with a TF AtDREB1A driven by a stress-inducible rd29A promoter. Transgenic lines showed enhanced tolerance to drought and salinity compared to the non-transgenic. Transgenic line showed higher RWC %, lower leaf temperature, and partially closed stomata.	Muthurajan et al. 2021
	<i>SiMYB19</i> improves salt tolerance in transgenic rice by regulating ABA synthesis and signal transduction.	Xu et al. 2022

Omics		Overexpression of OsRLCK241 conferred improved tolerance to salt and drought stresses in transgenic plants. OsRLCK241 expression improved ROS detoxification by enhancing the activities of ROS scavengers as well as the accumulation of compatible osmolytes to alleviate the osmotic stress evoked by salt and drought stresses.	Zhang et al. 2021a
		Overexpression of <i>OsRab7</i> gene improve tolerance to drought and heat stress in transgenic rice plants by increasing antioxidant enzymes activity and physiological parameters while hydrogen peroxide, electrolyte leakage, and malondialdehyde were reduced.	El-Esawi et al. 2019
		Genome editing generate loss of function mutants of two cyclic nucleotide-gated ion channel (OsCNGC14 and OsCNGC16) in rice. The mutants reduced survival rates proving that both gene are necessary for modulation of calcium signals in response to heat and chilling temperatures.	Cui et al. 2020
	<i>Oryza sativa</i> L	Physiology, proteomics and metabolomics analysis of plants submitted to different nitrogen management methods and drought stress. 234 differentially expressed proteins and 518 differential metabolites were closely associated with photosynthetic and redox pathways, sucrose and nitrogen metabolism, as well as resistance associated proteins.	Du et al. 2020
		Conducted a 3-years field experiment and assessed the metabolic changes in both source and sink organs in response to combined drought and heat stress during flowering and early grain filling.	Lawas et al. 2019
		Identified 631 and 4237 salt-induced differentially expressed genes (DEGs) related to heterosis under 7-day and 14-day salt stresses, respectively. Gene functional classification showed the expression of genes involved in photosynthesis activity after 7-day stress treatment, and in metabolic and catabolic activity after 14 days.	Jahan et al. 2021
		Evaluated the high night-time (HNT) temperatures on the phenotypic and metabolic profile in rice seeds. Sugar and sugar alcohols under HNT were differential in abundance between hyper (HNT > control) and hypo (HNT < control) suggesting a protective mechanism against HNT.	Dhatt et al. 2019
		Transcriptome analysis identified 4,070 heat stress-responsive genes in two rice cultivars under heat stress. 1,688 and 707 related to heat-resistant and heat-susceptible-cultivar, respectively. Gene ontology related to WRKY, HD-ZIP, ERF, and	Wang et al. 2019

		MADS transcription factor families.	
	<i>Glycine max</i>	Importance of phenylalanine and flavonoid metabolism in the soybean responses to drought stress. Identified two novel soybean MYB transcription factors (Glyma.17G099800 and Glyma.20G034100) using gene correlation analysis.	Zhao et al. 2021
		Salt stress increased the expression of antioxidant metabolism, stress response metabolism, glycine, serine and threonine metabolism, auxin response protein, transcription, and translation-related genes in salt-resistant cultivars (JD19 and LH3). Furthermore, metabolite profiles indicated that amino acid metabolism and the TCA cycle were important metabolic pathways of soybean in response to salt stress.	Jin et al. 2021
	<i>Solanum lycopersicum</i>	Metabolite profiling of tomato fruit under heat stress reveals, sucrose and triacylglycerols accumulation, membrane lipid unsaturation, affecting volatile profile.	Almeida et al. 2021
	<i>Solanum tuberosum</i> L.	Integration transcriptomics and metabolomics approaches revealed that 448 and 918 genes were up and downregulated under heat stress. Differentially expressed genes from RNA and protein process, cell wall degradation, photosynthesis. Differential metabolites included aa, secondary metabolism and flavonoids biosynthesis.	Liu et al. 2021
	<i>Solanum</i> sp.	Compared the transcriptomes of drought-stressed plants with and without the <i>Bacillus megaterium</i> strain inoculation. Identified that bacteria-induced transcriptome reprogramming, with highlights on differentially expressed genes including transcription factors, signal transduction, and cell wall biogenesis and organization. Metabolomics identified over 40 bacterial extracellular metabolites, including several important regulators or osmoprotectant precursors for increasing plant drought resistance.	Morcillo et al. 2021
	<i>Triticum aestivum</i>	Identified 5128 genes were differentially expressed (DEGs) under salt stress. The DEGs were classified into 227 KEGG pathways among which transporters, phenylpropanoid biosynthesis, transcription factors, glycosyltransferases, glutathione metabolism, and plant hormone signal transduction represented the most significant pathways involved in salt stress response.	Amirbakhtiar et al. 2019
	<i>Saccharum</i> spp.	Comparative analysis of physiological and transcriptome dynamics related to drought stress of highly drought-resistant (ROC22) and weakly drought-resistant (Badila) genotypes, in a time-course experiment (0 h, 4 h, 8 h, 16 h and 32 h). ABA-activated signaling pathway, response to water deprivation, response to salt stress and	Li et al. 2022

		photosynthesis-related processes showed significant enrichment in the two genotypes under drought stress.	
	<i>Cicer arietinum</i> L.	Untargeted metabolomics analysis revealed accumulation of allantoin, proline, arginine, histidine, isoleucine and tryptophan due to drought stress. Choline, phenylalanine, gamma-aminobutyric acid, alanine, tyrosine, glucosamine, guanine, and aspartic acid decreased under drought.	Khan et al. 2019
	<i>Zea mays</i> L.	Non-targeted metabolic profiling analysis of leaves for 385 maize natural inbred lines under well-watered as well as drought-stressed conditions. Identified 1035 metabolites differentially produced between the two conditions. Identified 3415 metabolite quantitative trait loci (mQTLs) and 2589 candidate genes.	Zhang et al. 2021b
MicroRNAs	<i>Glycine max</i>	Combined sRNA-seq, degradome-seq and mRNA-seq data to construct a comprehensive dataset for identifying the key regulatory miRNAs-targets network. Validated 42 miRNA–target pairs exhibited inversely related expression profiles. Among these pairs, gma-miR398 negatively regulates drought tolerance.	Zhou et al. 2020a
		Two arms of miR166m target different genes related to salinity stress (chloroplastic beta-amylase 1 targeted by miR166m-5p and calcium-dependent protein kinase 1 targeted by miR166m-3p), suggesting arm-switching of miR166m play roles in soybean in response to salinity stress.	Li et al. 2022
	<i>Oryza sativa</i>	Showed that osa-MIR171f, a conserved miRNA Family, is mainly expressed in response to drought stress and regulates the transcript levels of SCARECROW-LIKE6-I (SCL6-I) and SCL6-II in rice. CRISPR/Cas9 revealed that osa-mature-miR171a-f (osa-miR171) regulates the expression of flavonoid biosynthesis genes, consequently leading to drought tolerance.	Um et al. 2022
		Identified miRNAs miR156, miR160, miR162, miR167, miR168, miR169, miR397, miR398, miR1884 heat-responsive.	Saha et al. 2019
		Identified the osa-miR531b, osa-miR5149, osa-miR168a-5p, osa-miR1846d-5p, osa-miR5077, osa-miR156b-3p, osa-miR167e-3p and targets that are regulated by heat shock proteins or heat shock transcription factors.	Kushawaha et al. 2021
	<i>Solanum tuberosum</i> L.	The expression profiles of miR156 both in root and stem tissues and miR398 in stem tissues have been shown to be related to salt stress.	Çakır et al. 2021
		Identified 335 known miRNAs representing 55 miRNA families and 430 potential	Zhou et al. 2020b

	Solanum sp.	novel miRNAs. 61, 74 and 37 miRNAs were differentially regulated for combination (of both drought and heat stresses) vs control, combination vs drought and combination vs heat, respectively.	
	<i>Triticum aestivum</i>	Identified 589 transcripts and 84 miRNAs and 3 miRNA156, miR166 and miR393 validate that targeted superoxide dismutases and an array of homeobox leucine-zipper proteins, F-box proteins and protein kinases.	Ravichandran et al. 2019
		From 96 wheat heat-responsive miRNA-genes, they identified 3 potential candidates (HT-169j, HT-160a, and HT-160b) to marked-assisted selection program.	Tyagi et al. 2021
	<i>Zea mays</i> L.	Performed a miRNome analysis of two maize inbred lines with contrasting levels of drought tolerance. Identified in leaves 11 and 34 miRNAs uniquely responsive to drought in H082183 (drought tolerant) and Lv28 (drought sensitive), respectively.	Liu et al. 2019
	<i>Linum usitatissimum</i>	Identified 34 true HSF (heat shock factors). The promoters of those genes are enriched with regulatory elements including the HSE and LTRE, which respond to high- and low-temperature conditions, respectively.	Bhogireddy et al. 2021