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Abiotic Stress Tolerance in Rice: Insight in Climate Change Scenario

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Abstract

Rice, world's second major, staple cereal crop that feed the more than 50% of world's population. To safeguard the production and to fulfill the demand of ever the increasing population and urbanization there is need to increase the rice production. Though the rice yield has increased due to the development of modern technology and climate resilient high yielding cultivars but still it is 10–15 per cent lower than its potential yield due to various biotic and abiotic stress. Drought, extreme temperature, salinity, harmful radiation, heavy metals, gaseous pollutants are the most detrimental abiotic stresses factors that cause the morphological, physiological and biochemical changes in the rice crops and ultimate result is the reduction of rice production globally. Tolerance against these stresses through exploitation of potent biotechnological tools, molecular markers, QTL mapping omices approaches, phytohormones which could offer a more adequate and rapid solution to overcome these abiotic stresses and to enhance the ultimate grain yield of rice.

Keywords: Abiotic stress, QTL mapping, phytohormones, omices

1. Introduction

Rice (*Oryza sativa* L.) is the world's second-most-important cereal crop. Nearly half of the world's population utilizes it as a staple food. It belongs to the genus *Oryza* and family Poaceae, has 22 known species and has great economic importance [1]. These are adapted to variety of climatic conditions and can be grown both in dry and wetland habitats at high and low elevations. Green revolution substantially boosted rice productivity across Asia through a combination of modern new high yielding varieties and enhanced inputs like irrigation, fertilizer, and biocides [2]. Climate change is the only aspect that took away the breeder's concern from productivity despite plateauing yield in most of the cereals over the past decade. To feed the burgeoning population of the world, especially in Asia where the population is predicted to climb from 4.3 to 5.2 billion by 2050, rice production needs to expand and the quality of the grains must to be improved [3, 4]. Global warming and climate change has been predicted to decline irrigated rice yields by around 4% by 2020 and ~ 7% by 2050, while rainfed rice yields are expected to decrease by 6% and marginally (2.5%) by 2050, respectively [5]. Abiotic stress like drought,

salinity, and heat is the dominant drivers restricting agricultural growth and output of crops around the planet. Rice plants are sensitive to various abiotic stresses. Drought stress disrupts not just morphological features in rice plants, but also physiological and biochemical processes. It has been linked to a significant drop in crop yields due to detrimental effects on plant growth, physiology, and reproduction. Research studies tend to show that abiotic stress in combination of abiotic stress factors is the most harmful [6]. In rice, drought stress is the major limiting factor for rice production in both rainfed lowland (46 Mha) and upland (10 Mha) rice ecosystems across Asia [7, 8]. Soil salinity is rising exponentially with increasing sea levels in coastal areas and in irrigated lands where soluble salts washed away underwater are brought to ground level. Almost 40 Mha of rainfed lowland under rice cultivation in South and South-East Asia including India, Bangladesh, Myanmar, and Thailand, have been ravaged by unforeseen flash floods [9, 10]. Salinity stress affects the growth and development of rice plants at three different stages; germination, vegetative, and reproductive [11]. A major problem for stable rice production is high temperature in a number of tropical and sub-tropical countries, such as India, Bangladesh, China, Pakistan, Thailand, Sudan and many African countries. For the production of rice, atmospheric temperature at anthesis is crucial. Even 38°C, which is as such not high in tropical and subtropical countries, might cause substantial yield reduction due to pollen sterility [12]. The rice has emerged as a model genomic crop in the 21st century with its smaller genome size, high-quality genomic reference sequence, large genetic and genomic resources compared to every other crop. In the last 25 years a wide range of abiotic stress tolerance loci (QTLs) have been identified in rice [13]. The development of genome-wide DNA markers, i.e., simple sequence repeats, single nucleotide polymorphisms, and the identification of QTLs and marker trait associations, have prompted to new technologies in genomic and genetic engineering tolerant to various abiotic stress. Advancements in molecular biology techniques have enabled the discovery of many genes involved in abiotic stress tolerance through spatio-temporal gene expression analysis. Transgenic approaches have further validated functionally the identified candidate genes from the genetic expression analysis. Omics approaches such as genomics, proteomics, metabolomics, transcriptomics, epigenomics have emerged as powerful biotechnological tools, used for deciphering the abiotic stress responses as well as for producing climate-resilient abiotic stress-tolerant plants [14].

At present efforts are being made to identify several stress factors in the abiotic stress tolerance and to develop rice varieties with a tolerable stress through biotechnology, molecular breeding, genomics, transcriptomics, proteomics and metabolomics [15–18]. Abiotic stresses such as drought, salinity, and heat affect the productivity of many agriculturally important crops. Therefore, to meet the food requirements of a growing world population, it is necessary to develop sustainable high-yielding varieties that can persist under abiotic stress [19]. This chapter highlights abiotic stresses such as drought, high temperatures, salinity as well as abiotic stress tolerance techniques in rice plants with emphasis on increased rice yields.

2. Major abiotic stresses affecting rice crop

Rice is the world's most significant food crop, providing calories to more than half of the world's population of 7 billion people. In most cultivable rice habitats, it has become increasingly vulnerable to losses induced by abiotic factors such as drought, floods, salt, heat, and cold. Drought or water shortages are the most damaging abiotic challenges for rice farming in rainfed habitats. Another important limitation affecting the rainfed lowlands is the submergence of rice

plants for one to two weeks owing to flash floods. Long-duration cultivars are frequently affected by floods in the early phases of development, followed by drought during blooming, resulting in significant yield deficits [20]. Meanwhile, salinity, which is determined by a heavy concentration of soluble salts in the soil, is the second most common soil issue after drought, and it is a major constraint for rice production across the world. As a result of global climate change, heat stress is becoming a severe hazard to rice production. Heat stress hinders plant development, disrupts metabolic processes, and reduces output. Rice growing in temperate locations, as well as high-altitude conditions in tropical and subtropical zones, is hampered by low temperatures. Cold stress has a negative impact on rice crops throughout the germination, vegetative development, and reproductive phases, resulting in considerable production losses. Rice crops are sometimes subjected to numerous stressors (such as salt and drought, or drought followed by submergence), resulting in massive crop losses. Rice productivity would be significantly increased while water resources and soil quality were preserved if combined tolerance to several forms of abiotic stress was improved [21].

2.1 Drought stress

Drought is a severe abiotic stress that disrupts rice Morphological, Physiological, biochemical and molecular responses (**Figure 1**), resulting in considerable crop losses [22]. Drought stress has been linked to changes in plant length, biomass, and leaf area are associated with leaf senescence in a variety of crops, [23, 24] including rice (*O. sativa*) [25]. The occurrence of both drought and heat stresses in combination are more destructive (~70%) to crop production than other stresses occurring individually [26]. Drought stress causes oxidative stress by producing a buildup of reactive oxygen species in the chloroplast and mitochondria. Drought stress enhances the competitive ability of some weeds on crop plants by allowing them to use more water than crops [27]. The synergistic and antagonistic interactions between drought stress and pathogenic infection were similarly observed. [28]. According to Wang et al. [29] drought before and after heading, has detrimental effects on brown and milled rice rates by influencing its quality to a great extent. It is the primary constraint to rice production in both rainfed lowland (46 Mha) and upland (10 Mha) rice ecosystems throughout Asia [7, 8]. Drought stress can alter tillering, floret initiation, and subsequent spikelet sterility, as well as grain filling, throughout vegetative growth, blooming, and the terminal period of rice cultivation [30]. Terminal drought is the most detrimental abiotic stress factor to rice grain yield [31]. Several studies on the effects of drought stress and dehydration revealed physiological acclimation of plants by altered antioxidant responses [32, 33]. Understanding the mechanisms that cause physiological responses to drought stress and dehydration conditions is critical. Drought tends to reduce the rate of cell division and expansion, leaf size, stem elongation, and root proliferation in rice crops, as well as interrupts stomatal opening and shutting periods, and plant nutrient and water absorption and utilization performance [34]. Deficiency of water and moisture in rice crops increases the rate of abscisic acid (ABA) biosynthesis which diminishes stomatal efficiency and conductance which reduces transpirational losses [35]. The complex nature of drought stress in rice and its strong interaction with the environment has slowed the breeding programs to develop drought adapted varieties.

2.2 Salt stress

By the end of 2050, the world's population will have risen to about nine billion people. On the other hand, due to the accumulation of high salt content in the soil,

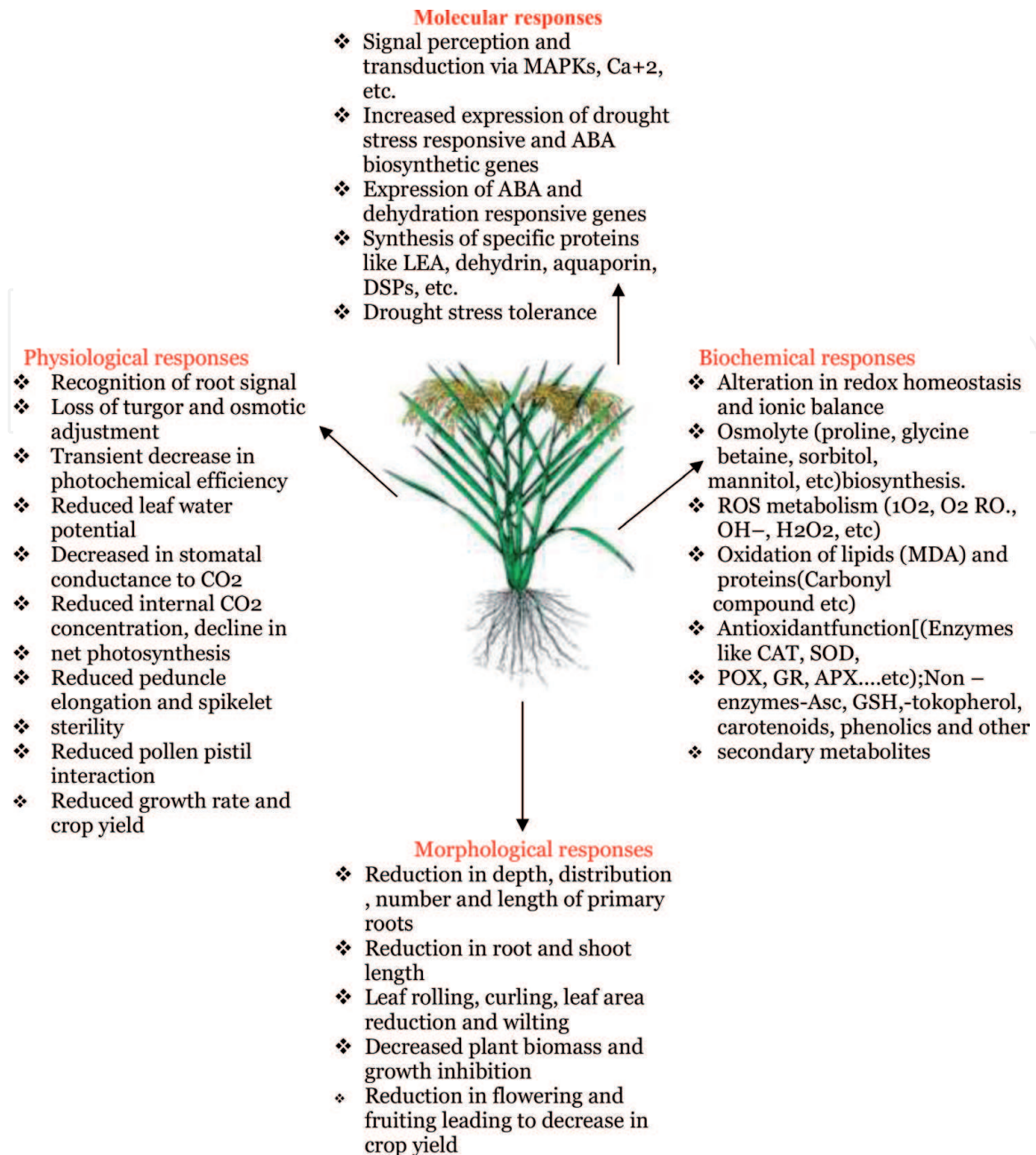


Figure 1.

Drought stress induces various morphological, physiological, biochemical, and molecular responses in rice.

worldwide agricultural production would almost probably remain static, resulting in crop growth inhibition and eventual crop mortality. Salt stress is a worrisome phenomenon because it diminishes soil agricultural productivity, leading to lower crop yields [36]. Salinity is becoming a critical threat because of diminishing irrigation water quality. (Flowers [37]. Salinity and water logging afflict 23% and 37% of worldwide cultivated land, respectively, and it is estimated that about 20% of all cultivated land and nearly half of irrigated land is salt-affected, greatly reducing yield well below the genetic potential [38]. The problem of salinity is particularly intense to agriculture in South and Southeast Asia, which produces about 90% of the world's rice [39]. By the middle of the twenty-first century, it is estimated that half of the cultivable land would be salt-affected [40]. It is suspected that the rise in soil salinity is due to poor irrigation water, its quality, and the use of brackish. Rice is a salinity-sensitive crop that performs poorly in soils with electrical conductivity (EC) as low as 3 dSm⁻¹, however salty soil is commonly defined as EC >4 dSm⁻¹ [41]. High-salt stress affects plants in several ways, such as ion toxicity, oxidative stress, alteration of metabolic processes, nutritional disorders,

genotoxicity, membrane disorganization, reduction of cell division and expansion as well as water stress. In order to cope with the antagonistic effects of soil salinity some new strategies like remediation of salinized soils, to increase the salt tolerance of crop plants through traditional as well as molecular marker-assisted breeding techniques, and biotechnology should be adopted [37, 42, 43]. Khatun and Flowers [44] observed that salt toxicity adversely affect panicle length, spikelets per panicle, and 1000-grain weight in rice crop. Salinity also delays flowering and ripening and reduces the number of tillers, biomass, and leaf area in rice crops. According to Asch and Wopereis [45], irrespective of seasons and growth stages, salt toxicity reduces rice yield, the number of panicles, and grains and causes sterility in all rice cultivars.

2.3 Temperature stress

Heat stress, characterized by prevalence of high temperature is one of the major abiotic constraints for rice production, next only to drought and salinity [46]. Vastly increased greenhouse gases in the air are predicted to significantly affect the climate and worldwide average air temperature guesstimated to significantly raise by 1.4–5.8°C between 1990 and 2100 [47, 48]. Increasing temperature with this magnitude and severity reduced global rice production [49]. The reduction in rice yield is mainly attributable to changes in critical temperature at each specific phase of growth, namely, germination, seedling, rooting, leaf elongation, tillering, panicle initiation, primordia, panicle differentiation, anthesis and maturing [50]. One of the most sensitive phenological phases to extreme temperatures is pollination that leads to poor seed set and low grain quality [51, 52]. Rice is particularly vulnerable to heat stress during the reproductive and ripening stages, as simply a few hours of heat stress causes flowering plants to become sterile. High temperatures during ripening, on the other hand, might result in a decrease in milling quality and grain filling, resulting in reduced crop yield [53].

Increase in temperature, that leads to higher humidity, can cause spikelet sterility. Consequently, amid heat stress, the floral buds are unable to mobilize carbohydrates [53]. Low temperature stress is another similar environmental stress that can cause the plant's development and growth to be slowed. Embrane structure and function, protein synthesis, and cellular cytoskeleton structure can all be severely affected by low temperature stress. Low temperatures also impede photosynthesis in both light and dark reactions; further, electron routes are disrupted, resulting in the formation of free radical species that can be harmful to rice crops, causing membrane deterioration. Japonica genotypes are more adaptable than indicas to cold temperatures and so are prevailing in high-altitude and latitude ecologies [54]. The respiratory rate of plants increase or decrease in accordance with the temperature, short-term low temperature stress leads to high respiration rate but in the case of long-term stress the cell gets damaged and eventually dies due to the reduced respiration rate.

3. Plant responses to abiotic stress

The signals of abiotic stress are a multi-faceted phenomenon due to a wide range of environmental abuses. Plants can produce appropriate responses that cause a particular change in conjunction with a specific stress condition, whereas there is significant overlap between abiotic signals. Typically, one sort of stress happens with or is followed by other stresses. The loss of water which is due to heat stress causes drought stress and in this way, both stresses are linked to each other. Signal

perception is the first phase in a signal transduction pathway which is tracked by the production of secondary signals. Secondary signals can trigger a protein phosphorylation cascade, which can then control the activation of specific transcription factors (TFs) or target genes. Additionally, these signals can modify the quantity of secondary signals; as a result, more signaling molecules are produced, providing an extra checkpoint for signals to flow in a given direction. Till date, many signaling pathways have been reported [55].

3.1 ROS signaling

Oxygen is a two-edged sword for plants, since it is a necessary element to be able to develop normal growth, but unavoidably promotes the formation of ROS like hydrogen peroxide (H₂O₂), superoxide radical, hydroxyl radical, singlet oxygen, etc. as a result of aerobic metabolic activities, such as photosynthesis and respiration. During stress circumstances in a plant, organelles such as mitochondria, peroxisomes, and chloroplast generate enormous amounts of ROS, which become highly corrosive and reactionary to nucleic acids, proteins, and lipids, inevitably leading to apoptosis or cellular damage [56].

Catalase (CAT), monodehydroascorbate reductase (MDHAR), superoxide dismutase (SOD), glutathione peroxidase (GPX), glutathione reductase (GR), dehydroascorbate reductase (DHAR), peroxiredoxin, and glutathione S transferase are all ROS foraging enzymes in plants (GST) [57]. These antioxidants work in the plant cells where they are present in different locations in order to detoxify ROS. The ROS homeostasis in plants must also be accompanied by non-enzymatic antioxidants, including tocopherols, Carotenoids, GSH, flavonoids and AsA [56]. Many other mechanisms, such as photosynthetic apparatus rearrangement, leaf movement, and leaf curling, can balance a plant's energy absorption with CO₂ supply, preventing ROS overproduction [57].

3.2 Phytohormone signaling

Phytohormones, a diverse set of signaling chemicals found in minute amounts inside cells, influence the responses. Plant growth, development, and nutrient allocation are all regulated by them. Responses to abiotic stress are triggered by a variety of stimuli, but phytohormones are responsible for the majority of them. Plants, which are sessile organisms, require phytohormones for survival [58]. They can carry out their function in their synthesis site or they can go to their action location [59]. Their family consist of cytokinin (CK), Indole acetic acid (IAA), salicylic acid (SA), ethylene, ABA, gibberellins (GAs), jasmonates, and brassinosteroids. The relatively newly discovered phytohormones are strigolactones. In regulating stress responses through interactions with some other hormones, ABA plays a major role. In order to regulate climate stress, it is the most exciting and indispensable hormone of the plant. In various phases of plant development, it plays a major role especially in opening and closing stomata, drought stress, seed germination and dormancy. PYR/PYL/RCAR-PP2C-SnRK2 is regarded as an ABA-generated signaling cascade, which effectively monitors seed dormancy even in occurrence of drought. ABA buildup amid drought stress restricts stomatal disclosure and modulates transpiration [60]. ABA signaling cascade consisted of 3 units, SnRK2/OST1 (Protein kinase), PP2C (protein phosphatases) and PYR/PYL/RCAR proteins have been investigated recently and their mechanism of operation was elucidated [61].

Ethylene is another major component of phytohormone. Ethylene is supposed to be the signaling path between plant growth and weather changes. Salinity, water logging, high temperature, frost, heavy metal interaction, nutritional inadequacy,

and drought are examples of abiotic stressors that influence ethylene production [62]. Ethylene response factors (ERFs) in plants are members of a large family of transcription factors (TFs) that are activated in response to a variety of physiological and environmental stress.

3.3 S_{os} (salt overly sensitive) signaling

Salinity is the most important abiotic stress that diminishes rice crop productivity. Plants suffer from severe osmotic pressure and a scarcity of water as a result of salinity, which causes ions to accumulate in their tissues. Different rice varieties have different levels of tolerance [63]. IR29, for example, is a salt-sensitive species that accumulates 5–10 times more Na⁺ in the leaves than Pokkali or BK [64]. Salt tolerance in rice is achieved by limiting Na⁺ translocation. The gene SKC1/ HKT8 is responsible for salt tolerance and a strong K⁺/Na⁺ balance in the shoots, as well as encoding a HKT family Na⁺ selective transporter that regulates Na⁺ transport over vast distances [65]. HKT1 is a similar gene that is ubiquitously expressed in the roots and leaves and seems to be involved in the long-distance trafficking of Na⁺. The Na⁺/H⁺ counter transporter salt overly sensitive (SOS)1 can facilitate the outflow of Na⁺ across the plasma membrane [66]. Plants lacking SOS1 become particularly salt sensitive and their transfer of Na⁺ over long distances is hampered. The root tip epidermis and xylem parenchyma cells are the primary sites of SOS1 expression. At the root-soil interface, it extrudes too much Na⁺ from the root epidermal cells. SOS1 seems engaged in the Na⁺ translocation in the roots and shoots. It's also responsible for providing ions from the xylem to the shoots in a manageable way. The SOS2/ SOS3 kinase complex utilizes SOS1 as a substrate. Plants lacking SOS2 or SOS3 have the same salt sensitivity phenotype as SOS1 plants [64]. Ion homeostasis could be maintained as a result of this.

3.4 Calcium signaling

Calcium plays a role in a variety of abiotic stress symptoms, with varied degrees of directivity. Many of the functions in plants are governed by changes in intracellular calcium levels. Calcium is a harmful ion whose concentration in eukaryotic cells is controlled. Calcium ions travel through specific calcium ion channels, the cell membrane, or organelles into the cytosol after activation. Calcium ions have therefore been progressively increased to provide a number of final preparations for calcium-dependent proteins such as calmodulin, CDPCs and calmodulin-dependent phosphatases. Local calcium increases may also occur in specific organelles, such as chloroplasts, and can easily govern specific actions in organelles [67]. The expanded accurate determination of calcium as a result of abiotic stress, their association with downstream end progressions, and the use of calcium ion homeostasis inhibitors, however, highlight its importance.

4. Biotechnological approach for improving major abiotic stress tolerance in rice

4.1 Genetic engineering

The biotechnological approach is an appealing complement to traditional strategies for improving rice genotypes because it allows for the stacking of more genes into the genome without disrupting their genetic background [68]. Drought resistance was greatly improved by overexpressing SNAC1 (STRESS RESPONSIVE NAC 1)

in rice, with 22–34 percent higher seed setting than control conditions in the field under acute drought stress during the reproductive stage, with no yield penalty or phenotypic alterations [36]. Similarly, under extreme field drought circumstances, overexpression of AP37 under the control of the OsCc1 promoter enhanced drought, salinity, and cold tolerance at the vegetative stage and also gave a 16–57 percent yield advantage over the control at the reproductive stage [69]. At the vegetative stage, overexpression of OsNAC10 with the GOS2 and RCc3 (root-specific) promoters improved drought tolerance, as well as high salinity and cold tolerance. RCc3:OsNAC10 transgenic rice cultivar showed yield advantages of 25–42 percent in the field under drought conditions [70]. OsPYL/RCAR5 (cytosolic ABA receptor) in rice plants functions as a positive inducer of abiotic stress-responsive genes [17, 18]. In contrast, rice plants exhibited a quick accumulation of soluble sugars, which act as interoperable solutes/osmoprotectants, lead to delays leaf drying and rolling [71]. Heat stress-induced gene expression and metabolite synthesis boost crop plant tolerance markedly [72]. HSFs function as molecular sensors to directly sense ROS such as H₂O₂ and control the expression of oxidative stress response genes during oxidative stress [73]. Binding of HSFs with heat shock elements (nGAAn) present in the heat responsive genes, including HSPs is critical for transcription induction of HSGs otherwise called heat shock response [74–76]. The enhanced expression of HSP70 assists in the translocation, proteolysis, translation, folding, aggregation, and refolding of denatured proteins [77]. HSP70 chaperones interact with a wide spectrum of proteins, particularly unfolded proteins generated in stressful situations [78]. Rice has 25 HSFs on 10 chromosomes other than chromosomes 11 and 12. Of these, 13 genes are class A, 8 are class B, and the remaining 4 are class C type HSFs [79]. Two HSBPs, namely OsHSBP1 and OsHSBP2, existing in rice plants and are abundantly expressed in all tissues under ordinary conditions, involved with HSR regulation, seed growth and found in considerably greater amount after heat shock recovery [80]. While considerable progress has been made in clarifying thermotolerance molecular systems, how plants perceive and translate heat stress signals is still not easy.

4.2 Marker-assisted breeding

Abiotic stress tolerance alleles were genetically eroded as a result of domestication and breeding for high yield. As a result, efforts are currently being conducted to restore allelic diversity for abiotic stress tolerance in modern high yielding varieties using locally adapted cultivars and germplasm. Stress sensitive genotypes/parents have contributed many advantageous alleles for abiotic stress tolerance, indicating the impact of a genotype's genetic background on its performance under stress [81]. A comprehensive screening and evaluation process, gene genetic background interaction, and gene environment interaction are all important factors in the utilization of QTLs in abiotic stress tolerance. The combination of whole genome expression data, QTL information, and meta-QTL analysis has proven to be a useful approach for narrowing down the search for abiotic stress tolerance candidate genes [82]. There are many success stories of introgression of QTLs for abiotic stress tolerance, and many varieties are in the advanced field trials stage [83] for tolerance to drought, salinity, and heat separately or in combination.

IRRI revealed the first important and persistent QTLs for grain yield under extreme drought stress [84]. Vikram et al [85] studied three populations: N22/IR64, N22/MTU1010, and N22/Swarna, and discovered a major consistent grain yield QTL, qDTY1.1, on chromosome 1 that can be used for marker-assisted breeding (MAB). Furthermore, in Vandana/IR64 populations, qDTY1.1 and the locus for plant height (sd1) were shown to be connected [86], suggesting that in large segregating populations, recombinant alleles with unlinked qDTY1.1 and sd1 could

create drought-tolerant plants with shorter stature [87]. In Apo/Swarna, Apo/IR72, and Vandana/IR72 genetic backgrounds, another large QTL “qDTY6.1” [88] was found on chromosome 6, explaining 40–66 per cent of the genetic variation for grain yield in aerobic conditions. Swarna and IR72, both drought-prone, performed better in aerobic conditions when this QTL was present. This was also the first report of a significant QTL that increases yield and yield potential in aerobic circumstances. Nevertheless, this QTL had no effect on lowland drought stress conditions. Three grain yield QTLs under drought stress namely qDTY2.2, qDTY3.1, and qDTY12.1 were introgressed into high quality Malaysian rice cultivar MRQ74 by MAB [89]. An Indian project in collaboration with IRRI: “From QTL to variety: marker assisted breeding of abiotic stress tolerant rice varieties with major QTLs for drought, submergence and salt tolerance” has introgressed seven consistent QTLs for grain yield under drought into high yielding, submergence-tolerant elite backgrounds of Swarna-Sub1, Samba Mahsuri-Sub1, and IR64-Sub1 [83].

Saltol QTL is a key salt-tolerant QTL that has been widely exploited to create excellent rice cultivars around the world Lin et al. [90] used an F₂ population resulting from a hybrid between “Nona Bokra” and “Koshihikari” to find multiple QTLs for Na₁ and K₁ absorption in shoots and roots, including a significant QTL responsible for SKC1 on chromosome 1. Ren et al. [63] cloned the SKC1 QTL, which maintains K₁ homeostasis in salt-tolerant cultivars under salt stress, and the SKC1 gene, which is a member of the HKT-type transporters and corresponds to the OsHKT8/Os01g0307500 locus. Using F₂ mapping populations, Zhou et al. [91] and Deng et al. [92] mapped QTLs qSKC-1 and qSNC-1 for SKC and SNC, respectively, between SSR markers RM283 and RM312. Deng et al. [93] used rice salt-tolerant 1 (rst1) mutant and showed that rst1 was controlled by a single recessive gene and QTL mapping between rst13Peiai 64 revealed the QTL loci on chromosome 6. Bizimana et al. [94] identified QTLs using RILs derived from IR29 (a salt-sensitive line) and Hasawi (a salt-tolerant line) and could not find Saltol or QTLs nearby this position indicating that tolerance in Hasawi is due to novel QTLs other than Saltol/SKC1. Emon et al. [95] and Kumar et al. [96] used association panel following a genome-wide association study approach to find marker-trait associations for salt stress tolerance. Kumar et al. [96] discovered 20 SNPs (loci) that were strongly related with Na₁/K₁ ratio at the reproductive stage, as well as the Saltol region, which is known to affect salt tolerance at the seedling stage. Many notable examples of transferring the Saltol QTL into elite rice varieties by MABC include PB1121 and PB6 [97], AS996 [98, 99], Bac Thom 7 [100, 101], Binadhan-7 [102], BRRI Dhan [103].

4.3 Omics approaches

Technological advancement in the omics area, the intrinsic genes for complicated abiotic stress in plants might be elucidated [14, 104]. Since high-strength omics approaches produced huge numbers of data, requiring both computer tools and storage resources, and data analysis, several online databases, servers and platforms were developed [105]. Proteomics and metabolomics have been shown to grow rapidly, allowing researchers to get extensive and accurate information on plant cell produced proteins and metabolites in response to environmental concerns [14, 106]. Both these emerging areas are highly expected to improve cereal crops. Similarly, profiling transcriptomics is extremely useful in ensuring a thorough understanding of regulatory molecules and their networks that are important to the communication of stress tolerance [106]. For illustrate, in order to learn more about regulatory processes and identify stress-responsive transcripts, researchers compared transcripts from tolerant and sensitive rice cultivars [107].

Despite significant improvements in high-throughput genotyping, phenotyping of complex abiotic stress responses (sometimes multigenic) remains a difficult task for molecular breeders [108]. Plants' epigenetic regulators have emerged as important regulatory mechanisms for responding to and inducing tolerance to abiotic stressors [109]. Epigenetic modulation of plant abiotic stress responses has been revealed thanks to breakthroughs in epigenomics. Short non-coding RNAs, such as miRNA, have emerged as critical epigenetic regulators of plant responses to stress [109]. However, more research is needed into how key crops, including rice, respond to abiotic stress, particularly at the epigenetic level. Overall, multiple omics techniques provide good platforms for understanding insights into plant responses and adaptation mechanisms, as well as developing abiotic stress tolerant, smart crops.

5. Perspectives and conclusion

Considering the massive losses of crop production due to severe environmental stresses, the development of crop varieties with increased tolerance or resistance to multiple stresses is presently indispensable. To date, relatively few genes reported to react to abiotic stress because agronomic characteristics of these stress tolerances have been controlled by many QTL, which show low inheritance and substantial interactions between the G/E systems. The discovery of possible genes for sustaining high pollen viability, effective gamete fertilization, and seed development in harsh conditions is not far off. With the progress of high-throughput techniques, many genes which are involved in stress regulation have been identified [110]. Plants that are subjected to several abiotic challenges at the same time must be investigated in order to comprehend the impact of various stresses. Every new combination of stresses has been suggested as a special type of stress, because it generates a totally new appropriate response. Enhanced and implementing tolerance mechanisms with the use of available low-cost sequencing and genotyping platforms, genetic and genomic resources and transgenic approaches provide huge opportunities for better rice cultivars in the near-coming future. Breeding and marker assistant selection, as well as modifying stress responses via plant hormones, are all ways that can be used to manage abiotic stress responses. Plant functional genomics perspectives which including proteomics, transcriptomic, and metabolomic analysis, as well as other high-throughput approaches and technologies, have yielded a number of drought-regulated genes, transcription factors, and cellular signaling components whose functions are crucial in rice stress tolerance.

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