

Climate resilient crops for improving global food security and safety

Abstract

Food security and the protection of the environment are urgent issues for global society, particularly with the uncertainties of climate change. Changing climate is predicted to have a wide range of negative impacts on plant physiology metabolism, soil fertility and carbon sequestration, microbial activity and diversity that will limit plant growth and productivity, and ultimately food production. Ensuring global food security and food safety will require an intensive research effort across the food chain, starting with crop production and the nutritional quality of the food products. Much uncertainty remains concerning the resilience of plants, soils, and associated microbes to climate change. Intensive efforts are currently underway to improve crop yields with lower input requirements and enhance the sustainability of yield through improved biotic and abiotic stress tolerance traits. In addition, significant efforts are focused on gaining a better understanding of the root/soil interface and associated microbiomes, as well as enhancing soil properties.

1 | INTRODUCTION

The United Nations Sustainable Development Goals (SDGs) present an urgent and formidable challenge to scientists and society alike, highlighting the urgent requirement to transform agriculture and the food sector to achieve food and nutrition security, ecosystem sustainability, economic growth, and social equity over the coming decades. Global food demand is predicted to grow by 70–85% as the population increases to over 9 billion people by 2050 (FAO, 2017; Ray, Mueller, West, & Foley, 2013). A “next generation Green Revolution” is required to achieve future food security. Radical new concepts and approaches are needed to achieve a more sustainable development of agriculture. The next Green Revolution requires a much broader and systems-based approach including environment, economy, and society, across all levels of organization (Nüsslein & Dhankher, 2016). Transformative science across the agri-food sector is required if a major crisis in food production to meet the needs of a growing world population is to be avoided. Future agriculture requires tailored solutions that not only incorporate fundamental step-changes in current knowledge and enabling technologies but also take into account of the need to protect the earth and respect societal demands.

Climate change has far-reaching implications for global food security and has already substantially impacts agricultural production worldwide through effects on soil fertility and carbon sequestration, microbial activity and diversity, as well as on plant growth and productivity. Negative environmental impacts are exacerbated in current

cropping systems by low diversity and the high intensity of inputs, climate-associated yield instabilities being higher in grain legumes such as soybean (Figure 1) and broad leaved crops than in autumn-sown cereals (Reckling et al., 2018). The predicted increased frequency of drought and intense precipitation events, elevated temperatures, as well as increased salt and heavy metals contamination of soils, will often be accompanied by increased infestation by pests, and pathogens are expected to take a major toll on crop yields (Figure 2) leading to enhanced risks of famine (Long, Marshall-Colon, & Zhu, 2015). For example, the frequency and intensity of extreme temperature events in the tropics are increasing rapidly as a result of climate change. Tropical biomes are currently experiencing temperatures that may already exceed physiological thresholds. The ability of tropical species to withstand such “heat peaks” is poorly understood, particularly with regard to how plants prevent precocious senescence and retain photosynthesis in the leaves during these high temperature (HT) conditions. Such environmental stresses are among the main causes for declining crop productivity worldwide leading to billions of dollars of annual losses. Throughout history, farmers have adopted new crop varieties and adjusted their practices in accordance with changes in the environment. But with the global temperatures rising, the pace of environmental change will likely be unprecedented. Furthermore, with the expansion of crop cultivation to nonoptimal environments and nonarable lands, development of climate-resilient crops is becoming increasingly important for ensuring food security (Kathuria, Giri, Tyagi, & Tyagi, 2007).

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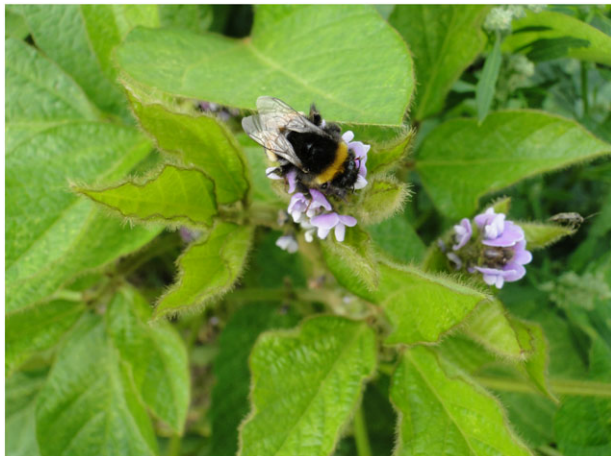


FIGURE 1 Pollinators such as bees are very attracted to legumes because of the high nutrient content of their pollen and nectar. Bumblebee feeding on soybean (variety Sultana) in a field experiment in 2015 in Müncheberg, Germany



FIGURE 2 Xerohalophytes growing in soil impacted by severe salinity and drought

Sustainable innovation of the agricultural sector within SDG constraints is urgently required to improve the way that food and animal feed are produced. Current scientific advances offer considerable potential to meet the challenges of increasing agricultural production with conservation of the environment and the earth's ecosystems, compliant to the SDGs. The papers published in this special issue cover basic and applied research focused on enabling crops to grow under over a wider range of environmental conditions with sustainable and reliable crop yields. Particular emphasis is placed on the development of climate-resilient crops that are able to adapt rapidly to changing climatic conditions and on how climate change impacts on the resilience of plant/soil interface and soil microbiomes. The manuscripts that comprise this volume address the challenges imposed by the increased frequency of abiotic and biotic stresses with a view developing strategies to minimize the impact of changing climate on agriculture and the environment.

1.1 | Abiotic stress tolerance

Of the multitude of diverse abiotic and biotic stresses faced by plants in the field, water availability is widely accepted to be one of the most

important constraints to crop yields. Drought stress alone is expected to limit the productivity of more than half of the earth's arable land in the next 50 years, competition for water between urban and agricultural areas compounding the problem. Several papers in this volume (Herzog, Konnerup, Pedersen, Winkel, & Colmer, 2017; Kerr et al., 2017; Pérez-Jiménez, Hernández-Munuera, Piñero, López-Ortega, & Amor, 2017) describe the physiological, molecular, and biochemical responses of plants to drought and flooding. Although the use of brackish and saline water could help alleviate the world's water problems, this option is only possible with the development of salt-tolerant crops (Figure 3) or management practices that alleviate salt stress. A number of manuscripts in this volume (Herzog et al., 2017; Joshi et al., 2017; Lakra, Kaur, Anwar, Pareek, & Pareek, 2017; Oyiga et al., 2017; Patishtan, Hartley, Fonseca de Carvalho, & Maathuis, 2017) describe how plants tolerate high levels of salt. Soil phytoremediation and tolerance to heavy metals are also highlighted (Fasani, Manara, Martini, Furini, & DalCorso, 2017). A number of papers describe the mechanisms that enable plants to withstand extremes of temperature (Bredow, Tomalty, Smith, & Walker, 2017; D'Amelia et al., 2017; Djanaguiraman et al., 2017; Djanaguiraman, Perumal, Ciampitti, Gupta, & Prasad, 2017; Charrier, Isabelle, Marc, & Thierry, 2017; Izydorczyk et al., 2017; Xia et al., 2017). Taken together, the new information provided in these manuscripts increases our current understanding of the biochemical and molecular basis of crop adaptation to abiotic stresses, highlighting promising candidate genes/enzymes that are targets for manipulation to improve the ability of plants to produce better yields under changing climate conditions. The acclimation mechanisms that facilitate optimization of photosynthesis and associated processes to changing irradiance are considered in two papers (Karpinska et al., 2017; Townsend, Ware, & Ruban, 2017). Within this context, the stress-induced accumulation of reactive oxygen species (ROS) controls numerous growth and developmental processes by modifying enzyme activity and protein-protein interactions. Several papers describe the roles of ROS, redox signalling and antioxidants in the plant stress signalling network, and in the interactions with phytohormone signalling cascades that govern plant responses to biotic and abiotic stresses (Ahamed et al., 2017; Karpinska et al., 2017; Song et al., 2017; Xia et al., 2017; Zhou et al., 2017). Cell proliferation and fate can also be regulated by control of



FIGURE 3 Cultivation of salt-tolerant crops such as *Agave sp.* on marginal lands in India

oxygen availability. The role of physiological hypoxia in the control of the bud burst is also discussed (Meitha et al., 2017).

Two manuscripts (Dixit et al., 2017; Gupta et al., 2017) describe the development of strategies for improving crop resiliency against multiple stresses for producing better yields with limited agronomic inputs. In particular, the paper by Gupta et al. (2017) reports the generation of rice plants with improved adaptation towards multiple abiotic and biotic stresses with reduced yield penalty through manipulation of the glyoxalase pathway. Methylglyoxal (MG) is a cytotoxic metabolite that is accumulated as a consequence of many abiotic and biotic stresses. MG accumulation may therefore be a linking factor in plant responses to diverse stresses. This paper reports that genetic manipulation of the two-step glyoxalase pathway that removes MG led to improved tolerance of rice to multiple abiotic and biotic stresses. The enhanced stress tolerance observed in the glyoxalase-overexpressing rice plants was attributed to improved MG detoxification, reduced levels of ROS accumulation, and better protection of photosynthesis (Gupta et al., 2017). Hence, prevention of MG accumulation is a promising strategy to develop improved crops with enhanced tolerance to a range of abiotic and biotic stresses.

The study described in the paper by Dixit et al. (2017) highlights the role of novel stress-associated proteins (SAPs) in providing tolerance to the multiple abiotic stresses experienced by plants. The Arabidopsis and rice genomes were found to contain 14 and 18 genes encoding SAP-related proteins, respectively. Most of the SAP genes in plants are differentially regulated in response to multiple environmental stresses such as low temperatures (LTs), salinity, drought, heavy metals, wounding, and submergence. Transgenic Arabidopsis lines overexpressing AtSAP13 were found to show improved tolerance to drought and salt stresses, and also toxic metals including arsenic (As), cadmium (Cd), and zinc (Zn) (Dixit et al., 2017). The mode of action of AtSAP13 proteins and their roles in tolerance to multiple abiotic stresses was analysed using DNA-protein interaction assays (Dixit et al., 2017). Several transcription factors related to abiotic stress tolerance were shown to bind to the AtSAP13 promoter. AtSAP13 and its homologs could therefore be used to develop climate resilient crops.

The role of abscisic acid-responsive transcription factors (ABFs) in the regulation of drought tolerance in cotton is described in detail in the paper by Kerr et al. (2017). A functional analysis of two genes that encode representative ABFs from Arabidopsis and cotton was undertaken. Expression of the Arabidopsis or cotton ABFs in transgenic cotton plants led to increased drought stress tolerance both under controlled greenhouse conditions and in the field (Kerr et al., 2017). Some of the transgenic lines analysed were better able to maintain yields during dry conditions in the field than the wild-type or nonexpressing controls. Hence, the increased expression of ABFs could provide a realistic mechanism to improve the performance of cotton in the field and develop more drought tolerant cotton varieties (Kerr et al., 2017).

Enhanced rice grain yields, achieved through manipulation of cytokinin homeostasis in the inflorescence meristem, are reported in the paper by Joshi et al. (2017). Cytokinin is degraded by the enzyme cytokinin oxidase (CKX) in the rice inflorescence. Knockdown of the inflorescence meristem-specific CKX, OsCKX2, resulted in elevated cellular cytokinin levels, which in turn, lead to enhanced panicle

branching with more grains filled per plant under unstressed and salinity stress conditions (Joshi et al., 2017). These findings shed new light on the complex crosstalk between cytokinin metabolism, abiotic stress tolerance, and grain yield.

Increasing soil contamination as a result of industrial activities and agricultural practices, such as use of recycled wastewater and underground water contaminated with heavy metals such as arsenic (Figure 4), has not only caused a decline in crop productivity but has also led to serious food safety concerns. Phytoremediation approaches are therefore crucial in the removal of toxic pollutants from soil and water so that crop production can be increased on (nonarable) contaminated soils. This topic is described in a comprehensive review by Fasani et al. (2017), which describes the problems associated with heavy metals toxicity in soil, as well as the potential of genetic engineering approaches to improve plant phytoremediation capacity in contaminated soils. The mechanisms that plants employ for uptake, translocation, detoxification, and accumulation of toxic metals are highlighted in this review, which also provides a comprehensive list of the recent studies undertaken in this field (Fasani et al., 2017). The use of phytoremediation to improve contaminated soils and/or water is proposed as a cost-effective and environmental friendly “green-clean” technology.

1.2 | Genomics and proteomics approaches to improve salt tolerance

Salinity is an ever-increasing menace to agriculture worldwide. This is particularly important for the cultivation of salt-sensitive crops such as rice and wheat. Rice is the second largest crop in the world and is planted on about one tenth of the earth's arable land and is the single largest source of food for half of humanity (FAO, 2015). Of the 130 million hectares of land used for rice cultivation, approximately 30% contain levels of salt high enough to affect rice yield (Vinocur & Altman, 2005; Wang, Vinocur, & Altman, 2003). The degree of susceptibility to salinity varies widely between rice cultivars, pointing to extensive genetic diversity that can be exploited to identify genes and their corresponding proteins that are important for rice salt tolerance. To develop crops tolerant to salinity, it is essential to understand



FIGURE 4 Field trials of rice germplasm grown on arsenic contaminated sites in West Bengal as a collaborative research project of CSIR-NBRI, Lucknow and RRS, Chinsurah, West Bengal, India.

the underlying physiological, molecular, and biochemical mechanisms and identify related genes and gene networks. Patishtan et al. (2017) report the results of a genome-wide association studies of salt-related traits in 306 rice cultivars. An important region on chromosome 8 was identified that contains a number of genes related to the ubiquitination pathway (Patishtan et al., 2017). The process of protein degradation is therefore proposed as a major target for improving salt tolerance in rice. Several hundred nonsynonymous single nucleotide polymorphisms were found in coding regions, specific genomic regions with increased numbers of nonsynonymous single nucleotide polymorphisms were identified.

Two rice genotypes (the salt-sensitive IR64 and the salt tolerant Pokkali) with contrasting responses to salinity stress were used to investigate the temporal differences in proteome profiles in the study reported by Lakra et al. (2017). This paper not only demonstrates the usefulness of the proteomics (2D-DIGE: two-dimensional differential in-gel electrophoresis) approaches to unravel the proteins involved in salt stress tolerance in rice genotypes but also highlights the finding that tolerant genotypes were "ready in anticipation" of stress, that is, the stress responsive machinery remained active and responsive to the stress signals (Lakra et al., 2017). The proteins identified in these studies will be helpful in improving salinity tolerance in crop plants. Genetic variations in salt tolerance were also reported in the paper by Oyiga et al. (2017), which reports a comprehensive evaluation and identification of quantitative trait loci conferring salt tolerance in 150 winter wheat cultivars, using a genome-wide association study approach. A large number of SNPs were reported in 37 quantitative trait loci associated with the salt tolerance traits. Candidate genes linked to these polymorphisms were identified and results confirmed by transcriptomics and qRT-PCR on samples harvested from plants grown under salt stress and control conditions (Oyiga et al., 2017). The polymorphisms identified in these two papers have biological relevance that can be exploited in future breeding programs directed at enhancing salt tolerance in wheat and rice.

The flooding of paddy fields is a common practice that could adversely affect global rice production because complete submergence can lead to severe damage and death of rice seedlings. Hence, the analysis of the role of gas films on leaves as a tolerance mechanisms presented in the paper by Herzog et al. (2017) has relevance for rice crop survival. The gas films on leaves of rice plants submerged in saline water were shown to delay the entry of salt. Moreover, the natural loss or removal of the leaf gas films resulted in a severe decline in photosynthesis and the growth of the rice plants (Herzog et al., 2017).

1.3 | Adaptation of extreme temperature stress

Exposure to extreme temperatures (chilling, freezing, or HT) causes detrimental effects on plant productivity and crop yields. The semiarid regions of the world are particularly vulnerable to the weather variability associated with climate change (Arab Water Council, 2009). Simulation studies have predicted extreme hot summers will occur twice a decade in the future in contrast to twice a century during 2000s (Christidis, Jones, & Scott, 2014). Russia recorded the worst ever heatwave in three decades in 2012 leading to about 55,000 casualties (Russo et al., 2014). Australia recorded doubling of the annual

number of hot days over the past 50–60 years with mean temperature increase by 0.9 °C (Deo, McAlpine, Syktus, McGowan, & Phinn, 2007). Warming over the Indian subcontinent (both land and ocean) has been recorded over first decade of this century (Roxy et al., 2015), and recent studies have warned the increased occurrences of heatwaves over the land (Rohini, Rajeevan, & Srivastava, 2016). Temperatures are projected to rise faster in Africa than in the rest of the world, with increases exceeding 2 °C by mid-21st century and 4 °C by the end of 21st century (Niang et al., 2014).

A mechanistic understanding of plant responses to HT, particularly when the stress is imposed at flowering, is crucial for the development of stress tolerant genotypes because plant reproductive organs are very sensitive to HT stress, (Farooq, Bramley, Palta, & Siddique, 2011; Prasad, Bheemanahalli, & Jagadish, 2017). HT reduce pollen viability and shorten the grain-filling period, temperature increases of 3–4 °C are likely to cause crop yields to fall by 15–35% in Africa and Asia and by 25–35% in the Middle East (Ortiz et al., 2008). Pearl millet (*Pennisetum glaucum*) has a higher HT tolerance than many other cereals and is hence considered to be an important climate resilient crop. Hence, like sorghum (*Sorghum bicolor*), pearl millet is an important cereal crop in the agriculture of arid and semiarid regions. The impacts of HT stress in pearl millet are reported in the paper by Djanaguiraman, Perumal, Ciampitti, et al. (2017), who identified sensitive stages and determined parameters such as temperature thresholds, genetic variability, and the fertility of pollen and the pistil. Exposure to HT stress was found to decrease pollen germination and seed yield per panicle (Djanaguiraman, Perumal, Ciampitti, et al., 2017), the periods of gametogenesis and anthesis being the most sensitive to HT stress in terms of effects on seed yield. Negative impacts of HT stress on the fertility of both pollen and pistil tissues were observed, the pistil being more sensitive than pollen (Djanaguiraman, Perumal, Ciampitti, et al., 2017). The screening of pearl millet germplasm and identification of HT tolerant lines in this paper will be extremely useful in future breeding programs designed to develop parental lines or hybrids with HT tolerance.

Understanding of mechanisms that afford tolerance will assist in the development of HT stress tolerant lines and hybrids. Similarly, deployment and adoption of HT tolerant genotypes and/or hybrids will increase the resilience of millet-based cropping systems to future climate changes. Both the pollen and pistil functions were found to decrease in response to HT stress in grain sorghum in the study reported by Djanaguiraman, Perumal, Jagadish, et al. (2017). In this case, an analysis of direct and reciprocal crosses showed that sorghum pollen was more sensitive to HT stress than the pistil, with greater decreases in seed-set (Djanaguiraman, Perumal, Jagadish, et al., 2017). Loss of sorghum gamete functions under HT stress were associated with changes in anatomy, and phospholipid composition and level of saturation, as well as ROS levels and antioxidant enzyme activities.

Like HT, LT stresses such as chilling and freezing also severely impair seedling survival and lower crop yields worldwide. Several studies in this volume provide new insights into the mechanisms by which plants perceive cold stress and how they transduce the LT signal to activate adaptive responses (Mantri, Patade, Penna, Ford, & Pang, 2012). For example, the *in planta* functions of an ice-binding protein

and ice recrystallization inhibition proteins, which play important roles in freezing tolerance via antinucleating activities that inhibit nucleation and formation of ice crystals were reported in the model grass *Brachypodium distachyon* (Bredow et al., 2017). Frost damage to flower buds is a particularly important stress for perennial crops, such as fruit trees, causing severe economic losses. The importance of frost damage at the developmental stage to walnut trees was highlighted using dynamic simulation modelling of temperature and photoperiod interactions (Charrier et al., 2017). Frost hardiness monitoring of three walnut genotypes at low and high elevation locations over 5 years revealed contrasting phenologies and maximum hardiness. Frost damage was shown to be controlled primarily by frost exposure and not the vulnerability of the walnut genotypes to frost damage during the dormant periods (Charrier et al., 2017). Such studies emphasize the importance of the mechanisms of perception of frost signals in order to minimize the damage. Phenolic compounds such as anthocyanins have been implicated in LT tolerance. Allelic diversity and the evolutionary significance of gene duplication on anthocyanin metabolism is reported in the paper by D'Amelia et al. (2017). This study highlights the role of the R2R3 MYB transcription factor called AN2, and its paralog AN1, in cold tolerant and cold susceptible potato (*Solanum tuberosum*) varieties. The duplication of MYB genes appears to have resulted in divergent functions, with AN1 specializing in anthocyanin production whereas AN2 serves to activate cold stress responses, inducing the synthesis of hydroxycinnamic acid derivatives (D'Amelia et al., 2017).

1.4 | Phytohormones signalling and stress tolerance in plants

Seasonal shifts in temperature induced by climate change are likely to affect seed germination and increase the risk of crop failure, particularly in economically important cereals such as wheat. Understanding the temperature-dependent mechanisms that influence seed germination is important in considerations of the resilience of wheat to changing environmental conditions. The molecular mechanisms underlying LT-regulation of abscisic acid (ABA) and gibberellic acid (GA) metabolism and signalling during wheat seed germination are reported in the paper by Izydorczyk et al. (2017). LT modulation of the spatiotemporal balance between ABA and GA levels and tissue sensitivity was reported to occur via altered expression of genes involved in the metabolic and signalling pathways of these phytohormones (Izydorczyk et al., 2017). Like ABA and GA, brassinosteroids (BR) play important roles in developmental processes as well as abiotic and biotic stresses tolerance (Vriet, Russinova, & Reuzeau, 2012; Zhou et al., 2014). The BR-mediated regulation of chilling stress in tomato plants was studied in the paper by Xia et al. (2017). BR is shown to positively regulate chilling tolerance through a signalling cascade involving glutaredoxin genes and the redox status of 2-Cys peroxiredoxin, as well as antioxidant enzymes activities (Xia et al., 2017). The BR-induced increases in antioxidant capacity that underpin enhanced chilling tolerance were found to be largely dependent on the activation of RESPIRATORY BURST OXIDASE HOMOLOG and associated increases in apoplastic ROS. Direct evidence of a crosstalk between BR and ROS in the resistance of tomato to root-knot nematodes is reported in the

paper by Song et al. (2017). Parasitic nematodes cause more than \$150 billion losses annually to susceptible crops worldwide (Hassan, Pham, Shi, & Zheng, 2013). BR were shown to be positive regulators acting to prevent infestation by root-knot nematodes via RESPIRATORY BURST OXIDASE HOMOLOG-dependent increases in mitogen-activated protein kinases (Song et al., 2017).

1.5 | Oxidative signalling, photosynthesis and biotic stress responses

ROS have multifaceted roles in plant biology. Despite the compelling evidence that ROS mainly act as beneficial signalling agents that protect plants against stress, the concept that oxidative damage is a major cause of stress-induced loss of cellular functions remains in the literature (Foyer, Ruban, & Noctor, 2017). This is particularly evident in the field of photosynthesis where the idea persists that light-induced damage to photosystem (PS)II causes photoinhibition requiring subsequent repair of the PSII D1 protein (Foyer et al., 2017). However, the interplay between photodamage and photoprotection in PSII is shown to be much more complex in the paper by Townsend et al. (2017). Light-induced photoinhibition is prevented by thermal energy dissipation processes in the thylakoid membrane that are together called nonphotochemical quenching (NPQ). Using a new pulse amplitude modulation fluorescence methodology, the relative contributions of NPQ and D1 repair to photoprotection were determined under short periods of illumination using photoinhibitors and mutant *Arabidopsis thaliana* lines. These studies show that NPQ makes a much greater contribution to PSII yield than D1 repair under short periods of illumination (Townsend et al., 2017).

ROS accumulation is controlled by a complex antioxidant scavenging system that includes enzymes such as superoxide dismutase, ascorbate peroxidase, catalase, glutathione peroxidase, glutathione reductase, and peroxiredoxins (Foyer & Shigeoka, 2011). However, enzymes that are considered to play important antioxidative roles such as peroxidases can also promote ROS production or ROS-dependent processes and different ROS forms (such as superoxide and H₂O₂) may antagonize each other in terms of the regulation of gene expression and low molecular weight antioxidants such as glutathione may play an integral role in transmitting oxidative signals as well as controlling ROS accumulation (Foyer et al., 2017). Photosynthesis is the major source of ROS in plants. H₂O₂ is generated in chloroplasts via the action of superoxide dismutase during photosynthesis, and this oxidant is also produced in the peroxisomes during photorespiration (Foyer & Noctor, 2005). ROS production, signalling, and removal by the antioxidant systems associated with photosynthesis provide flexibility and control in the management of high light and other stresses (Foyer et al., 2017). For example, using transgenic tobacco lines with low and high ascorbate oxidase activity, Karpinska et al. (2017) demonstrate how the redox state of the apoplast influences the acclimation of photosynthesis and leaf metabolism to the changing irradiance. High light-dependent changes in photosynthesis rates were significantly higher in high-light grown leaves when the apoplast was less oxidized, demonstrating that the redox state of the apoplast influences the extent of susceptibility of photosynthesis to high light-induced inhibition (Karpinska et al., 2017).

Stress-induced oxidation of the cellular environment leads to posttranslational modifications in protein structure and function that provide a high degree of plasticity and control in response to environmental stimuli. The influence of oxidative stress on two poorly characterized plant posttranslational modifications, protein succinylation and acetylation, is reported in the paper of Zhou et al. (2017). Using a proteomics approach to study the oxidative stress-induced interactions between the succinyl- and acetyl-proteomes, these authors provide evidence of the presence of H₂O₂-triggered interactions between the lysine succinylome and acetylome in rice leaves (Zhou et al., 2017). Large numbers of acetylated and succinylated proteins were identified in rice leaves. However, exposure to oxidative stress did not cause large global changes in the rice acetylome or succinylome profiles but rather led to modifications on a specific subset of the identified sites. Moreover, succinylation exerted a strong influence on the activities of catalase and glutathione S-transferase 6 recombinant proteins (Zhou et al., 2017).

A role for photorespiration in activating tomato leaf defenses against *Pseudomonas syringae* was reported in the paper by Ahammed et al. (2017). Climate change-associated increase in atmospheric CO₂ levels will shift the balance between photosynthetic carbon assimilation and photorespiration in C3 plants (Walker, VanLooke, Bernacchi, & Ort, 2016). Evidence is presented showing that photorespiration contributes to the basal defense against *P. syringae* via glycolate-oxidase-derived H₂O₂ production and hence climate changes associated decreases in photorespiration may impair such defense response (Ahammed et al., 2017). This report supports the concept that biotic defense pathways are promoted by photorespiration, which is inhibited at high CO₂. However, apparently contradictory observations show that growth under elevated CO₂ can induce salicylic acid-dependent defenses and thus increase plant resistance to pathogens (Noctor & Mhamdi, 2017). Moreover, elevated atmospheric CO₂ concentrations were shown to protect sweet cherry plants from the damaging effects of waterlogging (Pérez-Jiménez et al., 2017). Waterlogging often leads to hypoxia and decreases plant survival via inhibition of processes such as photosynthesis. However, high CO₂ was able to offset some of negative effects of hypoxia in sweet cherry (Pérez-Jiménez et al. 2017). Resolution of such apparently contradictory observations requires a much greater understanding of climate change-related changes in the relationships between primary metabolism, inducible defenses, and resistance to abiotic and biotic stresses (Noctor & Mhamdi, 2017).

The developmental control of hypoxia during bud burst in grapevine (*Vitis vinifera* L.) is reported in the paper by Meitha et al. (2017). The uniform control of bud burst is important in woody perennial species because it helps to synchronizing flowering, fruit set, and harvest. Evidence is presented in support of a role for oxygen-dependent signalling in the coordination of the resumption of transcriptional and metabolic processes during bud burst in grapevine after a period of dormancy (Meitha et al., 2017). The release from physiological hypoxia and associated transcript profiles are documented over the first 24 hr period during the resumption of growth in postdormant buds. Evidence is provided in support of oxygen-dependent signalling via the grapevine VII ethylene response factors during the transition from quiescence to bud burst (Meitha et al., 2017).

These studies presented in the different manuscripts that comprise this special issue not only increase current knowledge of the genes, processes, and underlying mechanisms of stress tolerance/resistance and associated crop resilience but they also identify potential new strategies for developing climate-resilient crops that will have enhanced and sustained productivity traits that will help to ensure global food security. These papers also contribute essential new ideas that are required to transform food production and so address the SDGs, with all their complex interactions and trade-offs.

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