Editorial

Crop Tolerance under Biotic and Abiotic Stresses

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Crop tolerance to both abiotic and biotic stresses is a crucial aspect of agricultural research since it directly impacts global food security and crop production sustainability. Biotic stresses encompass the challenges posed by various pests, diseases, and pathogens, while abiotic stresses involve adverse environmental factors such as drought, salinity, and extreme temperatures. Understanding and enhancing crop tolerance to these stresses are pivotal for ensuring stable agricultural production in the face of changing climate patterns and evolving pest and pathogen dynamics [1]. Related investigations contribute to the development of resilient crop varieties through breeding strategies and biotechnological interventions. Advances in omics technologies, including genomics, transcriptomics, and metabolomics, have provided valuable insights into the intricate networks governing stress responses in crops. Additionally, the identification of key stress-responsive genes and pathways has opened avenues for targeted genetic engineering to enhance crop tolerance [2].

The current Special Issue, titled "Crop Tolerance under Biotic and Abiotic Stresses," compiles one review and eleven original research papers from several research groups worldwide, including China [3,4], Colombia [5], Egypt [6], Hungary [7], Korea [8], Nigeria [9], Saudi Arabia [10–12], Spain [13], and Taiwan [14]. Concerning the experimental conditions, seven of the research studies were designed under controlled growth conditions [4,6–8,10,12,14], while the remaining four were field experiments [5,9,11,13]. Regarding the topics, three-quarters of the articles are concentrated on research related to abiotic stress, including multiple abiotic stresses [14], salinity [3,8,10–12], drought [5,6] and herbicides [7]. Additionally, three papers address the subject of biotic stress [4,9,13].

Investigating abiotic stress is essential for understanding how environmental factors, such as drought, salinity, or temperature fluctuations, impact plant growth and productivity. Liao and coworkers cloned and analysed two arabinosyltransferase sequences in the Sijichun tea cultivar, finding they were mainly expressed in young tissues and regulated by environmental changes, ethylene, and ABA signals [14]. Minor differences in their regulation patterns suggest slight functional variations. The study underscores the potential for informed cultivation practices based on arabinosyltransferase regulation, impacting tea metabolites and benefitting farmers. It also provides fundamental insights for further research and breeding, offering a pathway to modulate secondary metabolite profiles for improved tea quality through targeted approaches [14]. Abiotic stress, particularly in the form of salt stress, plays a pivotal role in shaping the resilience and productivity of crops, making it a critical research topic in agricultural science. It is no wonder that the review paper also deals with this topic. Noor and coworkers summarised the recent findings about the morphological, physiological, biochemical, and proteomic mechanisms of bermudagrass under salt stress [3]. They conclude that developing salinity-tolerant bermudagrass cultivars is crucial for overcoming growth challenges in saline soil, necessitating further exploration into genetically modified *Cynodon* cultivars. The review advocates for the use of salt-resistant species in high salinity risk areas, emphasising breeding programs to enhance bermudagrass' ability to withstand salt exposure through genetic, hormonal, and metabolic pathway regulation [3]. Breeding salt-tolerant genotypes in the case of other species is also an emphatic topic, so two research papers in this Special Issue found

effective tools for selecting these genotypes [10,11]. Javed and coworkers demonstrated that multivariate analysis, particularly with germination and seedling traits, proves essential for accurate barley genotype ranking [10]. Principal component and cluster analysis identify genotypes excelling in germination, seedling stages, or both, with confirmation through sequence-related amplified polymorphism markers. The study underscores the utility of multivariate analysis in barley breeding programs for comprehensively assessing complex relationships among genotypes, treatments, and traits, mostly in detecting salt tolerance during early growth stages [10]. Similarly, the results of Mubushar and coworkers affirm the utility of multivariate analysis with multiple traits in spring wheat breeding programs, offering a powerful tool for discriminating genotypes based on their salt tolerance, even at early growth stages [11]. Their study suggests that multivariate analysis, including principal component and cluster analysis, identified specific stress tolerance indices, such as the stress tolerance index, yield index, relative efficiency index, stress-weighted performance index, mean relative performance index, mean productivity index, geometric mean productivity index, and harmonic mean productivity index, along with plant dry weight, biological yield, and grain yield under salinity stress, as robust indicators for identifying salt-tolerant wheat genotypes. Conversely, the stress susceptibility index, tolerance index, relative salinity effect, and yield stability index were effective in isolating salt-sensitive wheat genotypes [11]. On the other hand, finding other options to help plants deal with salt stress is also important. Seleiman and coworkers showed that the application of 0.02 μM 24-epibrassinolide and 100 mg/L zinc oxide nanoparticles, either individually or in combination, alleviated the negative impact of salinity, leading to enhanced plant growth, so this treatment emerges as an effective strategy to mitigate salt stress in hydroponic systems and enhance the performance of maize plants [12]. Meanwhile, the determination and investigation of different cellular factors, which are involved in the salt-stress-induced pathways, are also essential because we have to better understand the background processes to produce salt-tolerant lines effectively. Huh investigated one of these cellular factors in *Arabidopsis thaliana*, namely Pumilio RNA-Binding Protein 6. The study proposes that this ER membrane protein plays a crucial role in the salt stress defence response by acting as a post-translational regulator that targets mRNA. The observed salt hypersensitivity of silenced lines suggests an association with an ABA-independent mechanism but indicates involvement in salt-stress-responsive genes [8]. Drought, characterised by a scarcity of water, poses a significant threat to global food security, as it adversely affects crop yields and quality. Understanding the mechanisms by which plants respond to and cope with drought stress is essential for developing resilient and drought-tolerant crop varieties. In the study of Morsi and coworkers, newly developed tissue-cultured canola genotypes demonstrated genetic diversity, showcasing varying responses to different irrigation regimes [6]. Notably, genotypes T2, T3, T1, and Torpe exhibited greater resilience to drought stress, outperforming other genotypes and commercial cultivars across multiple parameters. These superior physiological and agronomic traits in the identified genotypes could offer valuable contributions to enhancing canola production in water-limited environments [6]. The research of López-Hernández and coworkers reveals that the genetic basis of adaptation to drought stress varies among Caribbean localities [5]. Different response mechanisms dominate in dry and humid subregions, with commonality found in the photosynthetic pathway. The research suggests an environmentally dependent polygenic adaptation, emphasising the need for advanced interspecific ancestries and modern genome-wide association study approaches for common bean introgression breeding in the Caribbean coast of Colombia. The study advocates for enrichment pathway analysis to scrutinise interspecific panels, demonstrating the potential of integrating validated candidate genes into molecular editing strategies and genomic selection for enhanced drought tolerance in plant breeding programs [5]. Herbicide treatment is a form of abiotic stress imposed on plants, representing a human-induced environmental challenge with potential implications for plant growth and development. Herbicides are chemical substances designed to control or eliminate unwanted vegetation, yet their application can trigger various stress responses also in culti-

vated crops. The investigation of the cellular effect of an herbicide can help us their effect on different plant species. Gallé and coworkers studied the effect of flumioxazin in winter wheat and poppy weed plants, focusing on the role of different glutathione transferases in the process [7]. Applying the herbicide flumioxazin in the dark activates wheat defence mechanisms before the herbicide's effects appear in the light period. Differences in the response between wheat and poppy weed may be influenced by interspecies variations in glutathione transferase and type III peroxidase activity, with a notable absence of a tau glutathione transferase subgroup in poppy plants [7].

Studying biotic stress is crucial for understanding how plants respond to various pathogens, pests, and diseases, and for developing strategies to enhance crop resistance. The defence against pests can include different chemical or biological treatments. Dionisio and Calvo investigated the effect of *Trichogramma archaeae* release on a *Chrysodeixis chalcites* infestation on banana crops [13]. The study concludes that elevated natural parasitism by *T. achaeae* effectively controls *C. chalcites* in bananas, reducing reliance on a limited pesticide range. This offers a practical solution aligned with market demands for healthier, safer agricultural products and environmental protection. The release of *T. achaeae* also contributes to environmental sustainability, biodiversity conservation, and improvements in human health [13]. Selecting or engineering resistant lines is also a good strategy against biotic stress factors. The study by Job and coworkers identifies significant additive and non-additive effects for grain yield, agronomic traits, and fall armyworm-resistant traits in maize test cross hybrids, suggesting potential improvements under both artificial and natural fall armyworm infestations [9]. Two testers, 1393 and CKSBL10060 stand out as promising sources for developing fall armyworm-tolerant maize hybrids, and test crosses displaying high yield, stability, and fall armyworm tolerance could be valuable for creating adaptive open-pollinated maize varieties [9]. As in the case of any other stress-related studies, investigating the background processes and determining the key cellular factors related to disease signalling pathways is very important. Zhang and coworkers studied copine, a Ca^{2+}-dependent phospholipid membrane-binding protein in maize, which serves as a suppressor in the regulation of disease resistance and holds a crucial position in orchestrating the plant's response to disease resistance [4]. According to their results, copine could participate in defence processes associated with the R gene, SA pathway, JA pathway, and ABA pathway. Silenced lines exhibited significantly increased disease resistance, while overexpressed lines showed decreased resistance; however, silenced lines showed lower values for plant height, grain length, and 100-grain weight compared to control plants. The study establishes a foundation for understanding maize disease resistance mechanisms and contributes valuable insights for maize breeding [4].

Conflicts of Interest: The author declares no conflict of interest.

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