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Editorial

Genetic Identification and Characterisation of Crop Agronomic Traits and Stress Resistance

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1. Introduction

Enhancing crops' agronomic traits and resilience to stress is crucial for promoting food security and sustainable agriculture, particularly during climate change and for the growing global population. Genetic identification and characterisation are pivotal for comprehending the mechanisms underlying these traits and crops' responses to stress. Various genetic tools and methodologies, such as quantitative trait locus (QTL) mapping, genome-wide association studies (GWAS), marker-assisted selection (MAS), genomic selection (GS), and functional genomics techniques, like transcriptomics, proteomics, and metabolomics, have facilitated the recognition of crucial genomic regions associated with significant agronomic traits, like yield, quality, and resistance to both biotic and abiotic stresses. Hence, identifying leads for new genetic gains for crop breeding programs includes developing improved cultivars with heightened yield potential, enhanced nutritional quality, and resilience to stresses from pests and environmental factors. Leveraging genetic diversity through germplasm resources and molecular breeding strategies may be used to address these challenges.

Moreover, integrating multi-omics data and using advanced computational and statistical techniques have demonstrated roles in deciphering intricate gene-trait relationships and predicting trait performance across various environmental conditions. The emergence of high-throughput sequencing technologies and bioinformatics resources has hastened the progress of crop genetic investigations, revealing new genes and regulatory networks governing agronomic traits and responses to stress. This Special Issue consolidates the recent breakthroughs in genetic methodologies to pinpoint and describe agronomic traits, while enhancing stress resistance in a wide range of crops.

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2. Overview of the Special Issue

This Special Issue of *Agronomy* contains five original research articles and one review article on crop breeding and genetics.

A study by Wang 2023 et al. [1] evaluated the low-temperature tolerance of soybean cultivars during the early developmental (germination and seedling) stages in Northeast China. The results showed inhibited germination, a prolonged average germination time, a decreased plant height, dry weight and protein content, but accumulated proline and soluble sugars. Analysis suggested that the dry weight and proline content can be used as target traits for cultivar improvement.

Danaisilichaichon 2023 et al. [2] investigated bacterial leaf blight (BLB) caused by *Xanthomonas oryzae* pv. oryzae (*Xoo*), which poses a significant threat to global rice production. By employing genotyping-by-sequencing (GBS) and a genome-wide association study

(GWAS), they identified the causal SNPs associated with BLB resistance in 200 indica rice accessions inoculated with seven distinct *Xoo* isolates. This study identified 32 significant SNPs on chromosomes 1–8 and 12. Moreover, 179 genes within ±100 kb of the SNP regions were analysed, with 49 chosen as candidate genes based on their roles in plant defence mechanisms. These findings provide valuable insights for future functional studies and novel breeding strategies to enhance rice resistance against BLB.

Shaheen et al. (2023) [3] examined salinity's effect on the morpho-physiological and biochemical responses of cotton. The escalating soil salinity is exacerbated by climate change and irregular rainfall, necessitating the development of salt-tolerant cotton germplasm. This study assessed salt tolerance in 50 *Gossypium hirsutum* accessions under hydroponic conditions with various NaCl levels. The morpho-physiological (shoot length, root length, fresh shoot, and root weight) and biochemical attributes (Na^+/K^+ ratio, proline accumulation, catalase and peroxidase activity, and amount of reactive oxygen species (ROS) produced) were evaluated, revealing significant variations between the genotypes. These findings underscore the potential candidates for breeding salt-tolerant upland cotton genotypes, offering promising solutions for salt-affected areas.

Aslam et al. (2023) [4] estimated the drought tolerance indices in upland cotton under water deficit conditions. Water scarcity induced by global warming poses significant challenges to cotton production. Thus, identifying drought-tolerant cotton lines requires assessing their response to limited water availability without compromising the yield. This study evaluated the drought tolerance indices in fifty upland cotton accessions under varying water deficit conditions. Significant variations in the morphological (root and shoot length and fresh and dry root and shoot weights), physiological (relative water content, excised leaf water loss, cell membrane stability, and chlorophyll content) and biochemical traits (proline accumulation, catalase and peroxidase activity, and amount of reactive oxygen species (ROS) produced) were recorded. The new identified genotypes in this study may be used for breeding programs to develop drought-tolerant cotton germplasm for water-stressed regions.

Sen et al. (2022) [5] reported variations in the agro-morphological, yield and biochemical response parameters of wheat to salinity stress. Five salt-tolerant genotypes, one susceptible genotype, and a standard variety were exposed to four levels of salinity with electrical conductivities (0, 4, 8, and 12 dS m^{-1}). The data were recorded for the total height, total and effective tillers per plant, spike length, spikelet number per spike, grains per spike, thousand-grain weight, grain yield, accumulation of proline, glycinebetaine, soluble sugar, soluble protein, hydrogen peroxide, and malondialdehyde. Salinity stress significantly decreased the yield and attributes of all the genotypes, but the salt-tolerant genotype displayed the highest total tillers, effective tillers, grains per spike, and grain yield. The salt-tolerant genotypes also exhibited elevated levels of proline, glycine betaine, soluble sugars, and soluble proteins alongside reduced hydrogen peroxide and malondialdehyde accumulation, suggesting diminished oxidative stress and improved yield potential. This study identified promising wheat genotypes for soil salinity tolerance.

Sharma et al. (2023) [6] have reviewed the effect of heat stress (HS), which also poses a significant threat to crop productivity due to climate change. Understanding the impact of HS on plant reproduction is crucial, yet relatively understudied compared to other abiotic stresses. Plants employ diverse mechanisms to respond to HS at the molecular, biochemical, and physiological levels. This review discusses the molecular effects of HS on plant reproductive processes, focusing on leveraging transcription factors through omics studies and gene-editing techniques to enhance heat stress tolerance. Critical knowledge gaps in HS tolerance research have been identified, emphasising the need for judicious studies to develop resilient crop cultivars.

3. Conclusions

Gene identification and characterisation are crucial in enhancing crop agronomic traits and their stress tolerance mechanisms. Various genetic tools and methodologies show significant progress in identifying the critical genomic regions associated with important agronomic traits and stress responses. These findings provide valuable insights for crop improvement programs, offering the potential to develop improved cultivars with an enhanced yield potential, nutritional quality, and resilience to biotic and abiotic stresses. Further integration of multi-omics data and advanced computational methods holds promise for unravelling complex gene-trait associations and predicting trait performance under diverse environmental conditions.

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