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Editorial

Crop Yield Improvement in Genetic and Biology Breeding

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Food security remains one of the core issues for the sustainable development of human society, and with the continuous growth of the global population, accelerated urbanization, and changes in consumption patterns, agricultural production is facing unprecedented pressure. According to projections of the United Nations, the global population will approach 10 billion by 2050, leading to a significant increase in food demand from current levels, while arable land available for agricultural production continues to shrink due to urban expansion, land degradation, and the need for ecological conservation [1]. Against this backdrop, sustainably increasing crop yield and production efficiency under limited resources has become a key challenge for global agricultural science.

Simultaneously, climate change has further amplified the uncertainty of food production. Rising atmospheric carbon dioxide concentrations, significant changes in temperature and precipitation patterns, and the increasing frequency and intensity of extreme weather events have had profound impacts on crop growth and yield stability [2]. Abiotic stresses such as salinization, low temperature, high temperature, and drought have become major constraints on crop production, especially in marginal ecological zones and climate-sensitive regions [3]. Therefore, in the context of climate change, achieving high and stable crop yields requires not only improving potential yield levels but also enhancing crop adaptability to complex environmental conditions [4].

Over the past few decades, rapid advancements in genetics and molecular biology have brought revolutionary changes to crop breeding. The maturation of genome-sequencing technologies has enabled the gradual elucidation of the genome structure and function of major food and economic crops. Moreover, technologies such as gene editing, molecular marker-assisted selection, and genomic selection have provided unprecedented tools for the precise improvement of complex quantitative traits [5]. However, despite the significant increase in breeding efficiency brought about by modern breeding technologies, the growth rate of yield per unit area for major global crops has slowed or even stagnated in some regions [6]. This reality indicates that relying solely on traditional high-yield gene discovery or single-trait improvement can no longer meet future food demands, and new breakthroughs are urgently needed in integrating complex traits, multi-environment adaptability, and technology transfer [7].

Against this backdrop, the Special Issue of *Agriculture* titled "Crop Yield Improvement in Genetic and Biology Breeding" brings together six cutting-edge studies focused on crop yield improvement that systematically present the latest advancements in genetic and biological breeding for crop yield enhancement from multiple dimensions, including stress resistance regulation, structural trait improvement, multi-environment adaptability, and metabolic genetic regulation. These studies not only deepen the scientific understanding of yield formation mechanisms but also provide practical technical pathways for breed-

Check for updates

Received: 24 April 2026
Accepted: 27 April 2026
Published: 29 April 2026

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ing practices, fully reflecting the complete research chain from basic research to applied transformation in this field.

Abiotic stress is the primary limiting factor constraining global agricultural production and food security. It is estimated that approximately 45% of the world's arable land suffers from varying degrees of stress such as salinization, drought, and extreme temperatures, directly leading to an average crop yield reduction of 30–50%. Under stress conditions, the complex defense responses activated by plants to ensure survival often come at the expense of growth and development, creating a "stress resistance–growth" trade-off. This fundamentally limits the yield potential of crops under adverse conditions. Therefore, deeply understanding the genetic and physiological mechanisms of crop stress resistance and utilizing modern biotechnological approaches to breed new varieties that combine high stress tolerance with high and stable yields represent core strategies for addressing climate change and ensuring sustainable agricultural development.

In recent years, nanomaterials and plant biostimulants—as emerging green agricultural technologies—have shown significant application potential in enhancing crop stress tolerance. Among them, silicon has garnered considerable attention due to its unique physicochemical properties. Nano-scale silicon dioxide (NP-SiO_2), with its extremely high specific surface area, enhanced bioactivity, and utilization efficiency, can be more effectively absorbed by plants and participate in physiological regulation [8]. Previous research indicates that nano-silicon can significantly improve salt stress tolerance in crops such as wheat and maize through various mechanisms, including deposition in cell walls to enhance mechanical strength, regulation of ion transporters (e.g., NHX, SOS1) to maintain ion homeostasis, and activation of antioxidant enzyme systems [9]. These findings provide an important theoretical basis for using nanotechnology to regulate crop stress tolerance.

The study by Shin et al. in this Special Issue [10] offers systematic evidence for a deeper understanding of the molecular mechanisms by which NP-SiO_2 alleviates salt stress in soybeans. The research first screened NP-SiO_2 from six candidate biostimulants as the most effective material for mitigating the inhibitory effect of salinity on soybean germination. Under moderate salt stress, treatment with an appropriate concentration of NP-SiO_2 significantly improved soybean seed germination rate, germination index, and radicle length. At the physiological level, NP-SiO_2 treatment effectively enhanced the activities of peroxidase (POD) and ascorbate peroxidase (APX) while significantly reducing the accumulation of malondialdehyde (MDA)—a product of membrane lipid peroxidation—indicating its effectiveness in alleviating salt-stress-induced oxidative damage.

The most crucial discovery of the study came from transcriptomic analysis. Compared to the control, salt stress treatment caused significant changes in the expression of 4579 genes, while NP-SiO_2 treatment reduced this number to 2734, suggesting that NP-SiO_2 partially stabilized the drastic transcriptional reprogramming triggered by salt stress. Further cluster analysis revealed that NP-SiO_2 treatment specifically restored a set of genes suppressed under salt stress, which were enriched in pathways such as plant hormone signal transduction, phenylpropanoid biosynthesis, and flavonoid biosynthesis. Regarding the hormone network, NP-SiO_2 exhibited precise bidirectional regulation, down-regulating the excessive activation of some stress hormone pathways while simultaneously upregulating signaling for growth-promoting hormones. This restructuring of the hormone network aligns with the core theory proposed by Verma et al. [11], which posits that plants coordinate stress adaptation and normal growth through the dynamic balance of different hormone signals. NP-SiO_2 facilitates better survival and early establishment of soybeans in saline environments precisely through this molecular mechanism of "suppressing stress and promoting growth."

In addition to salt stress, low temperature is another critical abiotic stress affecting crop yield and quality, with particularly complex effects on lipid synthesis in oilseed crops. The study by Mi et al. [12] focused on the regulatory mechanisms of night-time low temperature on oil accumulation in rapeseed and innovatively expanded the research perspective from the seed itself to its source organ—the pod wall. Through field experiments at different altitudes and precisely controlled temperature greenhouse experiments, the study found that lower night temperatures significantly increased the oil content and erucic acid (C22:1) content in rapeseed, with this effect being particularly pronounced in strongly temperature-sensitive lines (STSL). To uncover the underlying mechanisms, the researchers conducted transcriptome sequencing (RNA-Seq) on pod wall tissues under low-temperature treatment. Analysis showed that low temperature did not simply inhibit the metabolism of the pod wall; instead, it significantly enhanced the synthesis of sucrose in the pod wall and its transport efficiency to developing seeds by upregulating a series of sucrose transporter genes and related transcription factors, thus providing more abundant carbon skeleton substrates for oil synthesis within the seeds. Concurrently, key genes for oil synthesis in the seeds were also activated. This study is the first to systematically reveal a synergistic regulatory pathway between sucrose supply in the source organ (pod wall) and oil synthesis metabolism in the sink organ (seed) under low-temperature conditions. This discovery not only complements previous theoretical frameworks regarding temperature effects on oil crop quality formation [13] but also provides new targets and approaches for directionally improving rapeseed yield and quality through cultivation management (e.g., utilizing low-temperature conditions in high-altitude areas or specific seasons) or molecular breeding (enhancing the synergistic regulation capacity of sucrose transport and oil synthesis).

Under the strategic framework of ensuring global food security, continuously increasing crop yield per unit area is the core pathway to address population growth and arable land resource constraints. Besides challenges posed by environmental stress, the improvement of crop structural traits is also crucial for ensuring stable yield under high-density planting. With increased agricultural intensification, high-density planting has become an important measure to increase yield per unit area. By increasing the number of plants per unit area to effectively utilize light and thermal resources, it significantly enhances the population's biological yield and harvest index. However, simultaneously, intensified competition among plants, altered canopy microenvironment, and the increased load borne by stems especially have made lodging an increasingly prominent problem, becoming a major bottleneck limiting the release of yield potential. Lodging is estimated to cause an average annual yield reduction of 10–15% in major global cereal crops. Crop lodging resistance primarily depends on stem mechanical strength, whose core determinants include the content and ratio of cell wall components (lignin, cellulose, hemicellulose), as well as the development status of vascular bundles [14]. In recent years, the application of multi-omics technologies has promoted the analysis of the genetic mechanisms underlying lodging resistance traits, providing important targets for molecular breeding [15].

The study by Xue et al. [16] in this Special Issue precisely utilizes an integrated transcriptomic and metabolomic strategy to systematically analyze the molecular mechanisms of lodging resistance trait formation in maize. Comparing stem traits of lodging-resistant and lodging-susceptible lines and their recombinant inbred lines, the study found that lodging-resistant lines exhibited superior stem mechanical strength at the mature stage, with significantly higher lignin and cellulose content in the cell wall. Deep integrative analysis of multi-omics data revealed that the molecular basis of lodging resistance is not established during the grain-filling stage but is progressively constructed through specific transcriptional and metabolic reprogramming at the mature stage. Pathway enrichment

analysis found that the phenylpropanoid biosynthesis pathway was specifically and significantly activated at the mature stage. Key genes in this pathway (such as PAL, HCT, CCR) were significantly upregulated in resistant materials, accompanied by the accumulation of lignin precursors (such as coniferyl alcohol) and other metabolites. This clearly explains the molecular pathway where gene expression drives metabolic flux, ultimately affecting cell wall strengthening. This finding is consistent with the "developmental stage-specific regulation hypothesis for complex trait formation" proposed by Li et al., addressing the technical challenge of negative correlation between lodging resistance and yield traits in traditional breeding.

Complementing studies that delve into mechanisms of single traits, the work by Kurasiak-Popowska et al. [17] in this Special Issue provides important insights into the genetic improvement of yield stability from the perspective of genotype-by-environment interactions. The study conducted a two-year multi-environment test on 280 early-maturing soybean genotypes at three locations in Poland, systematically evaluating the stability of yield, thousand-kernel weight, protein, and fat content. The study found that genotype × environment interaction effects had significant impacts on all traits. This indicates that the superior performance of a genotype may be highly dependent on specific environmental conditions; therefore, its adaptability and stability must be emphasized in variety selection. By applying the Additive Main effects and Multiplicative Interaction (AMMI) model and the Weighted Average of Absolute Scores (WAAS) index, the authors successfully combined high yield potential and broad adaptability for genotype screening. The study demonstrated that the synergistic improvement of structural traits such as plant height, lodging resistance, and thousand-kernel weight is crucial for enhancing yield stability. This work effectively supplements previous research on soybean G × E interactions [18] and provides empirical evidence and methodological tools for selecting suitable varieties under high-density planting models. It reminds breeders that while pursuing high-yield genes, stability evaluation must be incorporated into early breeding stages to cope with increasing environmental fluctuations under climate change.

The ultimate realization of crop yield depends not only on tapping genetic potential and optimizing plant structure but also highly on its performance stability and repeatability under different environmental conditions. Genotype × environment (G × E) interaction is a key factor determining varietal regional adaptability and production efficiency [19]. Against the backdrop of intensifying climate change and increasingly significant environmental heterogeneity, various uncertainties make multi-environment adaptability and yield stability of varieties core goals of modern breeding. The traditional screening model relying on a single advantageous environment is hardly able to meet the needs of sustainable agricultural production. Through systematically designed multi-location, multi-year trial networks to analyze the internal mechanisms and patterns of G × E interactions, thereby screening genotypes that can maintain high and stable yields under broad ecological conditions, has become an indispensable standard procedure in modern breeding programs. This process is not only an evaluation of genotype performance but also a deep exploration of the interaction patterns between breeding materials and the environment, providing scientific basis for precise breeding targeted at specific ecological regions.

The multi-environment evaluation study by Han et al. [20] in this Special Issue on the new soybean variety Heike 88, conducted over four years covering seven test sites in Heilongjiang Province, provides a classic case. This study not only confirmed that the average yield of Heike 88 was significantly higher than that of regional control varieties but, more crucially, revealed that its yield coefficient of variation showed a trend of decreasing year by year as the trial years progressed. This indicates that the variety's buffering capacity against environmental fluctuations strengthened, demonstrating excellent adaptability and

stability. Machine learning analysis found that accumulated temperature, year effect, and oil content were the main factors affecting yield. Through hybrid breeding, this variety achieved the aggregation of excellent traits from both parents, with its disease resistance characteristics forming a synergistic effect with high-yield traits. Simultaneously, its seed protein and oil content remained stable across different environments, highlighting the comprehensiveness of genetic gain. This practice is highly consistent in concept with the "complementary parental breeding strategy" advocated by Yu et al. [21], both emphasizing the foresight in parental selection and the systematic nature of trait integration, providing operable theoretical and practical frameworks for breeding work addressing complex environmental challenges.

On the other hand, in breeding aimed at specialty functional and high-value-added crops, the synergistic improvement of yield and quality becomes a focus, and its regulatory mechanisms are often more refined. The study on camelina by Gómez et al. [22] in this Special Issue focuses on the coordinated improvement of yield and quality in oilseed crops. By analyzing the expression patterns of key fatty acid synthesis genes at different stages of silique development in nine varieties, they found that some genes exhibited genotype-independent constitutive expression characteristics, while the expression of other genes was co-regulated by variety and developmental stage. Among them, the expression levels of genes related to polyunsaturated fatty acid synthesis in specific varieties during the late silique stage were significantly higher than in other varieties, and the α-linolenic acid content was prominent. This established a camelina variety screening system based on gene expression patterns, supplementing previous research on fatty acid synthesis regulation in Brassicaceae crops [23]. This provides a powerful tool for rapidly screening genotypes with ideal oil synthesis potential in advanced breeding materials, extending selection from phenotypic to genotypic + molecular phenotype-assisted selection.

In summary, this Special Issue systematically presents the latest advancements in genetic and biological breeding for crop yield enhancement through six original studies focusing on different crops and research dimensions. At the molecular mechanism level, it reveals the core roles of hormone signaling networks, phenylpropanoid metabolic pathways, sucrose transport systems, among others, in yield formation and stability. At the technical methodology level, it demonstrates the efficient application of technologies such as integrated multi-omics analysis, machine learning modeling, and multi-environment trial design. At the application and translation level, it validates the practical value of superior genotypes and breeding technology systems in crops such as soybean, maize, rapeseed, and camelina, providing practical solutions to address global food security challenges.

Although this Special Issue has achieved a series of breakthrough results, crop genetics and biological breeding still face many bottlenecks that need to be urgently overcome: The complexity of genotype × environment × management (G × E × M) interactions has not been fully resolved, making it difficult to accurately ensure yield stability of varieties in variable environments; the integration and functional validation efficiency of multi-omics data is relatively low, and there is a lack of mature technical systems for translating massive data into breeding decisions; the genetic analysis of complex quantitative traits remains insufficient, and the precision of multi-gene pyramiding breeding requires further improvement. Overcoming these bottlenecks depends on deep interdisciplinary integration and technological innovation.

In the future, crop breeding will fully enter the era of precision breeding. In terms of technology integration, artificial intelligence and big data technologies will be deeply integrated with whole-genome selection and gene editing technologies to achieve directional improvement of complex traits and significantly shorten the breeding cycle; the proliferation of environmental sensors and Internet of Things technology will aid in es-

tablishing dynamic G × E × M interaction prediction models, providing a scientific basis for regionalized variety promotion and field management optimization; developments in synthetic biology and metabolic engineering will break through the limitations of crops' inherent metabolic pathways, opening new directions for the synergistic enhancement of yield and quality. In terms of research priorities, the molecular mechanisms of G × E × M interactions, the role of non-coding RNAs and epigenetic regulation in yield traits, and efficient screening methods for multi-gene aggregation will become core research directions, further enriching the theoretical framework of crop yield regulation.

Global food security is a systemic project requiring deep synergy among basic research, breeding practice, and agricultural production. The research results presented in this Special Issue are a concrete manifestation of this collaborative concept. Basic research reveals molecular mechanisms that provide targets for breeding; innovation in breeding technologies accelerates the development of superior varieties, while field trials and production validation ensure the practical application value of varieties. With continuous innovation in genetic and biological breeding technologies, humanity will be able to continuously improve crop yield and production efficiency while addressing climate change and resource constraints, providing a more robust and sustainable guarantee for global food security. *Agriculture* will continue to follow the cutting-edge progress in this field, providing a communication platform for researchers and breeders, promoting the widespread application of genetic and biological breeding technologies in agricultural sustainable development, and contributing to the dual goals of global food security and green agricultural development.

Author Contributions: All the authors participated in the editing of this Research Topic, and all the other authors provided suggestive comments on the editorial. All authors contributed to the article and approved the submitted version. All authors have read and agreed to the published version of the manuscript.

Conflicts of Interest: The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as potential conflicts of interest.

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