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Editorial

Analysis of Complex Traits and Molecular Selection in Annual Crops

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1. Introduction

Annual crops, which include staple crops like rice [1], wheat [2], maize [3], cotton [4], and soybean [5], among others, have been extensively studied for their complex traits and the molecular basis of selection. Understanding these complexities is crucial for enhancing crop productivity, resilience to environmental stresses, and nutritional quality. The complex agronomic traits of crops are controlled by the effects of multiple genes, environments, gene–gene interactions, and gene–environment interactions [6]. For a long time, there has been a lack of effective research which analyzes complex agronomic traits. With the development of high-throughput sequencing technology, we can comprehensively and systematically understand the composition of complex agronomic traits and molecular selection breeding.

The past few years have seen a remarkable acceleration in our understanding of the intricate interplay between complex traits and the molecular mechanisms driving them. Researchers worldwide have delved deeply into the genetic architectures of key annual crops [7,8], unearthing novel insights into yield potential [9,10], stress tolerance [10,11], and nutritional quality [12,13]. Some researchers have constructed various mapping groups to analyze the genetic mechanisms of complex traits, such as F_2 populations [14], RIL populations [15], NAM populations [16], MAGIC populations [17], CUBIC populations [18], etc. Furthermore, genomic structural variation plays an important role in determining important complex traits in breeding and agriculture [19]. Phenotypic plasticity has also been shown to play a key role in phenotypic variation in the expression of various key agronomic traits under different environmental conditions [20], which also motivates the genetic analysis of complex agronomic traits. Through innovative applications of genome-wide association studies (GWAS) [21–23], high-resolution genomic selection strategies [24–26], machine learning and bioinformatics tools [27], and the revolutionary advent of CRISPR-Cas9 gene editing technology [11,28,29], we have moved closer to unlocking the full potential of these critical crops. This Special Issue captures complex traits and molecular selection in annual crops and contains five articles, which I will briefly describe in the following paragraphs. I want to clarify that the purpose of this editorial is not to elaborate on each article but to encourage readers to explore them.

2. An Overview of Published Articles

Genievskaya's study (contribution 1) sequenced 406 barley lines and investigated five quality traits (raw starch, protein, cellulose, and lipid content and grain test weight). Research has found that the environment significantly affects grain quality traits, particularly during grain filling, where heat and drought stress lead to increased protein content and decreased starch content. By combining genotypic and phenotypic data, GWAS was used to determine the key regions that affect barley grain quality characteristics such as starch and protein content and identify multiple quantitative trait loci (QTLs). Most of the identified candidate genes were desiccation stress and flowering genes, confirming that exposure to heat and drought stress during grain filling can lead to dramatic changes in

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grain quality traits, including lower starch and higher protein content. Nine QTLs are new and can be used in gene mining and breeding activities, including marker-assisted selection to improve grain quality parameters. In summary, this study successfully discovered SNPs closely related to grain quality through the genetic analysis of a large number of spring barley germplasms, providing the scientific basis and practical tools for further improving barley quality and optimizing breeding strategies.

Shen's article (contribution 2) used the comprehensive genome data of 890 upland cotton materials to analyze the degree of gene introgression between different geographical distributions and its impact on cotton selection and fiber quality. Genetic introgression was found to exist in different geographical distributions and was affected by artificial selection. GWAS was used to perform a meta-analysis on six fiber traits, and 261 QTLs were identified, of which 67 QTLs had genetic introgression signals and 123 QTLs had selection signals. In summary, this study provides clues to reveal the genetic introgression landscape at the population scale of cotton, shows that genetic introgression has a certain role in promoting cotton genetic improvement, and provides a useful reference for studying intraspecific genetic introgression in cotton with different geographical distributions.

Garramone's article (contribution 3) discussed the assessment of salt stress tolerance in wild potato species under in vitro conditions. The study selected a variety of potato-bearing wild potatoes, such as *S. bulbocastanum*, *S. commersonii*, *S. chomatophyllum*, *S. multidissectum*, *S. pinnactisectum*, *S. phureja*, and the cultivated species *S. tuberosum*, and tested them with different concentrations of NaCl (0, 40, 60, and 120 mM) to observe each variety's morphological changes. In vitro screening methods were used to detect significant variation in each phenotypic trait at all salinity levels. The results showed significant differences in the adaptability of wild potato germplasms under salt stress, demonstrating their potential as an important source of genetic diversity for improving crop salt tolerance. *S. commersonii* and *S. multidissectum* were selected as salt-tolerant breeding resources to utilize in subsequent genetic breeding.

Chalampuente-Flores's article (contribution 4) focused on the morphological and eco-geographic diversity of Andean lupins (*Lupinus mutabilis* Sweet) in the Ecuadorian Andes. The researchers collected a detailed description of the morphological and geographical ecological characteristics of 173 lupine germplasm resources and used geographic information systems technology to draw the optimal distribution map of this crop in Ecuador to identify hotspots with high morphological and ecological diversity. Through a series of morphological measurements and laboratory analyses, the differences between different lupine strains were examined, and statistical analysis methods such as principal component analysis, hierarchical cluster analysis, and variance analysis were used to analyze the environmental and genetic factors behind these differences. In short, this study not only revealed the impact of environment and genotype on lupine grain quality but also identified several excellent materials with promise for future genetic improvement. The authors also pointed out that continued work in germplasm resource assessment, farmland management, and the exploration of traditional uses is very necessary. These are essential to strengthening food security and local food autonomy.

Mao's article (contribution 5) constructed a high-density single nucleotide polymorphism (SNP) genetic map and used this map to locate QTLs related to early maturity in upland cotton. By analyzing the phenotypic data of F_2 and $F_{2:3}$ families in two different environments, they successfully identified the factors related to the number of the node of the first fruiting branch (NFFB), flowering time (FT), the whole growth period (WGP), and QTLs related to height of the node of the first fruiting branch (HNNFB), among which two stable QTLs were found. They further identified 125 candidate genes related to WGP and HNNFB traits and speculated that one of the genes, *Gh_D03G0857*, may play an important role in regulating the early maturity of cotton. These research results provide valuable information resources for subsequent research on the fine mapping of QTLs for early maturation traits, gene cloning, functional studies, molecular-assisted selection (MAS), and superposition breeding. In summary, this study successfully revealed the genetic basis of early maturity traits in upland cotton by applying high-density SNP genetic mapping technology and provided a large number of candidate genes and QTL information that can be used for further genetic improvement and early maturing cotton varieties.

3. Conclusions

As we conclude this Special Issue on the "analysis of complex traits and molecular selection in annual crops", we reflect with deep admiration and anticipation on the groundbreaking research presented within its pages. This collection of articles is not only a testament to the tireless dedication of agricultural scientists but also directs future systematic research on annual crops around the world to move towards a more sustainable, resilient, and nutritious future. This Special Issue highlights the power of interdisciplinary approaches, integrating classical genetics, advanced genomics, population genetics, and phenomics to unravel the mysteries of complex traits. From dissecting potato drought tolerance, the geographical morphology and ecological distribution of lupins, and barley quality to identifying cotton early maturity and fiber quality traits, previously unknown areas of related annual crop improvement are revealed.

The research results shared in this Special Issue provide the basis for crop improvement programs that are targeted, efficient, and environmentally friendly. They remind us that the pursuit of more productive, healthy, and resilient crops is an ongoing journey. Finally, we express our gratitude to all contributors, and we also thank the reviewers and editorial managers whose valuable work enriched this Special Issue and contributed to unraveling the mysteries of complex traits and molecular selection in annual crops. This Special Issue continues to advance research on complex trait analysis and molecular selection and lays a foundation for the future in-depth analysis of the huge untapped potential hidden in annual crop genomes.

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