agronomy

Editorial

Genetic Analysis in Crops

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1. Introduction

Crops contribute to global food production, energy, and medicine. Crop genetic studies focus on gene function and regulation, genetic variation and modification, genetic heredity, and gene interactions with their associated networks. Understanding crop genetics has major worldwide economic and environmental impact by providing new insights into improving crop nutrients, resistance to disease, and resilience to environmental stresses [1]. Traditional genetic analyses include morphological characterization, mutant screening, gene identification, molecular testing, biochemistry study, etc. With the aid of next-generation sequencing and gene editing techniques, crop genetics have shown great potential to promote agricultural breeding by improving crop's quality and quantity.

This Special Issue, entitled "Genetic Analysis in Crops", presents new developments and methodologies, best practices, and applications in crop science, including novel empirical research, reviews, and opinion pieces covering gene identification and analysis during crop development, gene regulation and molecular mechanisms in response to abiotic stress or biotic stress, genetic and genomic studies of crop genes, as well as novel approaches to investigate crop genes. The studies discussed illuminate a myriad of applications for advanced molecular techniques in agricultural research, including hops, triticale, rice, water yam, tobacco, and cotton. They offer invaluable insights into the genetic diversity of these crops and their potential applications beyond traditional uses. Additionally, they delve into the complex molecular mechanisms governing crop development, providing substantial contributions to genome annotation and efforts aimed at making genetic improvement across these crops. Moreover, the emphasis on genetic diversity underscores the critical need to expand our comprehension of genetic resources and reinforce genetic variation, particularly considering the challenges posed by both biotic and abiotic stressors.

2. Overview of This Topic Publications

Molecular markers to assess the variability of hop populations

Hop (*Humulus lupulus* L.) cones, primarily known for their role in providing bitterness and aroma to beer, have garnered attention for their multifaceted functions beyond brewing. Research on hops has primarily focused on three key aspects: its role as a bittering agent in beer, its contribution to aroma, and its preservative properties. Additionally, hops have a long history of use in folk medicine, with documented health-promoting effects dating back thousands of years. Calvi et al. investigated the genetic diversity of wild hop populations found in southern Italy, particularly in Calabria, utilizing simple sequence repeats (SSRs) as molecular markers to assess polymorphism and variability [2]. Their study encompassed twenty-two wild plants from three distinct geographical regions in southern Italy, alongside four commercial varieties, to explore genetic diversity and population structures. In their investigation, eight SSR markers were employed, alongside the analysis of four morphological traits: cone size, cone shape, cone diameter, and cone length. Their findings

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underscored the efficacy of microsatellites in hops due to their substantial polymorphism, making them valuable markers for identifying allelic forms within local germplasms. This ability holds promise for enhancing adaptability to new cultivation areas and isolating specific aromatic compounds, thus elevating the aromatic and gustative qualities of the final product.

Long-read cDNA sequencing in triticale

Triticale, a hybrid crop of wheat (*Triticum*) and rye (*Secale*), was initially developed in laboratories during the late 19th century in Scotland and Germany. In a recent study by Polkhovskaya et al., the spatiotemporal transcriptomic changes during seed development in triticale were investigated [3]. Through a comprehensive analysis utilizing long-read cDNA and direct RNA sequencing, the researchers identified novel genes at various stages of seed development 10 days post-anthesis (DPA), 15 DPA, and 20 DPA, and in different parts of the seed that were previously unannotated in the A, B, and R genomes. Among the novel genes detected were long non-coding RNAs (lncRNAs), protein-coding RNAs, and RNAs derived from transposable elements (TEs). Interestingly, some of the tested lncRNAs exhibited polymorphic characteristics within the triticale collection. With a cutoff of TPM > 2 and Gene Ontology (GO) analysis, it was revealed that lncRNAs comprise over 10% of the triticale developing seed transcriptome, indicating their potentially diverse roles in this biological process [3]. These findings not only provide valuable insights for enhancing genome annotation but also facilitate a deeper understanding of the functional dynamics within the developing seed transcriptome. Such an understanding holds significant promise for advancing the genetic improvement in triticale.

The catalase gene family in response to the abiotic stress in tobacco

Catalase (CAT) is a pivotal enzyme encoded by the catalase gene family, crucial for the elimination of reactive oxygen species (ROS). Its unique ability to detoxify H_2O_2 is essential for maintaining intracellular stability, thereby enabling cells to withstand oxidative stress. Liu et al. (2023) identified seven CAT genes, NtCAT1-7, through CD-Search, shedding light on the CAT gene family's response to stress in tobacco and its implications for tobacco resilience breeding [4]. The study delved into how NtCATs respond to various abiotic stresses such as NaCl, cold, and drought. Notably, NtCAT1, 2, 3, and 4 exhibited downregulation under abiotic stress, with no sensitivity to low temperatures, while NtCAT5, 6, and 7 showed upregulation specifically under cold conditions, with NtCAT6 displaying the highest sensitivity to abiotic stress [4]. GO annotation unveiled the involvement of all NtCATs in the oxidative stress pathway, except for NtCAT7. Predictions of CAT protein tertiary structures via PDBsum revealed conserved structures across all NtCATs, except for NtCAT7. Further gene structure analysis showed that NtCAT1–6 possesses six or seven introns, whereas NtCAT7 contains only one. The fluctuations in NtCAT expression under diverse stress conditions underscored their responsiveness to environmental cues and their active participation in tobacco's defense response, reinforcing their role in oxidative stress mitigation [4]. These findings advance our understanding of how NtCATs contribute to tobacco resilience and stress adaptation, informing strategies for enhancing tobacco resistance through genetic interventions.

Purple color genes in rice

Rice (*Oryza sativa*) stands as one of the world's most economically significant crops. Among rice cultivars, pigmented varieties hold appeal to both breeders and consumers due to their commercial viability and the health-enhancing properties attributed to pericarp anthocyanins [5–7]. Moreover, they serve as crucial morphological markers in hybridization efforts. In rice, the purple pericarp (Prp) trait and the purple leaf (Pl) trait exhibit epistasis, relying on the complement of the Pb and Pp genes for pericarp coloration and the Pl and Pp genes for leaf coloration, respectively. Cyanidin-3-glucoside (C3G) and peonidin-3-glucoside are the primary pigments deposited in the pericarps of purple rice [8,9]. Kang et al. examined the C3G content in the leaves and seed pericarps of colored leaf parents, elucidating the inheritance patterns of associated genes among progenies derived from crosses between two mutant lines, YUM051 and YUM144, showcasing distinct color pheno-

types in both leaves and pericarps [10]. Through high-performance liquid chromatography (HPLC) analysis of the anthocyanin content in leaves and grains, they underscored the independent genetic functions of the Pb and Pl genes, crucial in the pigmentation of purple pericarps and leaves in rice, respectively. Their research also highlighted the involvement of Pb and Pl in grain pericarp pigmentation, with Pb resulting in purple grains and Pl yielding purple leaves [10]. These insights into rice coloration mechanisms offer significant contributions to rice genetics and breeding endeavors, ultimately enhancing agronomic traits and fostering the development of improved rice varieties.

The spatial multivariate cluster analysis in water yam

Water yam (*Dioscorea* spp.) holds significant economic importance as a staple food for over 300 million people inhabiting the tropics and subtropics [11]. However, various biotic and abiotic stressors impose constraints, leading to low yields and inferior tuber quality in water yam production. Ouattara et al. conducted a comprehensive analysis of 285 water yam genotypes, evaluating eight key traits through ANOVA and PCA [12]. They explored the interrelationships among agronomic and tuber quality traits using Pearson's correlation coefficients, revealing noteworthy findings. A positive correlation emerged between tuber yield per plant and both plant vigor and the number of tubes per plant. Conversely, a significant negative correlation was observed between the dry matter content and tuber yield per plant, as well as tuber oxidation browning and boiled tuber quality [12]. Identifying superior genotypes possessing favorable characteristics is pivotal for enhancing water yam cultivation. Moreover, analysis using the multi-trait genotype–ideotype distance index (MGIDI) highlighted four traits exhibiting desired genetic gains across all families, including plant vigor, number of tubers per plant, yield per plant, and dry matter content. Conversely, yam anthracnose disease, tuber oxidation browning, boiled yam quality, and pounded yam quality displayed undesired gains in selection across the families [12]. These promising genotypes and traits hold potential as valuable contributors to water yam improvement programs, catering to the needs of both farmers and end users by enhancing agronomic and quality traits.

The genetic diversity and molecular studies in cotton

Cotton (*Gossypium* sp.) is a vital fiber crop with a global presence and significant economic importance. It holds a central position in the textile industry, contributing significantly to the global economy. The quality of cotton fibers is paramount as it directly impacts the excellence of textile products. These fibers, originating from single-celled structures on seed surfaces, are the most extensively utilized plant-based textile materials worldwide. With approximately 52 species and nine distinct cytogenetic genomes, including eight diploids and one tetraploid, cotton offers a rich reservoir of genetic diversity [13]. Among these species, *Gossypium hirsutum* and *Gossypium barbadense*, both tetraploids with (AD)n genomes comprising 52 chromosomes, reign as the most widely cultivated varieties worldwide [14–16]. In the face of escalating biotic and abiotic stressors and unpredictable climate shifts, the imperative for genetic diversity in cotton becomes even more pronounced. Aydin studied the genetic diversity of 47 cultivars across *Gossypium hirsutum* and *Gossypium barbadense*, employing 19 SSR markers and high-resolution capillary gel electrophoresis [17]. PCA utilizing Jaccard's similarity matrix offered fresh insights into the genetic relationships among these cultivars. Furthermore, Aydin used Bayesian cluster analysis to dissect the genetic associations between *Gossypium hirsutum* and *Gossypium barbadense* [17]. These comprehensive studies and analyses represent essential components in broadening our understanding of genetic resources and fortifying genetic variation. Such insights play an important role in developing cotton varieties tailored to exhibit desired traits despite challenging environmental conditions. Bai and Scheffler (2024) provided a comprehensive review of the recent progress made in molecular and genetic studies of cotton [18]. Understanding the genetic and molecular mechanisms underlying fiber development is essential for advancing breeding efforts aimed at enhancing cotton fiber quality and overall yield. Such insights are crucial for developing cotton varieties with desired traits for challenging environmental conditions. With advanced knowledge and techniques, breeders and

farmers can produce cotton varieties boasting superior fiber attributes, thus benefiting both industry and the economy.

3. Conclusions

The studies highlighted in this Special Issue emphasize the significance of interdisciplinary research in agriculture, particularly to unravel the genetic and molecular intricacies governing crop development, stress responses, and trait variation genetics. These findings carry profound implications for crop enhancement, resilience breeding, and the promotion of sustainable agricultural practices. They not only deepen our fundamental knowledge of plant biology but also provide researchers and breeders with the tools to engineer cultivars with enhanced traits, thereby fostering agricultural productivity and bolstering the global economy. As we continue to explore the complexities of plant genetics and molecular biology, the potential for innovation and advancement in crop improvement endeavors remains vast, promising a future characterized by sustainable agriculture and enhanced crop productivity and quality.

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