Editorial

Germplasm Resources Exploration and Genetic Breeding of Crops

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1. Introduction

A continuously changing climate has negatively impacted agriculture and threatened food security worldwide. Climate change and the fast-growing human population have caused the shrinking of arable land, soil erosion, water shortages, and the loss of genetic resources in their natural locations. Environmental changes force plant breeders to develop new and improved cultivars with better adaptability to biotic and abiotic stresses. The genetic diversity of crops, gathered and protected from extinction in genebanks worldwide, is essential for dealing with changing and more demanding environments.

Plant genetic resources are not only items to collect but are vital for securing breeding gains in agricultural crops. An estimated number of 7.5 million samples are stored in approximately 1800 genebanks worldwide [1], of which most are at least recorded in information systems. There is a compelling need for the genotypic and phenotypic characterization of whole genebank collections to efficiently increase their management and generate information that is useful for plant breeders. Precise and comprehensive characterization can be achieved through the intensive phenotyping and genotyping of genebank collections, current and historic cultivars, landraces, and breeding materials using advanced molecular, biochemical, and physiological tools and methods.

2. Overview of the Special Issue

The Special Issue "Germplasm Resources Exploration and Genetic Breeding of Crops" was planned to cover all aspects of the characterization of crop genetic resources and their applications in breeding, as well as genetics research and molecular breeding, including gene/QTL detection or gene functional analysis in crops. In our Special Issue, we have united 16 papers addressing various aspects around the topic of plant genetic resources, including quantitative trait loci (QTL) mapping/gene discovery [2,3], genetic diversity/variation [4–9], breeding products [9–13], and genetic resource profiles for crops [14–16].

2.1. QTL Mapping

The first contribution [2] employed QTL analysis to investigate the genetic architecture of panicle length in a biparental rice population that involved an accession of Dongxiang wild rice (*Oryza rufipogon* L.). Three out of the four QTL found were derived from wild species. After the development of a near-isogenic line for a major wild rice QTL on chromosome 7 and the establishment of a high-resolution genetic mapping population, the locus was pinpointed to a genomic region that contains the well-known *grain length on chromosome 7* (*GL7*) gene. Further studies suggested the locus in Dongxiang wild rice to represent a new variant of *GL7* that appears to control, besides grain size, inflorescence length.

A second QTL study [3] addressed blast resistance in the Thai rice landrace variety Phaladum through a QTL-seq approach. Inheritance studies indicated the presence of a single, all-stage *Magnaporthe oryzae* resistance gene. QTL-seq analysis located the gene in a 3.6 Mb region on chromosome 4 that harbours, among four other genes with putative functions in disease resistance, the dominant resistance gene *Pi63*. Kompetitive Allele-Specific PCR (KASP) marker-trait association analysis showed that all five genes were highly associated with variation in disease reaction, with the highest phenotypic variance explained by *Pi63*.

2.2. Genetic Diversity/Variation

The characterization of germplasm genetic diversity is critical for gaining information on desirable traits and maximizing genetic resource exploitation for cultivar development.

Lee et al. [4] characterized the genetic diversity of Korean black soybean (*Glycine max* (L.) Merr.) with green cotyledons. The evaluation of twenty seed composition traits in 469 accessions indicated that black soybean germplasm was divided into four clusters by the differences observed in crude fat, lutein, chlorophyll, cyanidin-3-glucoside, palmitic, α-linolenic, and oleic acid contents. This study highlights the genetic diversity of black soybean germplasm, which may be useful for soybean breeding programs.

Mehmood et al. [5] assessed the genetic divergence and population structure of potato genotypes collected from Punjab, Pakistan, using polymorphic retrotransposon-based DNA markers. Analysis of molecular variance (AMOVA) and STRUCTURE arranged the eighty genotypes into five distinct groups and indicated genotypes especially valuable for potato cultivar improvement.

Kadluczka and Grzebelus [6] comparatively investigated the fruit morphology and anatomy of 13 wild *Daucus* species and four closely related non-*Daucus* species as potential sources of genetic diversity for carrot (*Daucus carota* subsp. *sativus* Hoffm.) improvement. Evaluation of fruit morphology and anatomy and observation by light and scanning electron microscopy revealed a wide range of variation in fruit morpho-anatomical characteristics, including fruit size, shape, and weight, as well as fruit surface sculpturing and some other anatomical characteristics.

In the study conducted by Madhavan Samyuktha et al. [7], 52 mungbean (*Vigna radiata* L.) genotypes were evaluated for resistance to bruchids (*Callosobruchus* ssp., *Coleoptera*, *Bruchidae*), insects that cause severe damage to seeds during storage, and 2 highly resistant genotypes (V2802BG and V2709) were identified. In a population developed by crossing V2802BG with a high-yielding bruchid-susceptible cultivar, seven highly resistant families were identified and evaluated in the F_4 and F_5 generations. As a result, five highly resistant lines were developed, which can be used as a potential source of genetic material for improving bruchid resistance in mungbean breeding programs.

Noweiska et al. [8] used a fluorescence in situ hybridization toolbox and molecular markers linked to the leaf rust resistance gene *Lr63* (located on the short arm of the $3A^m$ chromosome—$3A^mS$) to track polymorphisms between *Triticum monococcum* subsp. *monococcum*, *T. boeoticum*, and *T. urartu* (A-genome donor for hexaploid wheat) accessions collected in different regions of Europe, Asia, and Africa. The authors distinguished three groups of accessions and concluded that the polymorphisms observed in cultivated forms of *T. monococcum* were induced by adaptation to local environmental conditions.

2.3. Breeding Resources and Breeding Products

Progress in plant breeding is achieved through the search for and introduction of new valuable trait-conditioning genes into breeding materials. In this section, the authors scanned plants of the *Avena* L., *Setaria italica* L., *Zea mays* L., and *Brassica napus* L. species, utilizing phenotyping or molecular genotyping to detect useful breeding materials and assess the diversity of the available breeding resources.

Ma et al. [9] investigated the genetic basis of the foxtail millet (*Setaria italica* L.) discoloration rate caused by carotenoid degradation during storage and identified *SiLOX4*

as a potential key gene in regulating millet discoloration. This study provided critical information on the mechanism of carotenoid degradation during millet storage and laid the foundation for further understanding of carotenoid metabolism in millet.

Thiam et al. [10] evaluated the diversity, productivity, and stability of eleven advanced breeding lines and the control cultivar 'Avery' of *A. magna* ssp. *domestica* in five locations across three cropping seasons in Morocco. Consequently, they verified that the tested lines were beneficial to be incorporated into breeding programs in Morocco and chose line AT5 as one with the highest grain yield and AT7 as the most stable in all environments, making them the most promising breeding material.

Sowa et al. [11] tested the crown rust resistance of Polish National Genebank resources for *Avena strigosa Schreb*. In addition to identifying *Avena* accessions that might be ideal crown rust resistance gene donors (PI 51887) and sources of putatively new *Puccinia coronata* resistance, they also proved the complexity and heterogeneity of the accessions gathered in the genebanks. This confirms that once many potential sources of oat resistance have been overcome, it is advisable to conduct a thorough search for desired breeding features among the population plants of a given accession.

Sobiech et al. [12] scanned maize breeding lines with different field resistance to *Fusarium* fungi using molecular markers linked to *Fusarium verticillioides* quantitative resistance loci. They confirmed the utility of the markers used in evaluating fusarium-resistant materials, presented optimal parental selection for crossbreeding, and developed multiplex PCR reactions to facilitate the maize breeding process.

In the study of Wasuwatthanakool et al. [13], the genetic effect and combining ability for both total carotenoids and their fractions of S_2 super sweet corn lines developed from a cross between tropical and temperate germplasm were examined. The authors identified lines potentially useful in hybrid breeding of high-carotenoid content and improved nutritional values and determined that the inheritance of carotenoid content was controlled by non-additive gene activity, enabling further breeding strategies.

Finally, Łopatyńska et al. [14] assessed double haploid oilseed rape lines with varied seed coat color and selected valuable breeding material connecting a light color of seeds with high yielding. Based on the obtained results, the authors concluded that the most crucial factors in breeding rapeseed with improved seed properties are seed weight and color. They also proved the usefulness of statistical multivariate methods in the selection of breeding material for rapeseed.

2.4. Genetic Resource Profiles

Three review articles in this Special Issue offer insights into the wealth of genetic resources for wheat/oats [15], chestnuts [16], and tobacco [17]. All three articles point out the significance of these plant materials to breeding for disease resistance and that the potential of the wild relatives can only be fully used when coupled with genomics-assisted breeding. Further, the utilization of gene signatures from distantly related species will be accelerated by genome-editing techniques, as cross-compatibility is no longer a prerequisite for information transfer.

3. Conclusions

This editorial summarizes the main scientific input from 16 research papers and reviews comprising the Special Issue "Germplasm Resources Exploration and Genetic Breeding of Crops". The papers cover studies on QTL mapping, genetic diversity/variation, breeding resources and breeding products, as well as the genetic resource profiles of a variety of important crops. The Special Issue presents a variety of ideas, concepts, and tactics for readers and researchers aiming to accelerate plant breeding through the exploration of germplasm resources.

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References

1. Keilwagen, J.; Lehnert, H.; Badaeva, E.D.; Özkan, H.; Sharma, S.; Civáň, P.; Kilian, B. Finding Needles in a Haystack: Identification of Inter-Specific Introgressions in Wheat Genebank Collections using Low-Coverage Sequencing Data. *Front. Plant Sci.* **2023**, *14*, 1166854. [CrossRef] [PubMed]
2. Li, S.; Rao, Y.; Duan, P.; Wang, Z.; Hu, P.; Yu, R.; Luo, C.; Tang, M.; Lu, C.; Wang, Y. Mapping and Candidate Gene Prediction of *qPL7-25*: A Panicle Length QTL in Dongxiang Wild Rice. *Agriculture* **2023**, *13*, 1623. [CrossRef]
3. Netpakdee, C.; Mathasiripakorn, S.; Sribunrueang, A.; Chankaew, S.; Monkham, T.; Arikit, S.; Sanitchon, J. QTL-Seq Approach Identified *Pi63* Conferring Blast Resistance at the Seedling and Tillering Stages of Thai Indigenous Rice Variety "Phaladum". *Agriculture* **2022**, *12*, 1166. [CrossRef]
4. Lee, J.Y.; Jo, H.; Son, C.K.; Bae, J.S.; Lee, J.D. Genetic Diversity of Korean Black Soybean (*Glycine max* L.) Germplasms with Green Cotyledons Based on Seed Composition Traits. *Agriculture* **2023**, *13*, 406. [CrossRef]
5. Mehmood, A.; Dracatos, P.M.; Maqsood, L.; Yousafi, Q.; Hussain, A.; Jaskani, M.J.; Sajid, M.W.; Haider, M.S.; Hussain, M.M. Genetic Variability and Population Structure of Pakistani Potato Genotypes Using Retrotransposon-Based Markers. *Agriculture* **2023**, *13*, 185. [CrossRef]
6. Kadluczka, D.; Grzebelus, E. Comparative Fruit Morphology and Anatomy of Wild Relatives of Carrot (*Daucus*, Apiaceae). *Agriculture* **2022**, *12*, 2104. [CrossRef]
7. Samyuktha, S.M.; Malarvizhi, D.; Mariyammal, I.; Karthikeyan, A.; Seram, D.; Dhasarathan, M.; Juliet Hepziba, S.; Sheela, V.; Thanga Hemavathy, A.; Kavithamani, D. The Hunt for Mungbean (*Vigna radiata* (L.) Wilczek) Genotypes and Breeding Lines Resistance to South Indian Bruchid Strain. *Agriculture* **2022**, *12*, 1050. [CrossRef]
8. Noweiska, A.; Bobrowska, R.; Kwiatek, M.T. Structural Polymorphisms of Chromosome 3Am Containing *Lr63* Leaf Rust Resistance Loci Reflect the Geographical Distribution of *Triticum monococcum* L. and Related Diploid Wheats. *Agriculture* **2022**, *12*, 966. [CrossRef]
9. Ma, Q.; Wang, J.; Cheng, L.; Li, Y.; Zhang, Q.; Li, H.; Han, Y.; Zhen, X.; Zhang, B. The Potential Function of *SiLOX4* on Millet Discoloration during Storage in Foxtail Millet. *Agriculture* **2022**, *12*, 1283. [CrossRef]
10. Thiam, E.H.; Jellen, E.N.; Jackson, E.W.; Nelson, M.; Rogers, W.; El Mouttaqi, A.; Benlhabib, O. Productivity and Stability Evaluation of 12 Selected *Avena magna* ssp. domestica Lines Based on Multi-Location Experiments during Three Cropping Seasons in Morocco. *Agriculture* **2023**, *13*, 1486. [CrossRef]
11. Sowa, S.; Mohler, V.; Paczos-Grzęda, E. Searching for Novel Oat Crown Rust Resistance in Diploid Oat *Avena strigosa* Schreb. Reveals the Complexity and Heterogeneity of the Analyzed Genebank Accessions. *Agriculture* **2023**, *13*, 296. [CrossRef]
12. Sobiech, A.; Tomkowiak, A.; Bocianowski, J.; Nowak, B.; Weigt, D.; Kurasiak-Popowska, D.; Kwiatek, M.; Mikołajczyk, S.; Niemann, J.; Szewczyk, K. Application Marker-Assisted Selection (MAS) and Multiplex PCR Reactions in Resistance Breeding of Maize (*Zea mays* L.). *Agriculture* **2022**, *12*, 1412. [CrossRef]
13. Wasuwatthanakool, W.; Harakotr, B.; Jirakiattikul, Y.; Lomthaisong, K.; Suriharn, K. Combining Ability and Testcross Performance for Carotenoid Content of S2 Super Sweet Corn Lines Derived from Temperate Germplasm. *Agriculture* **2022**, *12*, 1561. [CrossRef]
14. Łopatyńska, A.; Wolko, J.; Bocianowski, J.; Cyplik, A.; Gacek, K. Statistical Multivariate Methods for the Selection of High-Yielding Rapeseed Lines with Varied Seed Coat Color. *Agriculture* **2023**, *13*, 992. [CrossRef]
15. Mohler, V.; Paczos-Grzędarz, E.; Sowa, S. Loving the Alien: The Contribution of the Wild in Securing the Breeding of Cultivated Hexaploid Wheat and Oats. *Agriculture* **2023**, *13*, 2060. [CrossRef]
16. Braga, M.; Araújo, S.D.S.; Sales, H.; Pontes, R.; Nunes, J. Portuguese *Castanea sativa* Genetic Resources: Characterization, Productive Challenges and Breeding Efforts. *Agriculture* **2023**, *13*, 1629. [CrossRef]
17. Czubacka, A. The Use of the Polish Germplasm Collection of *Nicotiana tabacum* in Research and Tobacco Breeding for Disease Resistance. *Agriculture* **2022**, *12*, 1994. [CrossRef]