



Barley Genetic Resources: Advancing Conservation and Applications for Breeding

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1. Introduction

Barley (*Hordeum vulgare* L.) is one of the most important cereal crops in the world. It constitutes a staple food in several world regions due to its adaptation to high altitudes, drought, and soil salinity. Barley grains are used as livestock feed, malt, and foods, including roasted grains as a coffee substitute. In recent years, there has been a growing interest in barley for food because of recent research confirming its health benefits in human diets [1,2].

Barley is one of the oldest cereal crops and is widely grown across the world. The available evidence suggests that barley was first domesticated around 10,000 to 12,000 years ago in the Fertile Crescent. The genetic uniformity of barley modern cultivars is causing greater vulnerability to the negative effects of climate change [1,3,4]. Gene banks harbor a large "green treasure" of plant genetic resources (PGRs). More than 400,000 barley accessions are stored in 47 barley collections with more than 500 accessions and 25 smaller collections worldwide [4,5]. Currently, more and more breeding strategies are focusing on identifying novel sources of genetic basis of their initial plant material, barley breeding programs. By broadening the genetic basis of their initial plant material, barley breeders are continuing to make gains in terms of the productivity and quality of new cultivars, while at the same time they are efficiently responding to climate change [1,6].

The growing world population requires a constant increase in agricultural production. A changing climate is forcing plant breeders to develop plant cultivars with effective and durable resistance to biotic and abiotic stresses. These breeding activities can be supported by the broader exploitation of PGRs [7,8]. New Genomic Techniques (NGTs) are increasingly being used to characterize PGRs for breeding purposes. In addition, highthroughput technologies are being developed to enable extensive omics dataset analyses for genomics and phenomics. These technologies significantly advance plant research and provide information about existing biodiversity. This research is crucial to enable further plant genetic improvement concerning tolerance and resistance to biotic and abiotic stresses [9–14]. However, activities related to the conservation and characterization of PGRs in gene banks are costly and often have long-term returns. Therefore, there is an urgent need to coordinate efforts concerning the efficient utilization of available resources in plant breeding programs. Pre-breeding research activities are a very important part of this effort. They link gene bank activities with the effective use of PGRs by breeders. Pre-breeding programs are especially important for the characterization of crop wild relatives (CWRs), making them able to address major breeding aims, e.g., resistance to stresses [12–19].

The present Special Issue focuses on "Barley Genetic Resources: Advancing Conservation and Applications for Breeding". The selection of eight papers covers a wide range of research topics divided into three sections: (1) General characteristics of barley genetic resources for breeding to improve important agronomic traits (contributions 1, 2, and 3). (2) Barley genetic resources for breeding to improve disease resistance (contributions 4, 5, and 6). (3) The NGTs and PGR for breeding climate-change-resilient barley (contributions 7 and 8). These interesting papers present data on barley germplasm characterization, which



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Copyright: © 2023 by the author. Licensee MDPI, Basel, Switzerland. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (https:// creativecommons.org/licenses/by/ 4.0/). can be used by scientists and breeders. The final aim of the presented papers in this SI is to develop high-yielding barley cultivars with effective and durable resistance to biotic and abiotic stresses caused by changing climate conditions. These cultivars will provide farmers with stable and high income, making their farms resilient to more unpredictable weather conditions caused by climate change. In the next paragraphs, I briefly describe the papers in our SI; my purpose of this Editorial is not to elaborate on each of the texts but rather to encourage the reader to explore them.

2. General Characteristics of Barley Genetic Resources for Breeding to Improve Important Agronomic Traits

Three papers are grouped in this section that deal with the characterization of agronomic traits of barley genetic resources. The research conducted by Czembor and Czembor (contribution 1) described a genome-wide association study (GWAS) of agronomic traits in 431 European spring barley accessions, including landraces and old cultivars. These accessions originated from the Polish gene bank (National Centre for Plant Genetic Resources: NCPGR (KCRZG) at IHAR-PIB Radzików, Poland). The investigated accessions were classified into three groups to compare them in terms of phenological and other significant agronomical traits: group A (206 accessions) represented old cultivars cultivated prior to 1985, group B (178 accessions) represented modern cultivars cultivated after 1985, and group C (37 accessions) represented Polish landraces, i.e., traditional cultivars that had no breeding methods applied to them. All of them were phenotypically evaluated across 2 years under field conditions and genotypically evaluated using DarTseq to gain insight into the genetic architecture of phenology, biomass, yield components, and seed yield traits. In total, 16 traits of barley were analyzed to indicate marker-trait associations (MTAs). Overall, the genome-wide association study (GWAS) analysis identified 143 MTAs associated with these traits. This well-characterized barley collection and identified MTA markers will be used to create a Polish Genebank platform and will serve as a valuable resource for precise breeding programs. The presented research was conducted to develop and implement a national management system for crop plant genetic resources as part of the AGROBANK project at the Polish gene bank (NCPGR) (https://agrobank.cdr.gov.pl/index.php (accessed on 29 October 2021)). The authors discuss the importance of making phenotypic and genotypic data available for researchers and breeders through the bioinformatic platform (http://dane.agrobank.pcss.pl/jbrowse/ (accessed on 29 October 2021)).

The next article by Brbaklić et al. (contribution 2) describes the genetic diversity and population structure of a Serbian barley (*Hordeum vulgare* L.) collection during a 40-year-long breeding period using microsatellites and pedigree and phenotypic data. The set of 90 barley genotypes was phenotyped during three growing seasons and genotyped with 338 polymorphic alleles. The indicators of genetic diversity showed differentiation changes throughout the breeding periods. The population structure divided the breeding material into three distinctive groups. The principal coordinate analysis grouped the genotypes according to their growth habits and row types. An analysis of phenotypic variance (ANOVA) showed that almost all of the investigated traits varied significantly between row types, seasons, and breeding periods. The authors discuss a positive effect on yield progress during the 40-year-long breeding period. The investigated breeding material revealed a considerable diversity level based on microsatellite and phenotypic data without a tendency for genetic erosion throughout the breeding history. The authors concluded that plant material constitutes a great gene pool suitable for further barley improvement.

In the last article in this section, Dziurdziak et al. (contribution 3) present a multifaceted analysis of 64 barley landraces collected during gene bank expeditions in Poland at the end of the 20th century (72% were collected in the 1970s and 28% were collected in the 1980s). The authors used historical data from a standard field evaluation of agronomic traits, genetic data obtained from inter simple sequence repeat (ISSR) analysis, and grain morphometric data. The results presented in this paper confirm that the extensive genetic diversity in crop landraces deposited in gene banks can be an important part of future breeding programs. However, a prerequisite for this is a wide range of data available on its characteristics that are well analyzed, summarized, and reliable. The authors suggest that further studies are needed that use high-throughput genotyping, next-generation sequencing techniques applied to single-grain individuals, laboratory resistance tests, and qualitative analyses of grain chemistry.

3. Barley Genetic Resources for Breeding to Improve Disease Resistance

In this section, three papers are grouped that describe barley gene bank accessions as a source of resistance for breeding disease-resistant cultivars. The paper by Thauvin et al. (contribution 4) describes a GWAS for resistance to rhynchosporium in a diverse collection of spring barley germplasm. The 312 spring barley accessions were tested in four different locations over 3 years. High-density genotypes found via exome capture and RNA-seq were used to conduct high-resolution association mapping. Seven quantitative trait loci (QTL) were detected, including one in the Rrs2 region, amongst five containing known resistances. The frequencies and distributions of these novel and known QTL were superimposed onto the regional origin of the landrace genotypes comprising the genome-wide association study (GWAS) panel. The authors discuss the value of genetic resources as a source of diverse genetically controlled resistance to rhynchosporium. The detected QTL, along with their linked genetic markers, could be exploited either directly for breeding purposes or for candidate gene identification in future studies. The authors express an opinion that further work is still needed to clone the resistance genes underpinning the detected QTL. However, the described results provide insight into the location of rhynchosporium-resistantce QTL in a spring barley collection representing global diversity. The practical value of this paper is that the obtained results further expand the available resources for breeding varieties, which are required for sustainable barley production.

The next paper in this section is by Czembor et al. (contribution 5). It presents a GWAS for powdery mildew and rust adult plant resistances in European spring barley from the Polish gene bank. The presented research was conducted to develop and implement a national management system for crop plant genetic resources as part of the AGROBANK project at the Polish Genebank (NCPGR) (https://agrobank.cdr.gov.pl/index.php (accessed on 29 October 2021)). The 431 European barley accessions were phenotypically evaluated over 2 years (2018–2019) under field conditions, scoring APR to powdery mildew (PM), barley brown rust (BBR), and stem rust (SR), and genotypically evaluated using DArTseq. The accessions were grouped into sub-collections according to cultivation period and European country of origin or European region. A GWAS was conducted for PM, BBR, and SR and scored at the heading (HA) and milky-waxy (MW) seed stages in 2019, and maximum scores across all replicates were obtained from 2018 to 2019. Disease severity was sufficient to differentiate the collection according to cultivation time and country of origin and to determine SNPs. The GWAS analysis identified 73 marker-trait associations (MTAs) with these traits. The present study provides new knowledge about the genomic regions associated with barley APR to PM, BBR, and SR. The obtained results confirm that the landraces and old cultivars may offer added value for the preservation and use of barley biodiversity. The authors discuss the importance of incorporating the phenotypic and genotypic data of crop plants of agronomic importance in Polish agriculture into a Polish Gene Bank platform (http://dane.agrobank.pcss.pl/jbrowse/ (accessed on 29 October 2021)) to aid precise breeding programs.

In the paper by Mehnaz et al. (contribution 6), the authors describe the discovery, characterization, and postulation of the known *Rph* genes (resistance to *Puccinia hordei*) and the identification of novel sources of ASR (all-stage resistance) and APR (adult plant resistance) to *P. hordei*. A core set of 315 barley lines from Central Asia and the Middle East were rust-tested as seedlings for their response to eight Australian pathotypes of *P. hordei* and genotyped with molecular markers linked to the known characterized ASR and APR genes. The authors systematically conducted integrated seedling greenhouse tests and field evaluations and applied linked molecular markers. This resulted in the

characterization of resistance to *P. hordei* in a large set of lines. From a practical point of view, the identification of eight known ASR genes (*Rph1*, *Rph2*, *Rph3*, *Rph9.am*, *Rph12*, *Rph15*, *Rph19*, and *Rph25*) and three APR genes (*Rph20*, *Rph23*, and *Rph24*) that confer resistance to *P. hordei* is very interesting and important. Significantly, the authors also found several sources of resistance that appeared to potentially be novel. In the discussion, it was recommended that further characterization, genetic studies, and mapping should be conducted on lines carrying distinct novel resistance sources. This study is interesting because of the effective utilization of predictive molecular markers for APR genes *Rph20*, *Rph23*, and *Rph24* and ASR genes *Rph7* and *Rph15* and their utility for genotyping large germplasm collections and ultimately marker-assisted selection. This interesting study represents a useful resource of information about leaf-rust-resistant germplasm for breeders to further diversify the genetic basis of leaf rust resistance in barley.

4. The NGTs and PGR for Breeding Climate-Change-Resilient Barley

The possibility and problems of the genetic transformation of barley are discussed in the paper by Xu et al. (contribution 7). The comprehensive analysis in this paper provides insights into the molecular mechanisms of callus induction in barley. This may be helpful for improving the genetic transformation of barley. To reveal the key genes or factors controlling the callus induction and plantlet regeneration in barley, the authors compared the transcriptomic profiles of immature embryos of Golden Promise (GP) and ZU9, which differed dramatically in the efficiency of the genetic transformation. A total of 5386 up-regulated and 6257 down-regulated DEGs were identified in GP, respectively. From them, several genes identified exclusively in GP were selected and highlighted for further investigation. The authors discuss the involvement of these genes in protein metabolism, energy metabolism, stress response, detoxification, and ubiquitin-proteasome. Furthermore, they propose a regulatory network of DEGs related to the biosynthesis, response, and transport of auxin and cytokinin in response to in vitro culture of the two barley calli. This paper is very interesting and important because it provides valuable information on callus induction in barley that can improve the genetic transformation of barley, as well as other cereal crops.

The last paper presented in this SI by McAllister et al. (contribution 8) highlights a SHINE1/WAX INDUCER1 transcription factor that controls cuticular wax in barley. This issue is very interesting because cuticular wax is important for the hydrophobic barrier, which is the cuticle that protects plants from dehydration and generally from biotic and abiotic stresses. The authors exploited extensive allelic populations, near-isogenic lines, and powerful genotyping platforms to identify variation in the HvWAX INDUCER1 (HvWIN1) gene, encoding a SHINE transcription factor as underlying cer-x. The authors describe how they discovered that variation in HvWIN1 underlies alleles at the Cer-X locus, which are responsible for changes in cuticular integrity and cuticular waxes in barley. The authors stress the importance of a synergistic combination of access to germplasm resources and the development of advanced genotyping platforms in conducting their research. They also discuss how knowledge about the regulatory network controlling cuticular features in cultivars and wild species may become increasingly important for the development of more climate-resilient barley and cereal varieties.

5. Conclusions

In summary, this Special Issue brought together the recent findings and the literature on the characterization of barley germplasm. This information can be used by scientists and breeders investigating barley for resistance to biotic and abiotic stresses caused by changing climate conditions. This Special Issue provides valuable and novel knowledge about NGTs and the potential role of these methods in research and breeding efforts to obtain new cultivars with stable and high yields. The research presented in this Special Issue confirms that gene banks harbor a large "green treasure" of PGRs and that there is an urgent need to use them effectively in barley improvement to provide food for a growing human population.

The published articles in the current Special Issue do not constitute a fully comprehensive collection of this interdisciplinary research topic. This Issue lacks highly important topics such as the characterization of CWR and improvement in grain quality both for food and malt production. However, I hope that it provides a stimulus for action to generate more research in this very important field. With the support of the Editorial office, a new Special Issue was launched focusing on the same research theme, entitled "Barley Genetic Resources: Advancing Conservation and Applications for Breeding II". It is a continuation of the effort in the field, and we sincerely invite researchers to contribute to this new collection.

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List of Contributions

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