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Editorial

The Genetics, Genomics, and Breeding of Cereals and Grain Legumes: Traits and Technologies for Future Food Security

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1. Global Population and Food Security

According to the United Nations (UN), the world's population is expected to grow by more than one billion people over the next 15 years. Projections indicate that the world's population will reach 8.5 billion by 2030 and 9.7 billion by 2050 [1]. As the population grows, so will the demand for food and feed. By 2050, we will need 60–100% more food and feed than in 2010 [2]. At the same time, the High-Level Expert Forum on "How to Feed the World 2050" highlighted that the daily energy availability could reach 3050 kcal per person by 2050, while in developing countries it will reach 2970 kcal, up from 2770 kcal (2003/05), indicating an increase in calorie demand [1]. Future trends in food demand indicators have also confirmed that per capita food consumption will increase by an estimated amount of 41–51% [3]. In addition, since agriculture is dependent on fossil fuels, the uncertainty of fossil fuel prices and trends exacerbates the situation and thus affects food prices. According to the April 2023 edition of the Agricultural Market Information System market monitor, grain and oilseed prices have reduced over the past 10 months to levels seen before the Russia–Ukraine conflict (Figure 1A). However, this is a constantly evolving situation, as international deals for the import and export of food commodities are being cancelled or modified. The yearly Food and Agriculture Organization of the UN (FAO) Food Price Index showed a decreasing trend from 2011 to 2020, and then an increasing trend thereafter. The same was observed for the cereals and sugar price index (Figure 1B). These changes reflect the outlook for global food supply in the coming year(s). The FAO's report on the crop prospects and food situation (as of March 2023) indicates that 45 countries are in need of foreign food aid [4]. The impact of food cost and supply is evident in recent reports. For example, in 2021 alone, hunger affected 278, 425, and 56.5 million people in Africa, Asia, and Latin America and the Caribbean, respectively, representing 20.2, 9.1, and 8.6% of the respective regions' population. Globally, ~29.3% of the population (2.3 billion people) experienced moderate-to-severe food insecurity. According to the FAO's report "The State of Food Security and Nutrition in the World 2022", the global food security prevalence has increased to 9.3, 10.9, and 11.7 for 2019, 2020, and 2021, respectively. Projections have shown that, by 2030, 670 million people will still be undernourished, representing ~8% of the population. All these reports clearly indicate that the world will need more food in the next 2.5 decades [5].

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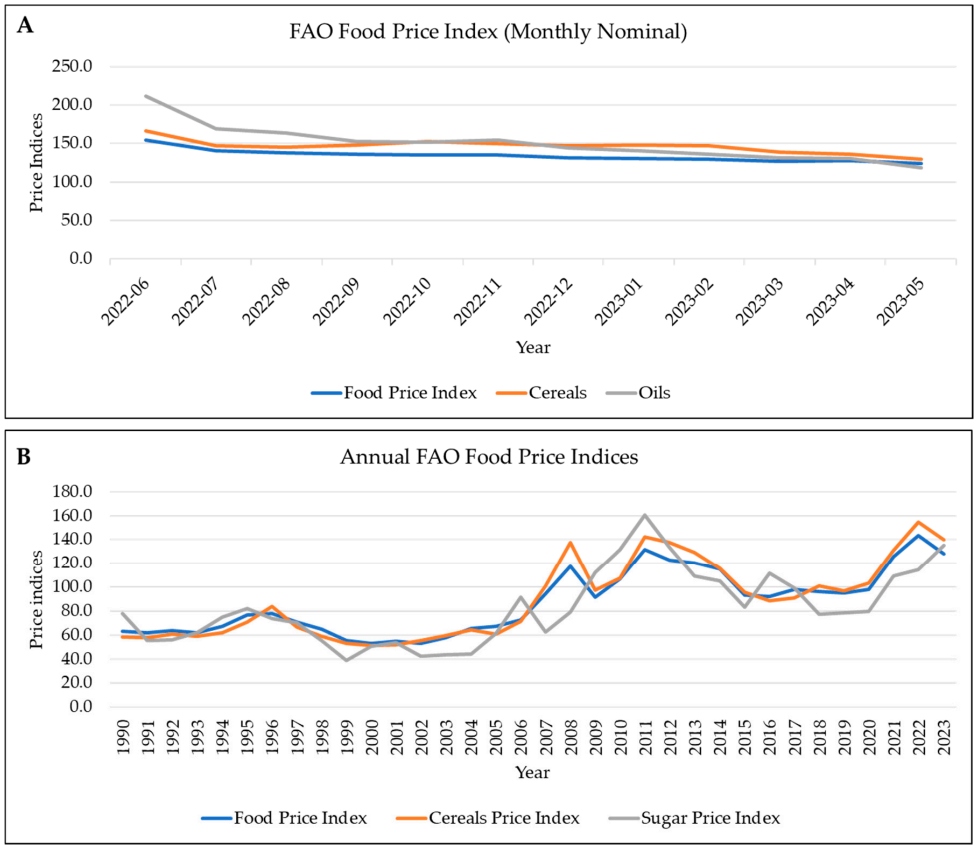


Figure 1. Food and Agriculture Organization food price indices. (**A**) Monthly food price index (June 2022 to May 2023). (**B**) Annual food, cereals, and sugar price indices. The food price index consists of an average of five commodity group price indices (meat, dairy, cereals, vegetable oils, and sugar) weighted with the average export shares of each of the groups for 12 months (in (**A**)) and 34 years (1990–2023) (in (**B**)). Each sub-index (cereals and sugar) is a weighted average of the price relatives of the commodities included in this group.

2. The Current Cereals and Legumes Situation

The major crops that feed the world are cereals and legumes, which covered ~1.3874 billion hectares (ha) in 2021 (Figure 2). Legumes (22,939 species) are members of the Fabaceae family that were domesticated in parallel with cereals. Major legumes, including chickpeas, lentils, soybeans, peanuts, faba beans, grass peas, and green peas, play an essential role in the human diet alongside cereals. While legumes provide protein, fiber, carbohydrates, minerals, and vitamins, cereals are important sources of lipids, carbohydrates, protein, minerals, and vitamins. Cereals are primarily members of the Gramineae family including wheat, rye, barley, oats, rice, millet, corn, sorghum, and triticale. Although legumes are a rich source of protein, the average global consumption of legumes is 21 g per day, which is comparable to meat consumption (112 g per person per day). However, legumes are an essential part of the traditional diets of most cultures, such as those in Asia [6]. In contrast to legumes, cereals, although lower in protein, are a major source of dietary protein in Mesoamerica and sub-Saharan Africa, West Africa, and Asia, including corn, millet, and rice (https://www.amis-outlook.org/; accessed on 31 July 2023). By 2050, the average global consumption of legumes may not increase significantly, but to feed the additional population, an estimated increase in production of 25% will be needed. In contrast, just to meet the calorie gap by 2050, an increase in global cereal production of 40% will be needed. Since cereals are also the main component of livestock feed, an increase in cereal production will lead to an increase in meat production; by 2050, the projected meat production is 455 million tons. This is important because meat consumption is projected to increase as per capita incomes rise (they are predicted to be 1.8 times higher by 2050).

Thus, the required cereal production by 2050 will be much higher. By 2021, global cereal and legume production will be 3070.64 and 876.87 million tons, respectively. The observed yield increase from 1961 to 2021 (Figure 2) is mainly due to breeding and selection efforts over the past four to five decades, as well as an increase in global harvesting area (Figure 2). These yield increases are promising but are not sufficient to sustainably feed a growing population. For example, a 2013 study based on statistics from 1961 to 2008 found that doubling yields (of four major crops, i.e., corn, rice, wheat, and soybeans) would require a yield increase of ~2.4% per year [7]. To increase the crop yields, either the yield gap should be reduced or the existing yield potential should be increased. However, yield gaps still exist in major crops. For example, in the case of rice, it has been reported that the average yield gap in Southeast Asia is 48% of the yield potential [8]. In contrast, yield gaps of 1.1 to 3.5 Mg·ha^{-1} still exist in the United States [9]. Similarly, a recent study reported that the estimated existing genetic yield gap was 51% [10]. In general, the yield gap in wheat is estimated to be in the range of 25 to 50% [11]. A review published in 2020 reported that the global potential for wheat, maize, and rice was 7.7, 10.4, and 8.5 t/ha, while their actual yields were 4.1 (53.24%), 5.5 (52.88%), and 4.0 (47.05%) t/ha, respectively [12]. The yield gap in soybean has also been reported to be around 40–52% in different countries, e.g., Brazil (42%), southwestern Ethiopia (5–51%), China (52%), and the USA (40%) [13–16].

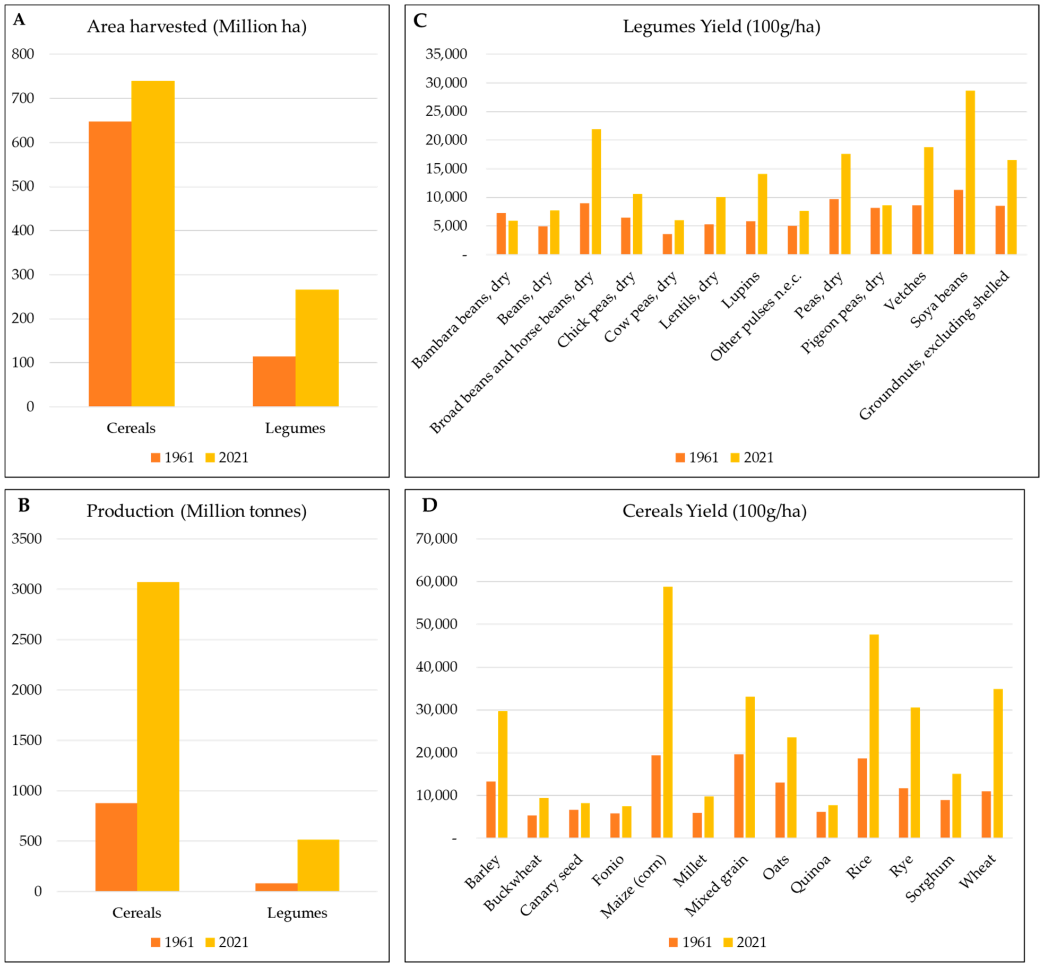


Figure 2. (**A**) Global total area and (**B**) production of cereals and legumes in 1961 and 2021. Yield of important (**C**) cereals and (**D**) legumes in 1961 and 2021. The cereal data in (**A**,**B**) includes barley, maize (corn), millet, rice, wheat, oats, rye, sorghum, triticale, canary seed, buckwheat, mixed grain, fonio, quinoa, and other cereals, whereas that of legumes (dry) in (**A**,**B**) include beans, broad beans, horse beans, vetches, chickpea, lentils, peas, lupins, cow peas, pigeon peas, Bambara beans, groundnuts, and soybeans. The data were accessed on 31 July 2023 from https://www.fao.org/faostat/.

3. The Way Forward in the Genetics, Genomics, and Breeding of Cereals and Grain Legumes

Reducing the yield gap in major crops is a challenge for researchers in genetics, genomics, and breeding. Sustainably feeding the world's population by 2050 requires strategies to close the yield gap in priority crops, i.e., legumes and cereals. The current yield potential of major crops is the result of multi-level efforts in classical breeding, advanced agronomic practices, and genetic engineering. However, as discussed above, yield increases due to these developments are declining or stagnating [17]. Technological advances in agronomy, breeding, and genomics offer opportunities to increase the efficiency of agriculture in general and crops in particular. To improve the productivity of crop plants, researchers have identified several traits that should be targeted for manipulation. The yield-determining traits could be grouped according to growth and development and interactions with the environment and other organisms. Traits related to growth and development include fertility, inflorescence architecture, biomass (shoot/root), photosynthesis, light-harvesting capacity, CO_2 fixation potential (partitioning and allocation), stomatal movement and density, senescence timing, root architecture, growth dynamics, and nutrient uptake, transport, and utilization [18,19]. Traits related to interaction with the environment and other organisms include root architecture, floral morphology, leaf pubescence, water potential in various plant organs, cuticular wax, symbiotic ability, secondary metabolite content, lysine and proline content, phytohormone content, nitrogen fixation, and many other physiological, morphological, and metabolism-driven traits related to plant–pathogen interactions (Figure 3) [20–22]. In addition, the literature also suggests the introduction of synthetic traits, such as seeding, attracting beneficial organisms, activating stress-specific responses in plants, and regulating target metabolites. With the knowledge of these target traits, the next major step is to find exploitable variations in these traits and understand the techniques to be used. The variation in these traits can be found naturally in wild relatives [23], spontaneous mutations, transposons, aneuploidy, and translocations. Variation can also be induced via artificial polyploidy, cross-breeding, and induced mutations with chemicals and ionization [24]. Genetic modification techniques can also be used to introduce mutations. In plant breeding, the use of classical breeding is complemented by modern techniques, i.e., genetic engineering, genomics, marker-assisted selection, and artificial intelligence. The use of phenomics, new breeding techniques, CRISPR-Cas, genetic engineering, genomics, bioinformatics, and artificial intelligence allows scientists to manipulate these traits and improve plant crop (Figure 1).

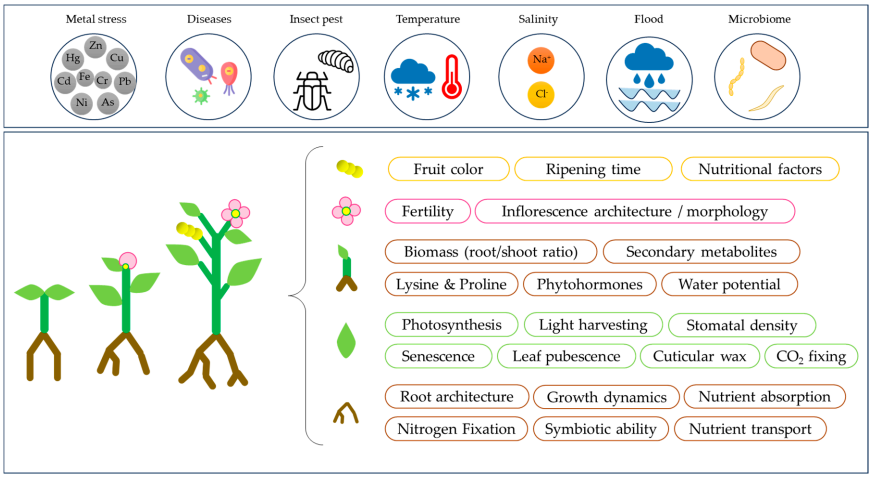


Figure 3. Stress and traits to be considered for improving yield gap through the use of breeding, genetic, and genomic approaches in cereals and grain legumes. The top panel shows the stresses (and microbiome). The bottom panel shows a plant and traits associated with each tissue type. The figure was prepared in Microsoft Power Point 2019 (Professional) ® (www.microsoft.com). The icons in top panel were downloaded from https://www.flaticon.com/ (accessed on 15 July 2023).

4. Special Issue Overview

Roy et al. [25] used a comparative transcriptome sequencing approach to study the different alternative splicing isoforms in soybean lines that differ in plant height. Their study highlights the usefulness of two approaches to understanding the role of alternative splicing in plant height. The first is the use of wild relatives and the second is next-generation sequencing technologies (PacBio RSII platform). The authors successfully detected 166,171 splice junctions and reported that 19% of the isoforms were novel. The study concluded that the isoforms were prevalent in annotated genes, especially those related to plant growth, hormone biosynthesis, and defense responses.

Basita et al. [26] performed association mapping for the quantitative trait loci (QTL) associated with five antioxidant traits in rice. For this work, they used both white and colored rice varieties and identified potential landraces with multiple antioxidant compounds from this panel. They detected 14 marker-trait associations as well as validated QTLs associated with anthocyanins, 2,2′-azino-bis-3-ethylbenzthiazoline-6-sulfonic acid. Interestingly, several QTLs associated with superoxide dismutase, flavonoid content, γ-oryzanol, and 2,2′-azino-bis-3-ethylbenzthiazoline-6-sulfonic acid activity were reported on chromosomes 11 and 12. This study highlights the combination of biochemical and molecular marker techniques for the identification of QTLs associated with rice traits that are linked to multiple health benefits.

Viana et al. [27] evaluated the effectiveness of a pedigree-based best linear prediction method for genetic evaluation of inbred progeny. They used eight years of data from more than 30,000 plants from multiple generations, progeny trails, and in silico populations. The authors were able to successfully predict the additive values for expansion volume. This study is important from the point of view that the adapted method proved to be superior when compared to phenotypic mass selection and can therefore be used for the genetic evaluation of inbred progeny.

Afzal et al. [28] used the genomic and proteomic data of *Vigna radiata* available from public databases and combined it with the wet lab experiments to identify the members of the two-component system gene family. This study highlights that the availability of genomic and transcriptomic data in public databases can significantly contribute to the understanding of gene structure, conserved sequence features (domains and motifs), evolution, chromosomal distribution, and the type of regulatory elements present in the promoter regions of genes. Using public genomic resources, the authors were able to identify 54 two-component system genes (and their subclasses) and determine how they have evolved in legumes. In particular, the authors determined the expression patterns in response to drought stress and proposed candidate genes.

Zhang et al. [29] used the genotyping-by-sequencing approach to genotype 410 faba bean accessions and identified 38,111 high-quality single nucleotide polymorphisms (SNP). This study highlights that the advent of genome sequencing techniques has enabled scientists to identify a relatively higher number of SNP markers and use them to understand population structure and genetic diversity in crop plants. Genetic relationships between groups from neighboring regions or countries with similar ecological environments and geographic origins were closer and more frequently found within the same group, while genetic variation between individuals was the primary source of their total genetic variation.

Mukuze et al. [30] identified genomic regions in soybean associated with resistance to *Callosobruchus chinensis* (commonly known as bruchids). The interesting perspective used in this study is the six multi-locus models for genome-wide association study. The approaches used in this work enabled the authors to identify 14,469 SNPs and 13 quantitative trait nucleotides (QTNs). This study also recommended three QTNs associated with several bruchid resistance traits in soybean for marker-assisted selection. The identification of 27 candidate genes potentially associated with resistance mechanisms in soybean confirms that modern genomic tools are increasing the efficiency of genetic studies and enabling researchers to explore molecular mechanisms.

Tajibayev et al. [31] characterized 151 durum wheat cultivars and lines developed in a Kazakhstan-Siberia Spring Wheat Improvement Network using phenotypic and genotypic methods. They used a promising molecular marker technique, i.e., iPBS retrotransposon markers, to study the genetic diversity in the population. The authors report the identification of superior and diverse germplasm for marker-assisted selection.

In summary, this Special Issue brings together studies on cereals and grain legumes and presents different strategies for crop improvement for yield and biotic and abiotic stress tolerance. The editors are grateful to the participating research groups for submitting their work to this Special Issue and for highlighting the importance of using modern genetic and genomic techniques for crop improvement. The editors hope that these datasets and results will play an important role in the improvement of the studied crops.

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