Chapter

Introductory Chapter: Recent Advances in Grain Crops Research

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1. Introduction

Grain crops produce small, hard, dry seeds that may or may not have an attached hull used for human and/or animal consumption. Grain crops are mainly of two different types, i.e., *cereals* and *legumes*. Grain crops are energy sources containing carbohydrates, proteins, and fats. Besides being the energy providing macromolecules, grain crops also contain health-supporting compounds, including dietary fibers, antioxidants, vitamins, and minerals [1]. The relatively higher durability of grain crops due to their low moisture content upon maturity has made them well-suited to industrial agriculture as compared to other fleshy fruits and vegetables that have very low shelf life due to higher moisture content. It is these attributes of easy storage, measurements, and transportation that may well be the reasons for selection and domestication of the grain crops by our earliest ancestors. It is now widely accepted that the development of grain agriculture is one of the most important factors in permanent settlements of human ancestors and their divisions into different social classes in history [2]. Earliest evidence of plant domestication comes from the middle east where rye grains with domesticated traits have been recovered [3], whereas the first evidence of cereal crop domestication comes from 9000 BCE. Later on, continued domestication and the resultant shift from a *hunter-gatherer* society to a *settled agricultural* society continued for thousands of years mainly consisting of grain crops. However, this domestication was primarily based on intermittent trial and error driven by a crude knowledge of selection and choice. Later, the selection and use of grain crops research were based on more scientific knowledge.

Among the grain crops, cereal grains occupied the central position concerning production, consumption, and health benefits. Cereal crops belong to the grass family, which is also known as Poaceae. The whole cereal grain consists of bran, endosperm, and the germ. Bran is the outermost layer having higher amounts of ω-3 fatty acids, fibers, macro and micro minerals, and vitamins. The endosperm mainly contains starch, where the germ consists of water and fat soluble vitamins, magnesium, and phosphorous. It is believed that the consumption of cereal grains has been co-started with human civilization that became the major part of human diet with the passage of time. Among the cereal grains, wheat, maize, rice, millet, buckwheat, and sorghum are used as a staple food by the people from different localities of the developed and under-developed world. It is assumed that about half of the daily caloric requirement is fulfilled through the consumption of cereal grains. A diet rich in cereals can in fact provide us with starches, soluble and insoluble fibers, digestible carbohydrates, essential fatty acids, appreciable amounts of proteins, higher amounts of folate, iron, magnesium, copper, phosphorus, zinc, and phytochemicals. The phytochemicals with antioxidant properties can lower the blood cholesterol levels and thus help in controlling heart diseases. In short, the whole cereal grain consists of a whole range of primary and secondary metabolites that not only provides energy, but also health supporting substances [4]. The phytochemicals or secondary metabolites of whole cereal grains are also known to be associated with significant health benefits. The phytochemicals that are rich in cereal grains include phenolics, lignans, phytic acid, phytosterols, saponin, squalene, tocotrienols, phytosterol, and oryzanol. Some of these phytochemicals can act as antioxidants and lower the blood cholesterol level, thus preventing the cardiovascular diseases and reduces the risk of cancer. On the other hand, industrial revolution led to the milling of the cereal grains that intensively involve the removal of the bran and germ. Albeit milling has improved the sensory attributes of the finished product, but the milled products lack important health beneficiary components, such as dietary fibers, phenolics, minerals, and vitamins [4]. Carbohydrates are the main class of primary metabolites that attribute the health benefits of cereal grains. It is known for the years that insoluble polysaccharides/fibers can relax constipation, whereas the soluble polysaccharides/mixed-link β-glucans can regulate the blood cholesterol level. The soluble and non-soluble polysaccharides that are present naturally in cereal grains have positive health implications in humans. These polysaccharides have the ability to hold water, give bulk to the stool, and can be broken down into short chain fatty acids. Such activities may help to resist the degenerative diseases, i.e., coronary heart diseases and cancer [5].

Another important group of grain crops include legumes that belong to the Leguminosae, which is also named as Fabaceae. Legumes are recognized as pulses after decortication or dehulling of seeds. Legumes are grown on a large area worldwide. The important grain legumes include chickpea, cowpea, lentil, green peas, etc. Pulses are cultivated in tropical and temperate regions around the globe, mainly in the South-East Asia. Food legumes are considered to be healthy plant-based food and are a good source of vitamins (B-complex), minerals (macro and microminerals), and dietary fiber [6]. Chickpea seed has high protein and carbohydrate with small amounts of fiber, oil, vitamins, and minerals. The digestibility of pulses proteins varies from 70–80%. Pulses have a hypocholesteremic effect, and the seeds are eaten fresh as green vegetables or boiled with condiments. The flour of some pulses, such as chickpea is used in food preparation as a dressing for vegetables (e.g., bringle and potato) and meat (e.g., fish and chicken). The flour of chickpea is utilized for making bread with pepper and salt.

Pulses are good sources of protein that add to the nutritional importance of cereal-based diets. Pulse proteins are abundant in amino acid, arginine and lysine, but they have lower amounts of cysteine and methionine, which are known as sulfur containing amino acids. The other limiting essential amino acids include the cyclic amino acid tryptophan, valine, and threonine. From the nutritional standpoint, it is necessary to provide the body with an appropriate amount of essential amino acids. To meet the human dietary needs the four most important essential amino acids of protein should be present in the ratio of: four parts of lysine, three parts of methionine, two parts of threonine, and one part of tryptophan. If any one of these amino acids is so low as to affect the above ratio, it becomes the limiting factor in determining the nutritive value of the protein. The content of the proteins in pulses is almost double as compared to the cereals. Moreover, pulses taken with cereals in diet can fulfill the basic requirements for protein and thus enhance the nutritional importance of cereal-based diets [7].

Pulses are known to be good sources of macro and macro-minerals, mainly calcium (Ca), magnesium (Mg), potassium (K), phosphorus (P), zinc (Zn), and iron (Fe). These minerals are important for the body because of their role in physiological as well as biochemical processes of the cells and tissues. Mg is an integral part of metabolic enzymes, K helps in the regulation of energy and metabolism, P gives strength to the bone and is involved in the formation of high-energy compounds, i.e., AMP, ADP, and ATP. Likewise, Zn also acts as a cofactor of certain enzymes, and Fe is a part of hemoglobin and myoglobin. The ionized minerals can help in blood coagulation and keep the membrane permeability intact. Besides, sodium (Na) and K are vital for the regulation of an acid-base balance and osmotic pressure of the cells. Legumes also contain antinutrients, i.e., phytate, which is rich in P. Phytic acid (Inositol hexaphosphoric acid) is abundant in legumes that can inhibit the absorption of Zn and other essential elements by the small intestine of humans and monogastric animals, thus making it unavailable to the body. Phytic acid forms complexes with the metal ions (Cu^{+2}, Ca^{+2}, Zn^{+2}, and Fe^{+3}), thus excreting them out of the body. The excretion of such essential elements may lead to various deficiency diseases. Phytate may also limit the absorption of vitamins and proteins, which can decrease the nutritional value of the legumes [8].

Furthermore, several grain crops are also required as a source of animal feed. Recent interest in wheat research is supported by the directives following the meeting of the G20 ministries of agriculture, of the wheat initiative [9] to profess the coordination of international research on wheat to fulfill global wheat production demand. Global population is predicted to increase up to over 9 billion by 2050 [10], which means that the demand will increase by 60% as compared to that in 2010. In order to meet this end, global wheat production must increase by 1.6% annually, compared to the current 1% global increase per year (2001–2010) – reviewed by Giraldo et al. [11]. Other initiatives such as the International Barley Hub [12] started to support the increasing demand of grain crops. In this chapter, we discuss the recent advances made in grain crops research, related to few important traits.

Seed shattering is a character that has probably played one of the most important roles in domestication of grain crops. Grain crop varieties or cultivars with less auto-shattering of the seeds, siliques, seed pods, and spikelets have been more desirable with regards to farming [13]. Evolutionary studies show that the loss of seeds shattering was a character independently acquired by monocots and dicots via "convergent phenotypic evolution" producing low dehiscent and/or indehiscent crop species. At tissue level, seed or seed pod shattering level is governed by histological modifications that involve the development of an abscission layer at the point where the seeds or spikelets/pods are attached with the plant [14–17]. Pourkheirandish et al. [18] demonstrated that a lower thickness of both primary and secondary cell walls of the abscission or separation layer results in higher seeds shattering in barley. Because of the importance that seed shattering carries in the adoption of grain crops for food and feed, it has been studied in detail in various grain crops at genetic level. A plethora of genes have been shown to regulate seed shattering in rice [19–22], barley [18], and legume crops such as soybean [23, 24], cow pea [25], common beans [26, 27], and medicago [28]. These genes encode various proteins such as the Shatterproof protein, NAC, Myc, and bHLH transcription factors, ALCATRAZ and the BEL-1-type homeobox SH5. Careful selection of crop varieties and cultivars by the farmers and scientific research have settled the seed shattering issue and most of the grain crop cultivars grown these days are indehiscent.

Other important aspects of research on grain crops include factors responsible for quantity and quality of the produce. Such factors have been studied by scientists throughout the world and in almost all grain crops. Most of these studies describe both negative or positive effects of different interventions and treatments. Research targeted toward the understanding of genetic basis of crop improvement is often conducted under restricted or unfavorable environmental conditions. Such projects include research on uptake and use efficiency of various macro and micro nutrients [29, 30]. Chen et al. [31] identified at least 10 genes related to nitrogen metabolism in different cultivars of barley. Most interestingly, these included the 2nd isoform of nitrate reductase enzyme (HvNIA2), which is responsible for catalyzing the 1st reaction in nitrate assimilation, i.e., the conversion of nitrate to nitrite and is also involved in the production of nitric oxide (NO) in plants [32]. Other genes induced under low nitrogen stress included those encoding enzymes such as the chloroplastic glutamine synthetase (HvGS2), ferredoxin dependent glutamate synthase (HvGLU2), and asparagine synthetase (HvASN1). Interestingly, the expression of these genes was found to be strictly regulated by nitrogen stress and in a tissue specific manner [31].

The elucidation of the genetic role played by the members of the plant nitrate transporters (NRT) or peptide transporters (PTR) is also of particular importance in the transportation of various nutrients from the soil to plants and ultimately crop production. Lin et al. [33] in the year 2000 cloned and functionally characterized NRT1 from rice. The NRT is constitutively expressed in the epidermis and root hairs of the roots. The importance of this gene in nitrate transport can be determined by the fact that even slight variations in the sequence of this gene results in nitrate-use divergence in different rice subspecies [34]. This is associated with the higher nitrate-absorption activity of Indica rice as compared to Japonica rice. As the Japonica rice plants expressing the Indica NRT1.1B allele showed significantly higher grain yield and nitrogen-use efficiency compared to Japonica plants that did not express the Indica allele [34]. The role of plant NRT and their functional applications has been reviewed by Fan et al. [35]. Plant NRT/PTR gene family has been renamed as NPF family [36] and contains a large number of genes that can be subdivided into at about 10 sub-families. The family has 93 known genes in rice [37]. NPF members not only transport nitrate but a wide range of other substrates including peptides [38], phytohormones such as auxin [39], abscisic acid [40], Jasmonates [41], and Gibberellins [42] further indicating the importance of these genes in plant physiology and crop production. Several members of the family have remained a focus of different scientific studies, especially in rice, describing significant increase in the overall yield, early maturity and the composition of soil microbiota [43–45] and should be a topic of future research in grain crops.

After decades of research in different living organisms, it has now become clear that practical utilization of recent advances in modern biotechnology is inevitable. Plant science has probably benefited the most from biotechnological advancements in terms of modifications at genome and proteome levels. With the advent of different gene editing techniques such as the CRISPR/Cas technology, any type of genetic modification has become easy and quick. A simple search on the web of science using "CRISPR rice" as keywords turns up 96 different research papers published from 2013 to 2020. Similarly, a search for "CRISPR wheat" shows up 25 research papers between 2017 and 2019, whereas searching for "CRISPR maize" shows up 17 research papers. This indicates the rapid adoption of newly developed techniques by plant scientists for genetic modifications in these plants. The use CRISPR/Cas technology for genetic modifications in grain crops has been described in the chapter by Hussain et al. [46] available as *online first* (https://www.intechopen.com/online-first/crispr-cas9-mediated-gene-editing-in-grain-crops). In this scenario, the availability of genome sequences and other genetic resources of grain crops such as rice (Rice Genome Annotation Project http://rice.plantbiology.msu.edu/), wheat (International Wheat Genome Sequencing Consortium https://www.wheatgenome.

org/), maize (Maize Genetics and Genomics Database https://www.maizegdb.org/), soybean (Integrating Genetics and Genomics to Advance Soybean Research: SoyBase https://www.soybase.org/), and other legumes (Legume Information system https://www.legumeinfo.org/) has further facilitated scientific research on grain crops at the cell or genome level. Further scientometric, informetric, and bibliometric studies are required to establish a detailed account for the impact of recent advances in grain crops research.

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References

[1] Belobrajdic DP, AR B. The potential role of phytochemicals in wholegrain cereals for the prevention of type-2 diabetes. Nutrition Journal. 2013;**12**(1):62

[2] Wessel TJA, Values H. The agricultural foundations of civilization. Agriculture Human Values. 1984;**1**(2):9-12

[3] Hillman G, Hedges R, Moore A, Colledge S, Pettitt P. New evidence of Lateglacial cereal cultivation at Abu Hureyra on the Euphrates. The Holocene. 2001;**11**(4):383-393

[4] Sarwar MH, Sarwar MF, Sarwar M, Qadri NA, Moghal S. The importance of cereals (Poaceae: Gramineae) nutrition in human health: A review. Journal of Cereals. 2013;**4**(3):32-35

[5] Kumar V, Sinha AK, Makkar HP, De Boeck G, Becker K. Dietary roles of non-starch polysaccharides in human nutrition: A review. Critical Reviews in Food Science. 2012;**52**(10):899-935

[6] Jukanti AK, Gaur PM, Gowda C, Chibbar RN. Nutritional quality and health benefits of chickpea (*Cicer arietinum* L.): A review. British Journal of Nutrition. 2012;**108**(S1):S11-S26

[7] Iqbal A, Khalil IA, Ateeq N, MS K. Nutritional quality of important food legumes. Food Chemistry. 2006;**97**(2):331-335

[8] Nkhata SG, Ayua E, Kamau EH, Shingiro JB. Fermentation and germination improve nutritional value of cereals and legumes through activation of endogenous enzymes. Food Science. 2018;**6**(8):2446-2458

[9] Wheat, Initiative. Available from: https://wwwwheatinitiativeorg/ [Accessed: November 2019]

[10] United Nations Department of Economics and Social Affairs. Population Division. Available from: https://www.un.org/en/development/desa/population/index.asp [Accessed: November 2019]

[11] Giraldo P, Benavente E, Manzano-Agugliaro F, Gimenez EJA. Worldwide research trends on wheat and barley: A bibliometric comparative analysis. Agronomy. 2019;**9**(7):352

[12] International Barley Hub. Available from: http://www.barleyhub.org/ [Accessed: November 2019]

[13] Di Vittori V, Gioia T, Rodriguez M, Bellucci E, Bitocchi E, Nanni L, et al. Convergent evolution of the seed shattering trait. Genes (Basel). 2019;**10**(1):1-16

[14] Liljegren SJ, Ditta GS, Eshed Y, Savidge B, Bowman JL, Yanofsky MF. SHATTERPROOF MADS-box genes control seed dispersal in Arabidopsis. Nature. 2000;**404**(6779):766-770

[15] Rajani S, Sundaresan V. The Arabidopsis myc/bHLH gene ALCATRAZ enables cell separation in fruit dehiscence. Current Biology. 2001;**11**(24):1914-1922

[16] Mitsuda N, Ohme-Takagi M. NAC transcription factors NST1 and NST3 regulate pod shattering in a partially redundant manner by promoting secondary wall formation after the establishment of tissue identity. The Plant Journal. 2008;**56**(5):768-778

[17] Mitsuda N, Iwase A, Yamamoto H, Yoshida M, Seki M, Shinozaki K, et al. NAC transcription factors, NST1 and NST3, are key regulators of the formation of secondary walls in woody tissues of Arabidopsis. Plant Cell. 2007;**19**(1):270-280

[18] Pourkheirandish M, Hensel G, Kilian B, Senthil N, Chen G, Sameri M, et al. Evolution of the grain dispersal system in barley. Cell. 2015;**162**(3):527-539

[19] Konishi S, Izawa T, Lin SY, Ebana K, Fukuta Y, Sasaki T, et al. An SNP caused loss of seed shattering during rice domestication. Science. 2006;**312**(5778):1392-1396

[20] Li C, Zhou A, Sang T. Rice domestication by reducing shattering. Science. 2006;**311**(5769):1936-1939

[21] Zhou Y, Lu D, Li C, Luo J, Zhu BF, Zhu J, et al. Genetic control of seed shattering in rice by the APETALA2 transcription factor shattering abortion. Plant Cell. 2012;**24**(3):1034-1048

[22] Yoon J, Cho LH, Kim SL, Choi H, Koh HJ, An G. The BEL1-type homeobox gene SH5 induces seed shattering by enhancing abscission-zone development and inhibiting lignin biosynthesis. The Plant Journal. 2014 Sep;**79**(5):717-728

[23] Funatsuki H, Suzuki M, Hirose A, Inaba H, Yamada T, Hajika M, et al. Molecular basis of a shattering resistance boosting global dissemination of soybean. Proceedings of the National Academy of Sciences of the United States of America. 2014;**111**(50):17797-17802

[24] Dong Y, Yang X, Liu J, Wang B-H, Liu B-L, Wang Y-Z. Pod shattering resistance associated with domestication is mediated by a NAC gene in soybean. Nature Communications. 2014;**5**(1):3352

[25] Suanum W, Somta P, Kongjaimun A, Yimram T, Kaga A, Tomooka N, et al. Co-localization of QTLs for pod fiber content and pod shattering in F2 and backcross populations between yardlong bean and wild cowpea. Molecular Breeding. 2016;**36**(6):80

[26] Koinange EMK, Singh SP, Gepts P. Genetic control of the domestication syndrome in common bean. Crop Science. 1996;**36**:1037-1045

[27] Rau D, Murgia ML, Rodriguez M, Bitocchi E, Bellucci E, Fois D, et al. Genomic dissection of pod shattering in common bean: Mutations at non-orthologous loci at the basis of convergent phenotypic evolution under domestication of leguminous species. The Plant Journal. 2019;**97**(4):693-714

[28] Fourquin C, del Cerro C, Victoria FC, Vialette-Guiraud A, de Oliveira AC, Ferrándiz C. A change in SHATTERPROOF protein lies at the origin of a fruit morphological novelty and a new strategy for seed dispersal in Medicago genus. Plant Physiology. 2013;**162**(2):907-917

[29] Cormier F, Foulkes J, Hirel B, Gouache D, Moënne-Loccoz Y, Le Gouis J. Breeding for increased nitrogen-use efficiency: A review for wheat (T. aestivum L.). Plant Breeding. 2016;**135**(3):255-278

[30] Hu B, Wang W, Ou S, Tang J, Li H, Che R, et al. Variation in NRT1.1B contributes to nitrate-use divergence between rice subspecies. Nature Genetics. 2015 Jul;**47**(7):834-838

[31] Chen Z, Liu C, Wang Y, He T, Gao R, Xu H, et al. Expression analysis of nitrogen metabolism-related genes reveals differences in adaptation to low-nitrogen stress between two different barley cultivars at seedling stage. International Journal of Genomics. 2018;**2018**:1-10

[32] Astier J, Gross I, Durner J. Nitric oxide production in plants: An update. Journal of Experimental Botany. 2018;**69**(14):3401-3411

[33] Lin CM, Koh S, Stacey G, Yu SM, Lin TY, Tsay YF. Cloning and functional characterization of a constitutively

expressed nitrate transporter gene, OsNRT1, from rice. Plant Physiology. 2000;**122**(2):379-388

[34] Hu B, Wei W, Ou S, Tang J, Hua I, Che R, et al. Nature Genetics. 2015;**47**:834-838

[35] Fan X, Naz M, Fan X, Xuan W, Miller AJ, Xu G. Plant nitrate transporters: From gene function to application. Journal of Experimental Botany. 2017;**68**(10):2463-2475

[36] Leran S, Varala K, Boyer JC, Chiurazzi M, Crawford N, Daniel-Vedele F, et al. A unified nomenclature of NITRATE TRANSPORTER 1/PEPTIDE TRANSPORTER family members in plants. Trends in Plant Science. 2014;**19**(1):5-9

[37] von Wittgenstein NJ, Le CH, Hawkins BJ, Ehlting J. Evolutionary classification of ammonium, nitrate, and peptide transporters in land plants. BMC Evolutionary Biology. 2014;**14**:11

[38] Komarova NY, Thor K, Gubler A, Meier S, Dietrich D, Weichert A, et al. AtPTR1 and AtPTR5 transport dipeptides in planta. Plant Physiology. 2008;**148**(2):856-869

[39] Krouk G, Lacombe B, Bielach A, Perrine-Walker F, Malinska K, Mounier E, et al. Nitrate-regulated auxin transport by NRT1.1 defines a mechanism for nutrient sensing in plants. Developmental Cell. 2010;**18**(6):927-937

[40] Kanno Y, Hanada A, Chiba Y, Ichikawa T, Nakazawa M, Matsui M, et al. Identification of an abscisic acid transporter by functional screening using the receptor complex as a sensor. Proceedings of the National Academy of Sciences of the United States of America. 2012;**109**(24):9653-9658

[41] Chiba Y, Shimizu T, Miyakawa S, Kanno Y, Koshiba T, Kamiya Y, et al. Identification of Arabidopsis thaliana NRT1/PTR FAMILY (NPF) proteins capable of transporting plant hormones. Journal of Plant Research. 2015;**128**(4):679-686

[42] David LC, Berquin P, Kanno Y, Seo M, Daniel-Vedele F, Ferrario-Mery S. N availability modulates the role of NPF3.1, a gibberellin transporter, in GA-mediated phenotypes in Arabidopsis. Planta. 2016 Dec;**244**(6):1315-1328

[43] Zhao M, Geng X, Bi W, Xu Q, Sun J, Huang Y, et al. Recombination between DEP1 and NRT1.1B under japonica and indica genetic backgrounds to improve grain yield in rice. Euphytica. 2017;**213**(12):265

[44] Wang W, Hu B, Yuan D, Liu Y, Che R, Hu Y, et al. Expression of the nitrate transporter gene OsNRT1.1A/OsNPF6.3 confers high yield and early maturation in Rice. The Plant Cell. 2018;**30**(3):638-651

[45] Zhang J, Liu YX, Zhang N, Hu B, Jin T, Xu H, et al. NRT1.1B is associated with root microbiota composition and nitrogen use in field-grown rice. Nature Biotechnology. 2019;**37**(6):676-684

[46] Hussain A, Imran QM, Yun B-W. CRISPR/Cas9-Mediated Gene Editing in Grain Crops. Recent Advances in Grain Crops Research: IntechOpen; 2019