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Cereal Grains

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Edited by Aakash Kumar Goyal

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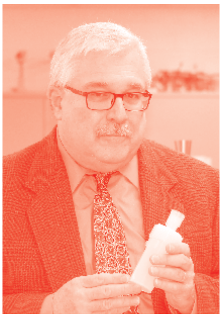

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Contributors
Oseni Kadiri, Timilehin David Oluwajuyitan, Babawande Origbemisoye, Babatunde Olawoye, Oladapo Fisoye Fagbohun, Oyekemi Popoola, Ruth Ukejeh, Mathew S. Baite, Mukesh K. Khokhar, Ram P. Meena, Casper Kamutando, Clemence Muitire, Martin Moyo, Abul Khayer Mohammad Golam Sarwar, Jiban Krishna Biswas, Ana Badea, Champa Wijekoon, Shonisani Eugenia Ramashia, Mpho E. Mashau, Oluwatoyin O. Oladayo Onipe, Véronique Bergougnoux, Mortaza Khodaeiaminjan, Ayman EL Sabagh, Fatih Çiğ, Seyithan Seydoşoğlu, Martin Leonardo Battaglia, Talha Javed, Muhammad Aamir Iqbal, Muhammad Mubeen, Musaddiq Ali, Mazhar Ali, Gülşah Bengisu, Ömer Konuşkan, Celaleddin Barutcular, Murat erman, Semih Açikbaş, Akbar Hossain, M Sohidul Islam, Allah Wasaya, Disna Ratnasekera, Muhammad Arif, Zahoor Ahmad, Fernando Cezar Juliatti, Laércio Zambolim, Suhel Mehandi, Anita Yadav, Ramanuj Maurya, Sudhakar Prasad Mishra, Syed Mohd. Quatadah, Nagmi Praveen, Namrata Dwivedi, Ajaz A. Lone, Zahoor A. Dar, Audil Gul, Asima Gazal, Sabina Naseer, Mudasir H. Khan, Ashraf Ahangar, Asif M. Iqbal, Aakash K. Goyal, Anuradha Singh, Jyotirmaya Mathan, Amit Yadav, Ashok Chaudhury

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Meet the editor

Aakash Goyal graduated with a degree in Biology from Maharshi Dayanand Saraswati University (MDSU), Ajmer, in 1999. He obtained a master's in Biotechnology with a specialization in Plant Biotechnology and Molecular Breeding from Guru Jambheshwar University of Science and Technology (GJUS&T), Hissar, in 2002, and a Ph.D. in Genetics and Plant Breeding with a specialization in Wheat Breeding from Chaudhary Charan Singh Universit (CCSU), Meerut, in 2007. After earning his Ph.D., Dr. Goyal completed a visiting fellowship with the Natural Sciences and Engineering Research Council of Canada (NSERC) and joined the wheat and triticale breeding program at Lethbridge Research Center, Agriculture and Agri-Food Canada (AAFC), Lethbridge. In 2012, he received an honorable position of Wheat Breeder for Bayer Crop Science, Saskatoon, Canada. In 2014, he took a senior research scientist position with the International Center of Agriculture Research in Dry Areas (ICARDA). In 2017, he moved back to Canada and joined InnoTech Alberta as a Native Plant Research Scientist. Since November 2019 he has been working as an agriculture specialist with Palm Gardens, Inc. in Edmonton, AB, Canada In July 2021, he joined RAYN Cultivation Inc., Edmonton, Alberta, Canada as Chief Executive Officer (CEO). Dr. Goyal has published ten books and fifty research papers, review articles, book chapters, and book reviews. He is also an elected fellow member of the International College of Nutrition (FICN) and Society of Applied Biotechnology (FSAB).

Contents

Preface

Cereals, Grains: Importance, Challenges and Future Prospects.

Cereal crops such as maize, rice, wheat, sorghum, and barley were the foundation of human civilization. Not only are they important sources of human and animal feed but they are also useful for fuel production. Over the past 50 years, cereals have emerged as rapidly evolving crops because of new technologies and advances in agronomy, breeding, biotechnology, genetics, and so on. Population growth and climate change have led to new challenges, among which are feeding the growing global population and mitigating adverse effects on the environment. One way to deal with these issues is through sustainable cereal production. This book discusses ways to achieve sustainable production of cereals via agronomy, breeding, transcriptomics, proteomics, and metabolomics. Chapters review research, examine challenges, and present future prospects in the field.

I would like to thank all the contributing authors for their outstanding efforts and timely work in producing such fine chapters. I greatly appreciate all the reviewers for their helpful comments. I would also like to thank the staff at IntechOpen, particularly Sara Gojević-Zrnić and Lucija Tomicic-Dromgool, for their assistance, advice, and encouragement during the development of this book. Lastly, I express my heartfelt thanks to my family for their love, encouragement, and vision that unveiled in me the desire to reach the highest mountain in everything I do.

Aakash Kumar Goyal, Ph.D.
CEO,
RAYN Cultivation Inc.,
Edmonton, Canada

Section 1

Breeding

Chapter 1

Current Scenario of Breeding Approaches in Rice

Suhel Mehandi, Anita Yadav, Ramanuj Maurya,
Sudhakar Prasad Mishra, Syed Mohd. Quatadah,
Nagmi Praveen and Namrata Dwivedi

Abstract

Rice is the predominant crop in India and is the staple food in eastern and southern Indian populations. One of the oldest grown crops is rice. The initial discovery of cytoplasmic male sterile (CMS) three-line system made it possible to produce hybrids that significantly increase rice yields compared to its inbred counterparts. Further genetic and molecular studies help elucidate the mechanisms involved in CMS male sterility. Additional CMS types were also discovered with similar genetic control from wild sources by interspecific hybridization. In India more than 1200 varieties were released for cultivation suitable different ecosystems and out of them 128 varieties have been contributed from NRRI, Cuttack. A list of these varieties are furnished below with their duration, grain type, yield potential, reaction to major disease and insects grain quality and tolerance to different adverse situations. Recent advances in molecular approaches used in modern rice breeding include molecular marker technology and marker-assisted selection (MAS); molecular mapping of genes and QTLs and production of hybrids and alien introgression lines (AILs). Genomic selection (GS) has been projected as alternative to conventional MAS. GS has huge potential to enhance breeding efficiency by increasing gain per selection per unit time. Due to the adaptation of semi dwarf high yielding varieties, combined with intensive input management practices, the country witnessed an impressive rice production growth in the post-independent period. Rice production was increased four times, productivity three times while the area increase was only one and half times during this period. The projected rice requirement by 2025, in order to keep up with increasing population, is about 130 m.t. The challenge of growing rice production is made more difficult by declining trends in HYV's yields, decreasing and degrading natural resources such as land and water and a severe labour shortage.

Keywords: Rice, Hybrid, Heterosis, Marker Assisted Selection, Genomic Selection

1. Introduction

Rice (*Oryza sativa* L.) is one of the most important staple foods that feed more than half of the world's population; Asia and Africa are the major consuming regions [1]. For at least half of the world's population, rice is the most significant source of calories. As a result, many countries have developed strategies to achieve rice self-sufficiency by growing the area under cultivation or increasing yield per unit area. In case of rice, however, grain quality is just as critical as yield. Heterosis is the ability of F_1 offspring to outperform either parent and it is the only way to achieve full hybrid vigor in crop plants. For decades, this has been a factor in the production of superior cultivars for many crops in agriculture and enthusiastic geneticists [2]. In a hybrid compared to HYVs, the appropriate combination and manipulation have produced benefits [3]. Since the discovery and growth of the cytoplasmic male sterile (CMS) source in the middle of the twentieth century, heterosis was possible due to its self-pollinating existence (0.3–3.0% outcrossing). Nanyou 2, the first indica rice hybrid, was released for cultivation in China in 1974.

Subsequently, relatively heterotical hybrid rice (HR) breeding approaches were adopted, such as two-line system and super hybrids, which complemented Chinese food security and liveling standards significantly in India. In 1989, the Indian Council of Agricultural Research (ICAR) launched a special goal-oriented and time-bound project for rice called "Promotion of Research and Development Efforts on Hybrids in Selected Crops," which included 12 network centres. Around four years of intensive research (1989–1993) paid off handsomely, and India became the second country after China to grow and commercialize hybrid rice. APRRI, Maruteru, launched the first hybrid variety APRH-1 in 1993–1994 for Andhra Pradesh. So far, 117 rice hybrids (36 from public organization and 81 from private sector) have been produced, with duration ranging from 115 to 150 days and a total area of 3.0 mha, accounting for 7.0 percent of India's total rice acreage [4]. As a result, breeding for consumer-favored grain qualities has become a major target for breeding programs all over the world. Grain quality must be clearly identified and the genes underlying their regulation deciphered before it is possible to breeder for fastidious customer preference. Rice is a staple food crop that accounts for more than a fifth of all calories consumed by humans [5]. Since rice is the most common cereal crop in most Asian countries and is the staple food for more than half of the world's population, even a small increase in rice grain micronutrient content could have a major effect on human health. Hybrid rice is the product of a cross between two rice parents with genetically different traits. When the right parents are chosen, the hybrid can outperform both parents in terms of vigor and yield. Higher yields, increased vigor, and increased resistance to diseases and insect resistance are all advantages of hybrid rice [6].

2. Hybrid rice breeding program in India

Rice is the predominant crop in India and is the staple food in eastern and southern Indian populations. One of the oldest grown crops is rice. The two cultivated species of rice are (i) *Oryza sativa* - Asian rice Cultivated Species of Rice (A) Asian Rice (*Oryza sativa* L.). It is predominant species which has spread to different part of world. (B) African Rice (*Oryza glaberrima* L.) [7]. It's also only found in Africa's tropical region. Based on morphological and physiological characteristics as well as geographical adaptation, Asian rice is divided into three ecological forms. **1.** *Indica*: Grown in tropical climate such as India, Sri- Lanka, China, Thailand, Malaysia, Taiwan *2. Japonica*: Japan and Korea have a temperate climate *3. Javanica:* Indonesian hybrid of Indica and Japonica (**Table 1**).

3. IRRI's hybrid rice program

Germplasm, parents and hybrids are being developed through new breeding and seed technology by researcher. Currently scientists are working for the hybrids rice production with the Collaboration of NARS and private sectors.

S.No.	Year	Remarks
1	1926	Heterosis in rice reported
2	1964	China started hybrid rice research
3	1970	China discovered a commercially usable genetic tool for hybrid rice (male sterility in a wild rice = Wild Abortive)
4	1973	PTGMS rice was found in China
5	1974	First commercial three-line rice hybrid released in China
6	1976	Large scale hybrid rice commercialization began in China
7	1979	IRRI revived research on hybrid rice
8	1981	PTGMS rice genetics and application was confirmed
9	1982	Yield superiority of rice hybrids in the tropics confirmed (IRRI)
10	1990s	- India and Vietnam started hybrid rice programs with IRRI
11	1991	More than 50% of China rice land planted to hybrids
12	1994	First commercial two-line rice hybrid released in China
13	1994–1998	Commercial rice hybrids released in India, Philippines Vietnam

Table 1.
Brief history of hybrid rice.

4. Wild species

The genus Oryza contains tweny valid species, two of which are cultivated, namely *Oryza sativa* and *Oryza glaberrima.* There are nine diploid species among the remaining 18 species (**Table 2**). Six of them are tetraploid. Some of the wild species utilized in breeding programme are *Oryza perennis* - Co 31 GEB 24 x *O. perennis* [8–10].

5. Breeding component and system in hybrid rice development

For breeding technique, there are three approaches (1) the three-line method also known as CMS (cytoplasmic male sterility) system (2) the two-line method also known as the PTGMS (photo/temperature sensitive genic male sterility) system and (3) the one-line method, also known as the apomixis system. Inter-varietal hybrids, Inter-sub-specific hybrids and inter-specific or intergeneric hybrids are three ways to increase the degree of heterosis (**Table 3**).

5.1 Two-line hybrid rice

The two-line hybrid rice research began in China and was successfully scaled up in 1995. The thermo-sensitive male sterile lines (TGMS) lines are those whose sterility expression is regulated by temperature, whereas photoperiod-sensitive male sterile (PGMS) lines are those whose expression is controlled by day-length duration. Backcrossing has successfully transferred the PGMS trait to many *Indica* and *Japonica* rice cultivars in China. In China, rice hybrids produced by this male sterile system are being tested in multiple locations. The degree of heterosis in two-line hybrid rice is close to that of three-line hybrid rice, but the technique methods is different. Unlike three-line hybrids, the male parent of two-line hybrid is not limited by restorer genes, allowing us to use both good restorer lines with high combining potential and good traditional varieties without restorer genes as male

Botanical Name	Chromosome No.	Genome	Origin
O. sativa	24	AA	Asia
O. nivara	24	AA	Asia
O. meridionalis	24	—	- Australia
O. longistaminata	24	AA	Africa
O. rufipogan	24	AA	Asia
O. glumaepatula	24	—	America
O. grandiglumis	48	CCDD	America
O. glaberrima	24	AA	Africa
O. barthii	24	AA	Africa
O. australiensis	24	EE	Australia
O. latifolia	48	CCDD	America
O. alata	48	CCDD	America
O. eichingeri	24, 48	CC, BBCC	Africa
O. minuta	48	BBCC	Asia
O. punctata	48	BBCC	Asia
O. officinalis	24	CC	Asia
O. granulata	24	—	Asia
O. meyeriane	24	—	Asia
O. ridleyi	48	—	Asia
O. longiglumis	48	—	New Guninea
O. brachantha	24	FF	Africa
O. schlechter	—	—	New Guninea

Table 2.
Wild species of Rice.

parents. Since restorer genes are not limited, there's a better chance of breeding elite hybrids [12]. The developed PTGMS lines such as PA64S, GZ63S, Zhun S, etc. have many advantages for hybrid combinations, such as larger freedom for crossing, higher yielding, better quality and diseases resistance. The yield of improved two-line hybrid rice combinations is usually higher than of three-line hybrids used as controls. Meanwhile, seed processing and cultivation techniques for two-line hybrids have advanced to the point that they can be used in commercial production. Breeding of elite restorer lines is the key for matching heterotic combinations [13] (**Table 4**).

5.2 Three-line system hybrid rice

5.2.1 Identification and utilization of cytoplasm male sterility

The role of rice cytoplasm in male sterility was first discovered in 1954 [16]. They studied cytoplasmic differences among rice varieties in 1965 and formed a male sterile line for the first time by transferring the nuclear genotype of rice cultivar Fujisaka [17]. However, due to its instability, poor plant form and photoperiod sensitivity, this cytoplasm male sterility (CMS) line could not be used to breed rice. Yuan Long Ping proposed the concept of using heterosis in rice in 1964, and for the

Sl. No.	**Rice Hybrids**	**Year of Release**	**Duration**	**Developed by**	**Recommended for**
1	DRRH- 3	2010	131	DRR, Hyderabad	Andhra Pradesh, Gujarat, Madhya Pradesh, Odisha, Uttar Pradesh
2	US - 312	2010	125–130	Seed Works International, Hyderabad.	Andhra Pradesh, Bihar, Karnataka, Tamil Nadu, Uttar Pradesh, West Bengal.
3	CRHR-32	2010	125	CRRI, Cuttack, Odisha	Bihar, Gujarat.
4	INDAM 200–017 (IET 20419)	2011	120–125	Indo-American seeds, Hyderabad	Odisha, Chhattisgarh, Gujarat Maharashtra, Andhra Pradesh.
5	27P11	2011	115–120	PHI Seeds (P) Ltd.	Karnataka, Maharashtra.
6	VNR 2245 (VNR-204)	2011	90–95	VNR Seeds Pvt. Ltd., Raipur	Chhattisgarh, Tamil Nadu.
7	VNR 2245 (VNR-202)	2011	100–105	VNR Seeds Pvt. Ltd., Raipur	Uttar Pradesh, Uttarakhand, West Bengal, Maharashtra, Tamil Nadu.
8	Shyadri-5 (Hybrid)	2011	110–115	RARS, Karjat (BSKKV)	Konkan Region of Maharashtra.
9	CO (R) H-4	2011	130–135	TNAU, Coimbatore	Tamil Nadu.
10	Hybrid CO 4	2012	130–135	TNAU, Coimbatore	Tamil Nadu.
11	US 382	2012	125–130	Seed Works International Pvt. Ltd., Hyderabad	Tripura, Madhya Pradesh, Karnataka.
12	27P31	2012	125–130	PHI Seeds Pvt. Ltd. Hyderabad	Jharkhand, Maharashtra, Karnataka, Tamil Nadu, Uttar Pradesh, Bihar, Chhattisgarh.
13	27P61	2012	132	PHI Seeds Pvt. Ltd. Hyderabad	Chhattisgarh, Gujarat, Andhra Pradesh, Karnataka, Tamil Nadu.
14	25P25	2012	110	PHI Seeds Pvt. Ltd. Hyderabad	Uttarakhand, Jharkhand, Karnataka.
15	Arize Tej (HRI 169)	2012	125	Bayer Bio Science Pvt. Ltd., Hyderabad	Bihar, Chhattisgarh, Gujarat, Andhra Pradesh, Tamil Nadu.
16	PNPH 24	2012	120–130	Nuziveedu Seeds Limited, A.P.	Bihar, West Bengal, Odisha.
17	PNPH 924–1	2012	125–135	Nuziveedu Seeds Limited, A.P.	West Bengal, Assam
18	NK 5251	2012	NA	NA	Tamil Nadu, Karnataka, Andhra Pradesh, Maharashtra, Gujarat.

Sl. No.	Rice Hybrids	Year of Release	Duration	Developed by	Recommended for
19	VNR 2245	2012	120–125	VNR Seeds Pvt. Ltd., Raipur	Chhattisgarh, Tamil Nadu.
20	VNR 2355 Plus	2012	130–135	VNR Seeds Pvt. Ltd., Raipur	Uttar Pradesh, Uttarakhand, West Bengal, Maharashtra, Tamil Nadu.
21	CR Dhan 701	2012	140–145	NA	Bihar, Gujarat.
22	JKRH 3333	2013	135–140	JK Agri Genetics Ltd., Hyderabad- 16.	West Bengal, Bihar, Chhattisgarh, Gujarat, Andhra Pradesh.
23	RH- 1531	2013	118–125	Devgen Seeds & Crop Technology, Hyderabad	Major Hybrid rice growing regions (Madhya Pradesh, Uttar Pradesh, Andhra Pradesh, Karnataka, Maharashtra).
24	CO 4 (IET 21449)	2013	NA	TNAU, Coimbatore	Tamil Nadu, Gujarat, Maharashtra, Uttarakhand, Uttar Pradesh, Bihar, Chhattisgarh, West Bengal.
25	Arize Dhani	2013	NA	Bayer Bio-Science, Hyderabad	Odisha.
26	27P52	2013	NA	PHI Seeds Pvt. Ltd. Hyderabad- 82.	Andhra Pradesh, Chhattisgarh, Gujarat, Odisha, Uttarakhand.
27	27P63	2013	NA	PHI Seeds Pvt. Ltd. Hyderabad- 82.	Andhra Pradesh, Chhattisgarh, Karnataka, Uttar Pradesh.
28	KPH - 199	2013	NA	Kaveri Seed Company Limited, Secunderabad	Andhra Pradesh, Chhattisgarh, Madhya Pradesh.
29	KPH - 371	2013	NA	Kaveri Seed Company Limited, Secunderabad	Chhattisgarh, Jharkhand, Karnataka, Kerala.
30	VNR 2375 PLUS	2013	NA	VNR Seeds Pvt. Ltd., Raipur	Bihar, Karnataka, Punjab, Maharashtra, Uttarakhand.
31	US 305	2013	NA	Seed Works International Pvt. Ltd., Hyderabad	Andhra Pradesh, Tamil Nadu, Maharashtra.
32	US 314	2013	NA	Seed Works International Pvt. Ltd., Hyderabad	Andhra Pradesh, Bihar, West Bengal, Uttarakhand.
33	Ankur 7434	2014	NA	Ankur seed Pvt. Ltd.	Chhattisgarh.
34	PAC 807	2014	NA	Advanta India Ltd. Hyderabad	Chhattisgarh.
35	PAC 801	2014	NA	Advanta India Ltd. Hyderabad	Uttar Pradesh.

Sl. No.	Rice Hybrids	Year of Release	Duration	Developed by	Recommended for
36	CSR 43	2014	NA	—	Uttar Pradesh.
37	JKRH-401	2014	NA	JK Agri Genetics Ltd., Hyderabad- 16.	Uttar Pradesh.
38	Arize 6444 Gold	2015	130–135	Bayer Crop Science, Hyderabad	Assam, Chhattisgarh, Odisha, Uttar Pradesh, Bihar Meghalaya, Karnataka, Tamil Nadu.
39	SAVA 127	2015	115–120	Savannah seed Pvt. Ltd.	Uttar Pradesh.
40	Arize Tej (HRI 169)	2015	120	Bayer Crop Science, Hyderabad	Bihar, Chhattisgarh, Gujarat, Andhra Pradesh, Tamil Nadu, Jharkhand.
41	27P31	2015	NA	PHI Seeds Pvt. Ltd. Hyderabad- 82.	Jharkhand, Maharashtra, Karnataka, Tamil Nadu, Uttar Pradesh, Bihar, Chhattisgarh, Madhya Pradesh, Odisha.
42	PAC 801	2015	NA	Advanta India Ltd., Hyderabad	Uttar Pradesh, Jharkhand.
43	NK 16520	2016	132	Syngenta India Ltd., Secundrabad	Chhattisgarh, Uttar Pradesh, Bihar, Jharkhand, Odisha, Telangana.
44	KPH 467	2016	126	Kaveri Seed Company Limited	Chhattisgarh, Madhya Pradesh, Maharashtra.
45	KPH 272	2016	126	Kaveri Seed Company Limited	Telangana, Karnataka, Tamil Nadu.
46	37P22	2017	126	PHI Seeds Pvt. Ltd. Hyderabad	Punjab, Haryana.
47	GK 5022	2017	123 (Aerobic)	Ganga Kaveri Seeds Pvt. Ltd., Hyderabad	Bihar, Chhattisgarh.
48	27P36	2017	NA	PHI Seeds Pvt. Ltd. Hyderabad	Bihar, Madhya Pradesh, Jharkhand.
49	NPH 8899	2017	168 (Boro)	Kaveri Seed Company Limited	Uttar Pradesh, Bihar, Assam.

NA = Not available.
Source: [11].

Table 3.
List of hybrid Rice released/notified in India during 2010–2017.

first time in China, hybrid rice research was started. The discovery of WA, a nationwide cooperative program was immediately established to extensively testcross with the WA and screen for its maintainers and restorers. Soon in 1972, the first group of CMS lines such as Erjiunan 1A, Zhenshan 97A and V20A were developed all using WA as the donor of male sterile genes and all using successive backcrossing method. In 1973, the first group of restorer lines such as Taiyin 1, IR24 and IR661 were screened using direct test crossing system. Nanyou 2 and Nanyou 3 hybrids

Sl. No.	Variety	Ecology	Year of release	Duration	Grain type	Recommended for
1	Phalguni	Irrigated	2010	117	LS	Odisha
2	Reeta (CR Dhan 401)	Shallow low land	2010	150	MS	Odisha
3	Luna Suvarna (CR Dhan 403)	Coastal Saline	2010	150	MS	Odisha
4	Luna Sampad (CR Dhan 402)	Coastal Saline	2010	140	SB	Odisha
5	Nua Chinikamini (Aromatic)	Shallow low land	2010	145–150	SB	Odisha
6	CR Dhan 501	Semi-deep	2010	152	LB	UP, Assam
7	CR Dhan 701	Shallow low land	2010	142	MS	Bihar, Gujarat, Odisha
8	CR Dhan 601	Boro	2010	160	MS	Orissa, WB and Assam
9	CR Dhan 500	Deep Water	2011	160	MS	Odisha, UP
10	Satyabhama (CR Dhan 100)	Upland	2012	110	MS	Odisha
11	Pyari (CR Dhan 200)	Aerobic	2012	115–120	SB	Odisha
12	Hue (CR Dhan 301)	Irrigated	2012	135	LS	Odisha
13	Improved Lalat	Irrigated	2012	130	LS	Odisha
14	Improved Tapaswini	Irrigated	2012	130	SB	Odisha
15	Sumit (CR Dhan 404)	Shallow lowlands	2012	145	LB	Odisha
16	Poorna Bhog (CR Dhan 902)	Shallow lowlands	2012	140	LS	Odisha
17	Jalamani (CR Dhan 503)	Deep Water	2012	160	MS	Odisha
18	Jayanti Dhan (CR Dhan 502)	Deep Water	2012	160	MS	Odisha
19	Luna Barial (CR Dhan 406)	Coastal Saline	2012	150	SB	Odisha
20	Luna Sankhi (CR Dhan 405)	Coastal Saline	2012	110	MS	Odisha
21	CR Dhan 907 (Aromatic)	Irrigated Late	2013	150	MS	Chhattisgarh, Odisha, Andhra Pradesh, Gujarat
22	CR Dhan 300	Irrigated	2013	140	LS	Maharashtra Gujarat Odisha, Bhar
23	CR Dhan 303	Irrigated	2014	125	SB	MP, UP, Odisha
24	CR Dhan 305	Irrigated	2014	125	SB	Jharkhand, Maharashtra and Andhra Pradesh

Sl. No.	**Variety**	**Ecology**	**Year of release**	**Duration**	**Grain type**	**Recommended for**
25	CR Dhan 304	Irrigated	2014	130	SB	Odisha and West Bengal
26	CR Dhan 201	Aerobic	2014	118	LS	Chhattisgarh and Bihar
27	CR Dhan 202	Aerobic	2014	115	LB	Jharkhand and Odisha
28	CR Dhan 407	Rainfed shallow lowland	2014	150	LB	Odisha and West Bengal
29	CR Dhan 505	Deep water	2014	162	MS	Odisha and Assam
30	CR Dhan 204	Aerobic	2014	120	LB	Jharkhand and Tamil Nadu
31	CR Dhan 306 (IET 22084)	Irrigated	2014	120–125	SB	Madhya Pradesh, Bihar, Puducherry
32	CR Dhan 205 (IET 22737)	Aerobic	2014	110	SB	Tamil Nadu, Gujarat, Odisha, Madhya Pradesh, Punjab
33	CR Dhan 101 (Ankit)	Upland	2014	110	MS	Odisha
34	CR Dhan 203 (Sachala)	Aerobic	2014	110	LS	Odisha
35	CR Dhan 206 (Gopinath)	Aerobic	2014	115	SB	Odisha
36	CR Dhan 307 (Maudamani)	Irrigated	2014	135	SB	Odisha
37	CR Dhan 408 (Chaka Akhi)	Shallow lowland	2014	165 PS	LB	Odisha
38	CR Dhan 310	Irrigated	2015	125	MS	Odisha, Madhya Pradesh and Uttar Pradesh.
39	CR Dhan 207 (Srimati)	Aerobic	2016	110–115	MS	Odisha
40	CR Dhan 209 (Priya)	Aerobic	2016	112–115	LS	Odisha
41	CR Dhan 409 (Pradhan Dhan)	Semi-deep	2016	160–165	LS	Odisha
42	CR Dhan 507 (Prasant)	Deep Water	2016	160	MS	Odisha
43	CR Dhan 800	Shallow lowland	2016	140	MS	Odisha
44	CR Sugandh Dhan 910 (Aromatic)	Irrigated Late	2016	142–145	MS	Odisha
45	CR Dhan 311 (Mukul)	Irrigated	2016	120–126	LB	Odisha

Sl. No.	Variety	Ecology	Year of release	Duration	Grain type	Recommended for
46	CR Dhan 508	Deep Water	2017	187	LB	Odisha, West Bengal, Assam
47	CR Dhan 506	Semi-deep	2017	165	MS	Assam, Andhra Pradesh and Karnataka.
48	CR Sugandh Dhan 908 (Aromatic)	Irrigated Late	2017	145	MS	Odisha, West Bengal and Uttar Pradesh
49	CR Sugandh Dhan 909 (Aromatic)	Irrigated Late	2017	140	MS	Assam, Bihar, UP, Maharashtra
50	Gangavati Ageti (Aromatic)	Upland	2017	85	LS	Karnataka
51	Purna	Upland	2017	90	SB	Gujarat
52	CR Dhan 309	Irrigated	2019	115	LS	Assam, Chhatisgarh, Uttar Pradesh
53	CR Dhan 801	Shallow lowland(for submergence and drought prone areas)	2019	140	SB	AP, Telengana, Odisha, UP and WB
54	CR Dhan 802 (Subhas)	Shallow lowland(for submergence and drought prone areas)	2019	142	SB	Bihar, Madhya Pradesh
55	CR Dhan 510	Semi-deep	2019	160	SB	WB and Odisha
56	CR Dhan 511	Semi-deep	2019	160	SB	West Bengal, Odisha
57	CR Dhan 312	Irrigated	2019	135–140	MS	Maharashtra and Chhattisgarh
58	CR Dhan 102 (Santha Bhima)	Upland	2019	105–110	SB	Odisha
59	CR Dhan 210 (Sarumina)	Aerobic	2019	110–115	LS	Odisha
60	CR Dhan 410 (Mahamani)	Rainfed shallow lowlands	2019	160–165	LS	Odisha

Source: ICAR-NRRI [14, 15].
Grain: LS: Long Slender, MB: Medium Bold, MS: Medium Slender, SB: Short Bold, MB: Medium Bold.

Table 4.
Rice varieties developed by ICAR-NRRI, Cuttack during 2010–2019.

with high heterosis were published in 1974 [18–20]. In another word, the discovery of WA led to successful breakthrough in hybrid rice production, resulting in the establishment of three-line hybrid rice system. As a result, China became the first country in the world to commercialize hybrid rice for food production. For commercial rice hybrids processing, a three-line hybrid system with the CMS line (A), maintainer line (B) and restorer line (R) is used. The A line cannot produce viable pollen due to the interaction between cytoplasmic and nuclear genes, so called cytoplasmic male sterile, which anthers are pale or white and shriveled. The A line is also known as the CMS line and the seed parent because it is used as a female parent for hybrid seed development. Since the CMS line is male sterile, it cannot replicate itself and requires the assistance of a maintainer. The B line is the maintainer line, and its morphology is very similar to that of its CMS line, with the exception of its reproductive feature. However, the B line has viable pollen grains and normal seed setting, it may pollinate the A line, resulting in male sterile F1 plants. In this way, the male sterility of the A line is maintained, and the A line can be reproduced for further use or commercial purposes. Similarly, the R line will pollinate the A line because it has viable pollen grains and normal seed setting. Unlike the pollination with the B line, the F1 plants from the pollination with R line are extremely fertile, or the male sterility of the A line is restored into fertility in their progeny by R line. As a result, the R line is often referred to as the pollen parent or restoring line [21–25].

6. Genetic mechanism of rice heterosis

Heterosis, also known as hybrid vigor, is the phenomenon in which progeny of diverse inbred varieties outperform both parents in terms of yield, panicle size, and number of spikelets per panicle, number of productive tillers, stress tolerance and other factors. This phenomenon has been extensively exploited in crop production as a powerful force in plant evolution. After the successful development of hybrid maize in 1930, other crop breeders, including rice breeders, were inspired to use the concept of hybrid production by exploiting heterosis. In fact, the exploitation of heterosis has been the most practical achievement of genetics and plant breeding research [26]. The impact of this phenomenon can be judged by the fact that the number of grains per square meter in rice varies significantly between (1) wild ancestors with just a few hundred (2) improved inbred varieties with about 40,000, and (3) rice hybrids with about 52,000. Rice heterosis was first reported by Jones (1926) who observed that some F1 hybrids had more culms and greater yield than their parents. Between 1962 and 1967, a variety of proposal came from around the world for commercial exploitation of heterosis to become a major component of national and international rice improvement programs. Rice breeders from Japan, China, United States, India, the former Soviet Union and Philippines, for example, began working on projects to use rice heterosis. However, progress had been hampered by rice's inability to be strictly self-pollinated crop, as opposed to corn which is needed for hybrid seed development, extremely difficult [27–29].

7. Molecular technique to enhance rice breeding activities

Recent progress in molecular biology and biotechnology increases opportunities to use rice genetic tools not addressed in previous programs for rice production. The availability of genomic, phenotypic, geographical, and ecological information among other sequence data, when analyzed together, enables researchers to strategically plan experiments based on established models predicting plant performance [3, 30]. Molecular marker technology and marker-assisted selection (MAS), molecular mapping of genes and QTLs and the generation of hybrids and alien introgression lines [31–34] are just a few of the molecular approaches used in modern rice breeding. MAS is a form of genomic assisted breeding that uses molecular markers to map QTLs or unique genes linked to phenotypes or target traits in order to select individuals with desirable alleles for desired traits [32]. MAS has many benefits over traditional phenotypic selection, including the fact that it is easier than phenotypic screening, that selection can be performed at the seedling level, and that a single plant can be selected based on its genotype [35].

Breeding for improved grain is complex because many of the quality traits are phenotyped using subjective and or expensive biochemical methods. As a result, scientists have been able to map/clone several QTLs/genes for various quality traits and developed molecular markers to aid in grain quality selection. Co-dominant marker, making it ideal for marker-assisted backcrossing for recessive trait like aroma, since lines carrying the aroma gene can be selected in the heterozygote state without having to screen progeny [36, 37]. Other researchers have produced markers for the 8-bp deletion in exon 7 of chromosome 8. Other alleles in the BADH2 gene, such as a 7-bp deletion in exon 2 [38–40] and a 3-bp insertion in exon 13 found in aromatic rice varieties from Myanmar [41], have also been functionally identified. Around the world, functional markers for RM 190, a waxy gene SSR and waxy SNPS on intron (In1), exon 6 (Ex6) and exon 10 (Ex10) are used to select for AAC and RVA around the world [42]. The waxy SNP haplotypes have been found to be more effective in selecting for AAC and RVA than the RM 190 haplotype across these three SNPs in the waxy genome [43–47].

8. Outstanding elite hybrid rice varieties in India

In India many verities of rice have been released by Indian Council of Agriculture Research (ICAR) institute, state agricultural universities and private seed companies.

9. Future trends in rice breeding

Rice production would have to double by 2050 to keep up with population growth. If the world's population grows, so will consumers demands for higher-quality rice. In addition to this challenge, climate change is combining new biotic and abiotic stresses. As a result, when designing new lines, rice breeders must consider a large number of simple and quantitative traits in combination while preserving and enhancing grain quality. MAS has been effective in improving certain biotic, abiotic and quality traits in rice, but it is purposeful on broad impact QTLs/genes and ignores epistatic and genetic context effects. Most traits of interest to rice breeders are regulated by a combination of several small effect and/or major genes rather than a few large-effect genes. The use of genomic selection (GS) as an alternative to traditional MAS has been proposed. By the benefits per selection per unit time, GS has a huge potential to improve breeding efficiency. GS breeding enables breeders to use genome-wide DNA marker data to choose the most suitable parents for the next generation. The association between genome-wide markers and phenotypes of the individuals under selection is used to choose these parents. The major benefits of GS over MAS is that genotyping is not limited to a subset of markers that target genes with significant effects, but instead uses all available marker data to predict breeding value. This aids in the prevention of data loss. Genes with a minor effect can be tracked and chosen based on all of the markers results. As the cost of genotyping decreases, GS will become more efficient method for improving rice breeding performance [48, 49].

Author details

Suhel Mehandi[1*], Anita Yadav[1], Ramanuj Maurya[2], Sudhakar Prasad Mishra[3], Syed Mohd. Quatadah[4], Nagmi Praveen[4] and Namrata Dwivedi[5]

1 Faculty of Agricultural Sciences and Allied Industries, Rama University, Kanpur, Uttar Pradesh, India

2 Department of Botany, University of Lucknow, Lucknow, Uttar Pradesh, India

3 Mahatma Gandhi Chitrakoot Gramodaya Vishwavidhyalaya, Chirakoot, Satna, Madhya Pradesh, India

4 ICAR-Indian Institute of Pulses Research, Kanpur, Uttar Pradesh, India

5 Jawaharlal Nehru Krishi Vishwa Vidyalaya, Jabalpur, Madhya Pradesh, India

*Address all correspondence to: suhelgpb@gmail.com

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Chapter 2

Cereal Grains of Bangladesh – Present Status, Constraints and Prospects

Abul Khayer Mohammad Golam Sarwar
and Jiban Krishna Biswas

> *"Bangladesh has emerged as a global model for combating hunger and obtained great success in becoming a country of food surplus from a country lagged with chronic food shortages"*
>
> *– The Christian Science Monitor.*

Abstract

The edible seeds or grains of the grass family Poaceae (conserved name Gramineae) is commonly known as cereals and are cultivated for the edible component, grain consisting of the germ (or an embryo), endosperm and bran. Bangladesh, predominantly an agrarian country, has a long tradition of cereal grains cultivation, consumption and conservation. Rice is the staple food for millions (of people) across the globe including Bangladesh. It occupies more than 96% of the land area under "Cereal Agriculture" in Bangladesh. Maize occupies the 2nd position both in acreage and production followed by wheat and other minor cereals *viz*. barley, sorghum and millets. In this chapter, the historical development and production scenario of different cereal crops and their present status, constraints, challenges and opportunities has been described and discussed. The information presented here would provide a clear inside of the "Cereal Agriculture of Bangladesh" to students, researchers, administrators, policymakers, and the common people as well.

Keywords: Cereal agriculture, Historical development, Production trends, Food and nutritional security, Bangladesh

1. Introduction

The name "cereal" derives from *Ceres*, the Roman and Greek goddess of harvest and agriculture. The edible seeds or grains of the grass family Poaceae (conserved name Gramineae) is usually referred to as cereals (botanically, a sort of fruit called a caryopsis) and are cultivated for the edible component highly nutritious grain consisting of the germ (or an embryo), endosperm and bran. The cereal grains have a high starch content and also contain varying amounts of protein, the embryos often contain oil, and vitamins occur in the outer tissues of the seed. The comparative nutrient composition of different cereal crops is presented in **Table 1**. Cereal grains have

Cereal	Protein (%)	Fat (%)	Crude fiber (%)	Ash (%)	Starch (%)	Total dietary fiber (%)	Total phenol (mg/100 g)
Rice	7.5	2.4	10.2	4.7	77.2	3.7	2.51
Wheat	14.4	2.3	2.9	1.9	64.0	12.1	20.5
Maize	12.1	4.6	2.3	1.8	62.3	12.8	2.91
Barley	11.5	2.2	5.6	2.9	58.5	15.4	16.4
Sorghum	11	3.2	2.7	1.8	73.8	11.8	43.1
Oats	17.1	6.4	11.3	3.2	52.8	12.5	1.2
Rye	13.4	1.8	2.1	2.0	68.3	16.1	13.2
Finger millet	7.3	1.3	3.6	3.0	59.0	19.1	10.2
Pearl millet	14.5	5.1	2.0	2.0	60.5	7.0	51.4
Foxtail millet	11.7	3.9	7.0	3.0	59.1	19.1	106

Source: Saldivar [1].

Table 1.
Nutrient composition of cereal grains.

been the most important suppliers of dietary energy for more than 24 centuries and hope to be continued in the coming years. The importance of cereals (in the human diet) is well represented within the logo of the Food and Agriculture Organization of the United Nations, a wheat ear with a Latin inscription below "*Fiat Panis*" (Eng. Let there be bread). Cereals also have a wide array of virtues and benefits. For example, a long time storage ability due to the yield of mature and imperishable grains that can be gradually used as food or seed for future sowing. The cereal grains were first domesticated by ancient farming communities about 8,000 years ago in the Fertile Crescent region, considered to be the cradle of agriculture and food production [2]. Rice and millets were starting to become domesticated in East Asia by the year 7,500 BC. Around the same time, Sorghum and millets were also being domesticated in sub-Saharan West Africa. On average, cereal grain products supply approximately 55% of calories and 48% of their protein requirement of a human diet [2].

Bangladesh, a low-lying, riverine country, lies in the north-eastern part of South Asia between latitude $20^0$34′ and $26^0$38’ N and longitude $88^0$01′ and $92^0$41′ E. The country, with an area of 147,570 sq. km (56,977 sq. mi), is bounded by India on the west-north and north-east while Myanmar on the south-east and the Bay of Bengal on the south [3]. Bangladesh, predominantly an agrarian country, enjoys generally a subtropical monsoon climate. The country comprises a wide range of agro-ecosystems spread over the wetlands, (deltaic) flood plains as well as the hills. The agriculture sector contributes about 14.23% of the country's GDP and employs around 40.60% of the total labour force [4]. Due to its very fertile land and favorable weather conditions, a wide diversities of crops e.g., cereals, pulses, oilseeds, spices and condiments, fibers, vegetables, etc. grow abundantly in this country. Cereal crops occupied more than 75% of the total cropped area of Bangladesh [4].

Among the cereal crops, rice is the staple food for millions across the globe including Bangladesh. In Bangladesh, rice occupies more than 96% of the land area under "Cereal Agriculture". Bangladesh is the third-largest rice producer in the world after China and India [5]. Maize occupies the 2nd position both in acreage and production, but its production is insufficient to meet the national demand, followed by wheat and other minor cereals *viz*. barley, sorghum and millets. Minor cereals, sometimes also called poor man's crops, are rich in dietary fibers, phenolics and polysaccharides, antioxidants, mineral nutrients, etc. These are commonly used as constituents of special food preparations e.g., kheer or payes, moa (sweet ball of fried millets), porridge, pitha or cakes, pudding, flour, bread, sometimes cooked as rice, etc. and for feeding birds, poultry, livestock fodder and feed in developed countries. In Bangladesh, cereals provide a major part of the calorie intake, although their share in total calorie consumption has decreased from 92% in 1990 to 89% by 2010 with a projection of further decrease to 87% by 2031 and 86% by 2050 [6]. Cereal crops are also a dominating component of the present cropping patterns of Bangladesh. Presently, 316 different cropping patterns were recorded in this country excluding the minor ones, individually occupied less than 0.0001 per cent of the net cropped area [7]. Rice (Boro)-Fallow-Rice (T. Aman) was the most dominant cropping pattern which occupied 26.92% of the net cropped area; whereas the last cropping pattern was the Barley-Fallow-Fallow which occupied only 0.0002% of the net cropped area. Some of the most prominent cropping patterns among these are sown in **Table 2**.

No.	Cropping pattern	Area (ha)	% of NCA	District (no.)	Upazila (no.)
001	Boro–Fallow–T. Aman	2306005	26.919	63	426
002	Boro–Fallow–Fallow	1139530	13.302	59	342
003	Fallow–Fallow–T. Aman	509480	5.947	36	162
004	Boro–Aus – T. Aman	209015	2.440	47	177
005	Fallow–Aus – T. Aman	193275	2.256	30	108
006	Mustard–Boro–T. Aman	184620	2.155	51	203
007	Boro–B. Aman	183070	2.137	32	113
008	Potato–Boro–T. Aman	180380	2.106	33	115
009	Wheat–Jute–T. Aman	147210	1.718	43	216
010	Vegetable–Vegetable–Vegetable	143270	1.672	61	283
011	Mustard–Boro–Fallow	143130	1.671	37	112
012	Grasspea–Fallow–T. Aman	108150	1.262	25	80
013	Maize–Fallow–T. Aman	101460	1.184	39	126
014	Wheat–Fallow–T. Aman	90910	1.061	39	100
015	Mungbean–Fallow–T. Aman	89650	1.047	22	70
016	Grasspea–Aus – T. Aman	81610	0.953	19	61
017	Vegetable–Fallow–T. Aman	74710	0.872	45	170
018	Vegetable–Vegetable–Fallow	63935	0.746	59	168
019	Onion–Jute–T. Aman	54185	0.633	39	102
020	Mungbean–Aus – T. Aman	53730	0.627	14	43
021	Chili–Fallow–T. Aman	52995	0.619	45	146
022	Lentil–Jute–T. Aman	51875	0.606	34	96
023	Vegetable–Vegetable–T. Aman	51745	0.604	49	127
024	Wheat–Jute–Fallow	48700	0.568	32	82
025	Potato–Maize–T. Aman	47690	0.557	19	68

Source: Nasim et al. [7].

Table 2.
List of prominent cropping patterns in Bangladesh.

In this chapter, the historical development and production scenario of different cereal crops of Bangladesh, their present status, constraints, challenges and opportunities have been described and discussed.

2. Major cereals

2.1 Rice (*Oryza sativa* L.)

In our tradition, rice is synonymous with food, the world's second-largest per capita rice consumption at 179.9 kg yr.$^{-1}$ [8], and is dominating the entire crop sector. It provides nearly 48% of rural employment, about two-thirds of the total calorie supply and one-half of the total protein intake of an average person in the country. The rice sector contributes one-half of the agricultural GDP and one-sixth of the national income in Bangladesh [3]. Due to favorable weather conditions (e.g., temperature, relative humidity, rainfall, day length, etc.), rice is grown all the year-round in three growing periods *viz*. Aus (summer rice; April–August), Aman (monsoon rice; July–December), and Boro (winter rice; November–June) in Bangladesh. The growth of rice production in Bangladesh was 2.8% yr.$^{-1}$ in the 1980s and 3.5% yr.$^{-1}$ from 1990 to 1991 until recently [9]. Since the late 1980s, most of this growth has occurred through the development and adoption of improved and stress-tolerant rice cultivars through irrigation in Boro rice (dry season) and supplementary irrigation in Aman rice. The introduction of Boro rice in low-lying areas by replacing rain-fed traditional Aus rice cultivars, jute and the other upland crop cultivars also played an important role [9].

The total rice coverage was about 11.52 million hectares (m ha) over three rice growing seasons in 2018–2019 (**Table 3**). Most of the modern rice cultivars are photoperiod insensitive, therefore, they could be cultivated almost throughout the year. Even in some specific ecosystems, farmers may harvest three rice crops a year from the same piece of land. The recent coverage of Aus, Aman and Boro area were 9.60, 48.82 and 41.58 per cent, respectively. Boro and Aman contributed 53.75 and 38.62 per cent, respectively of the total rice production whereas Aus only 7.63 per cent, although total production of Aus rice increasing very slowly [9].

Though the total rice-growing area did not change much during the last four and a half decades (**Figure 1**), rice production nearly quadrupled from 9.8 million metric tons (m t) in 1971–1972 to 36.4 m t in 2019, helping Bangladesh to achieve self-sufficiency in rice production and ensuring food security. There had been a major shift in ecotype based (Boro-Aus-Aman) rice cultivation. The area under HYVs of Boro rice was 0.32 m ha in 1971–1972, 4.11 m ha in 2007–2008 and 4.79 m ha in 2018–2019. Most of the traditional Aus cultivars were in the process of replacement with the introduction of HYVs. Around 50 per cent of the traditional Deep Water

Season	Coverage (m ha)	Total production (m t)	Yield (t ha^{-1})	% of total area	% of total production
Aus	1.11	2.78	2.51	9.60	7.63
Aman	5.62	14.06	2.50	48.82	38.62
Boro	4.79	19.56	4.08	41.58	53.75
Total	11.52	36.30		—	—

Source: BBS (Bangladesh Bureau of Statistics) [4].

Table 3.
Rice statistics in 2018/19.

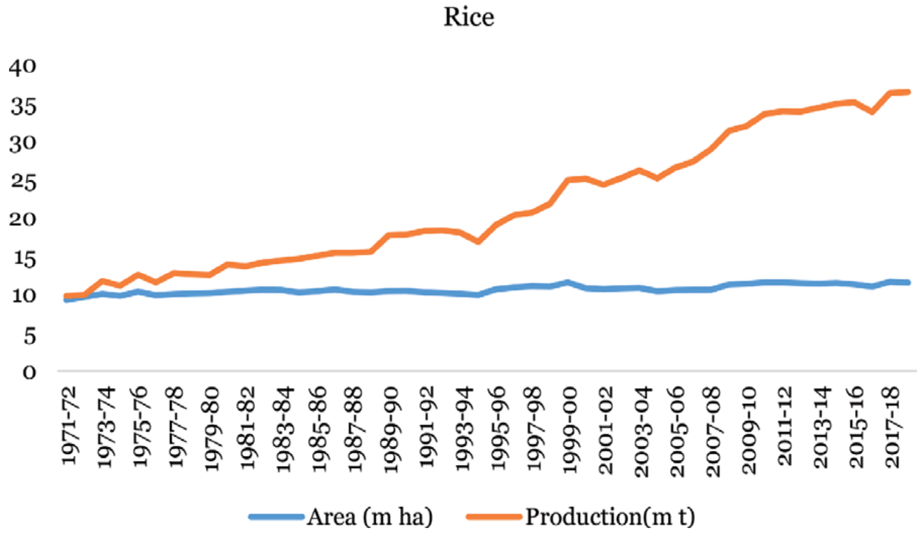

Figure 1.
Area coverage and production trend of rice. M ha million hectare; m t million metric ton. Source: BBS [4, 10].

Rice (DWR) lands were transformed into irrigated Boro land [9]. In 1971–1972 traditional Aus coverage was 2.95 m ha. More than two-thirds of the Aus area was given up mostly to Boro by 2014–2015. The coverage under Aman has experienced little change since 1971. The trends in area coverage and production under different rice ecotypes are described and discussed in detail in [9]. Recently, researchers of the Bangladesh Rice Research Institute (BRRI) and their collaborators had developed the rice vision leading to 2050 and beyond for Bangladesh [11]. They reported that rice production could reach 47.2 m t, having a surplus of 2.6 m t in 2050 and targeted to be continued thereafter, at the present increment rate of rice production. Several measures were also recommended to achieve the rice vision of Bangladesh leading to 2050 and beyond [11]. Although rice is the component of most of the cropping patterns of Bangladesh, 17 cropping patterns exclusively contained rice crops [7]. Five of them were most dominant among cropping patterns of Bangladesh.

2.1.1 Rice cultivars of Bangladesh

Bangladesh was very rich in rice genetic resources. Name of nearly 12,500 traditional cultivars, those were cultivated in different seasons of Bangladesh, were listed [12]. The International Rice Research Institute (IRRI) Gene Bank contains more than 8,000 traditional rice cultivars collected from Bangladesh. Rice breeders used many of these landraces as donors to develop elite lines that have been used as parents for popular improved rice cultivars grown throughout Asia [13]. The Genetic Resource and Seed Division of Bangladesh Rice Research Institute (BRRI) has collected and conserved more than 8,000 landraces of rice were as long medium, and short-term storage (**Table 4**). Most of the traditional cultivars are out of cultivation due to comparatively low yield, although these have many exceptional qualities e.g., fineness, taste, aroma, etc. Only around eight per cent of the recorded landrace cultivars are still available with the farmers in some fragile pocket areas like saline, drought, deep water area and hilly areas of Bangladesh [13]. In recent years, the cultivation of traditional rice cultivars with exceptional features e.g., long grains, fineness, taste, aroma, etc. is retrieving popularity for a premium price, customer's preferences, national and international demand, etc. Presently, one specialized research institute, the BRRI and a few other organizations like Bangladesh Institute of Nuclear

Cultivar/Line	**Registered in accession**
Indigenous *indica*	
Local landraces	5202
Pure line selection	1030
Exotic *indica* landraces (IRRI, China, USA, Turkey)	790
Exotic/breeding lines	968
Wild Rice of Bangladesh (*Oryza rufipogon*, *O. officinalis*, *O. nivara*, and *O. sativa* f. *spontanea*)	42
Wild rice from IRRI	12
Total	8044

Source: DoE [14].

Table 4.
Rice genetic resources in the BRRI Gene Bank.

Season	**Cultivar**
Aus	Broadcast – BR20, BR21, BR24, BRRI dhan27, BRRI dhan42, BRRI dhan43, BRRI dhan65 and BRRI dhan83.
	Transplant – BR1, BR2, BR3, BR6, BR7, BR8, BR9, BR14, BR16, BR26, BRRI dhan27, BRRI dhan48, BRRI dhan55, BRRI dhan82, BRRI dhan85, BRRI dhan98 and BRRI hybrid dhan7; Iratom 24, Binadhan-19.
Aman	BR3, BR4, BR5, BR10, BR11, BR22, BR23, BR25, BRRI dhan30, BRRI dhan31, BRRI dhan32, BRRI dhan33, BRRI dhan34, BRRI dhan37, BRRI dhan38, BRRI dhan39, BRRI dhan40, BRRI dhan41, BRRI dhan44, BRRI dhan46, BRRI dhan49, BRRI dhan51, BRRI dhan52, BRRI dhan53, BRRI dhan54, BRRI dhan56, BRRI dhan57, BRRI dhan62, BRRI dhan66, BRRI dhan70, BRRI dhan71, BRRI dhan72, BRRI dhan73, BRRI dhan75, BRRI dhan79, BRRI dhan80, BRRI dhan87, BRRI dhan90, BRRI dhan91, BRRI dhan93, BRRI dhan94, BRRI dhan95, BRRI hybrid dhan4 and BRRI hybrid dhan6; Binashail, Binadhan-4, Binadhan-7, Binadhan-11, Binadhan-12, Binadhan-13, Binadhan-15, Binadhan-16, Binadhan-17, Binadhan-19, Binadhan-21, Binadhan-22, Binadhan-23; BAU dhan1, BAU dhan2.
Boro	BR1, BR2, BR3, BR6, BR7, BR8, BR9, BR12, BR14, BR15, BR16, BR17, BR18, BR19, BR26, BRRI dhan28, BRRI dhan29, BRRI dhan35, BRRI dhan36, BRRI dhan45, BRRI dhan47, BRRI dhan50, BRRI dhan55, BRRI dhan58, BRRI dhan59, BRRI dhan60, BRRI dhan61, BRRI dhan63, BRRI dhan64, BRRI dhan67, BRRI dhan68, BRRI dhan69, BRRI dhan74, BRRI dhan81, BRRI dhan84, BRRI dhan86, BRRI dhan88, BRRI dhan89, BRRI dhan92, BRRI dhan96, BRRI dhan97, BRRI dhan99, BRRI dhan100, BRRI hybrid dhan1, BRRI hybrid dhan2, BRRI hybrid dhan3 and BRRI hybrid dhan5; Binadhan-5, Binadhan-6, Binadhan-8, Binadhan-10, Binadhan-14, Binadhan-18, Binadhan-24; BAU dhan3.

Source: BRRI [15]; http://www.bina.gov.bd/; http://www.sca.gov.bd/

Table 5.
Seasonal distribution of modern, both inbred and hybrid, rice cultivars in Bangladesh.

Agriculture (BINA), Bangladesh Agricultural University (BAU), are working on the development of high yielding rice cultivars, both inbred and hybrids, for different seasons (**Table 5**). Seeds of some hybrid cultivars are imported by different organizations and seed companies from different countries.

2.2 Wheat (*Triticum aestivum* L.)

Wheat, one of the first cultivated plants, possesses unique dough-forming properties and is the leading source of plant (cereal) protein in the human diet, having higher protein content (14.4%) compared to other major cereals i.e., maize

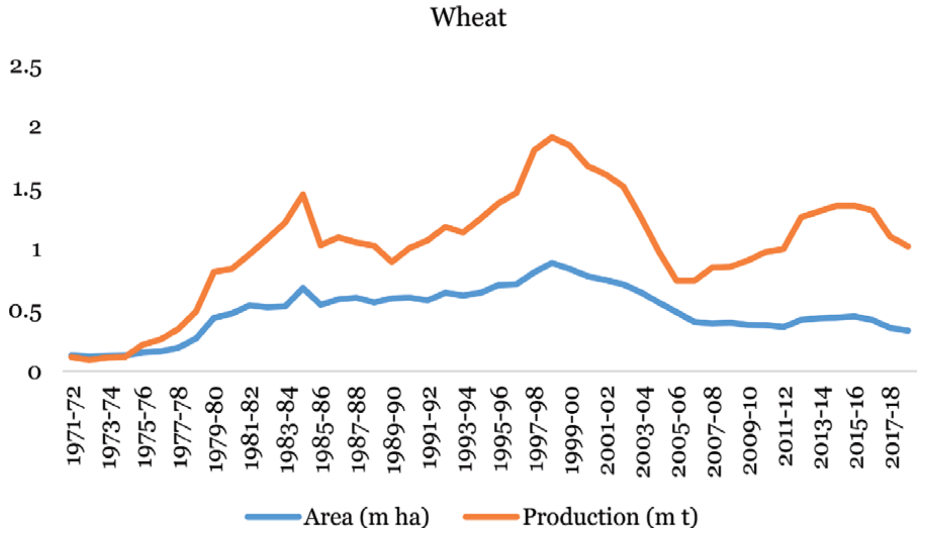

Figure 2.
Area coverage and production trend of wheat. M ha million hectare; m t million metric ton. Source: BBS [4, 10].

(corn) and rice (12.1 and 7.5%, respectively) (**Table 1**). In terms of total production tonnages used for food, it is currently second to rice as the main human food crop and ahead of maize, allowing for more extensive use in animal feeds. The increasing income level and urbanization lead to dietary changes such as switching from traditional rice to wheat and to livestock, poultry, and fish products, which in turn require large amounts of maize for their production [16].

In Bangladesh, it is a crop of Rabi (Winter; Mid-October to Mid-March) season; it requires dry weather, bright sunlight and well-distributed rainfall between 40 and 110 cm for congenial growth. Although wheat has some advantages in its cultivation compared to Boro and other winter crops i.e., less water requirement, echo-friendly, high nutritional value, diversified use, etc.; the command area under wheat cultivation showed a decreasing trend (**Figure 2**). In 1971–1972, the coverage was 0.127 m ha and the total production was only 0.113 m t. Since then the coverage area remarkably went up to 0.88 m ha in 1998–1999 which is almost 7 times in 27 years. However, the area declined to 0.39 m ha in 2006–2007 and maintained more or less the same level up to 2011–2012, thereafter, an increasing trend up to 2015–2016 and the 0.33 m ha in 2018–2019 (**Figure 2**). The total production followed the same trend until 2006–2007 having the highest peak (1.90 m t) in 1998–1999. However, despite a small increase in the coverage area (compared to 1971–1972), the production trend is quite inspiring (**Figure 2**). This might be due to the application of innovative approaches in wheat research and development [9]. A specialized research institute, the Bangladesh Wheat and Maize Research Institute (BWMRI) has very recently been established in 2017. Formerly, it was a (Wheat) Research Centre under the Bangladesh Agricultural Research Institute (BARI). Until today 33 high yielding wheat cultivars are developed by BARI (**Table 6**). Just getting separated from BARI very recently, BWMRI has released three cultivars, *viz*. WMRI Gom 1, WMRI Gom 2 and WMRI Gom 3, within a short period. The Plant Genetic Resources Centre (PGRC), BARI has also collected and conserved 602 wheat accessions in its gene banks and conservatories [18]. Despite the governmental heartfelt afford and policy supports the wheat-growing area declining day by day due to climate change impacts e.g., shorter winter, high temperature, early or late monsoon rainfall, etc. Among the cropping patterns, the number of wheat-based cropping

Serial Number	Name of cultivar	Year of Release	Yield (t ha^{-1})
1	Kalyansona	1968	2.6–3.2
2	Sonora 64	1974	1.6–2.2
3	Norteno 67	1974	2.8–3.2
4	Mexi 65	1974	2.6–3.6
5	Inia 66	1974	2.5–3.0
6	Sonalika	1974	3.0–3.5
7	Tanori 71	1975	2.8–3.2
8	Jupateco 73	1975	3.0–3.2
9	Nuri 70	1975	2.5–3.0
10	Balaka	1979	2.6–3.0
11	Doel	1979	2.5–3.0
12	Pavon 76	1979	3.0–3.6
13	Akbar	1983	3.5–4.5
14	Kanchan	1983	3.5–4.5
15	Ananda (BAW 18)	1983	2.1–3.4
16	Barkat	1983	3.4–3.8
17	Agrahani	1987	3.5–4.0
18	Protiva	1993	3.5–4.5
19	BARI Gom –19 (Sourav)	1998	3.5–4.5
20	BARI Gom –20 (Gourab)	1998	3.6–4.8
21	BARI Gom –21 (Shatabdi)	2000	3.6–5.0
22	BARI Gom –22 (Sufi)	2005	3.6–5.0
23	BARI Gom –23 (Bijoy)	2005	4.3–5.0
24	BARI Gom –24 (Prodip)	2005	4.3–5.1
25	BARI Gom-25	2010	3.6–5.0
26	BARI Gom-26	2010	3.6–5.0
27	BARI Gom –27	2012	4.0–5.4
28	BARI Gom –28	2012	4.0–5.5
29	BARI Gom –29	2014	4.0–5.0
30	BARI Gom –30	2014	4.5–5.5
31	BARI Gom –31	2017	4.5–5.0
32	BARI Gom –32	2017	4.6–5.0
33	BARI Gom –33	2017	4.0–5.0

Source: Azad et al. [17].

Table 6.
Modern wheat cultivars developed by Bangladesh Agricultural Research Institute.

patterns was 27 which occupying 5.36% of the net cropped area [7]. Wheat-Jute-T. Aman was the most dominant cropping pattern followed by Wheat-Fallow-T. Aman with a net cropped area of 1.72% and 1.06%, respectively. Late planting of wheat due to delayed harvesting of T. Aman rice, a longer time for land preparation, formation of plow pan due to puddling in transplanted rice, low organic matter and micro-nutrients deficiency in the soil, unavailability of labourers, hotter winter, late monsoon rain and some cases of excess moisture in the soil, causes a significantly lower yield in every year.

2.3 Maize (*Zea mays* L.)

Maize, indigenous to the Americas and staple in South and Central America and Southern Africa, occupied the second position both in area and production and mainly used for animal and poultry feed industries in Bangladesh. It was an insignificant crop, still reported as a minor cereal in Bangladesh perspective [4], and a little development was observed until 2000. Then the area started increasing progressively while the total production increased quite significantly (**Figure 3**). Maize is now cultivated in both Rabi (Winter; Mid-October to Mid-March) and Kharif-1 (Early monsoon; Mid-March to Mid-July) seasons, and area and production of maize increased considerably. Now, it secured second position pushing wheat to third. In 1971–1972, the coverage and total production were 0.0028 m ha and 0.002 m t respectively which increased to 0.445 m ha to produce 3.569 m t in 2019 (**Figure 3**). The corresponding increments in percentages were *ca*. 16,000 and 180,000, respectively. The phenomenal rise in area and production of maize was mainly due to the favorable environment for higher productivity and a stable and expanding market as feed for the poultry and livestock. From 2010 to 2019, maize production increased at an average annual rate of 11.40%, with some wheat producers switching to the cultivation of maize [9]. Since maize is used mostly as poultry feed, the substitution of the wheat-growing area by maize hampered the supply of staple food for people and has put more pressure on other cereals (i.e., rice) to meet the growing food grain demand. And a substantial increase in wheat import is observed to meet up the local demand [3]. So far, 26 maize cultivars have been released by BARI (**Table 7**); and 92 maize accessions are conserved at the PGRC, BARI [18]. A total of forty-three maize-based cropping patterns were listed for Bangladesh [7]. The most dominant cropping pattern with maize was Maize-Fallow-T. Aman, which occupied 1.18% of the net cropped area. Maize-based cropping patterns altogether covered 3.85% of the net cropped area [7].

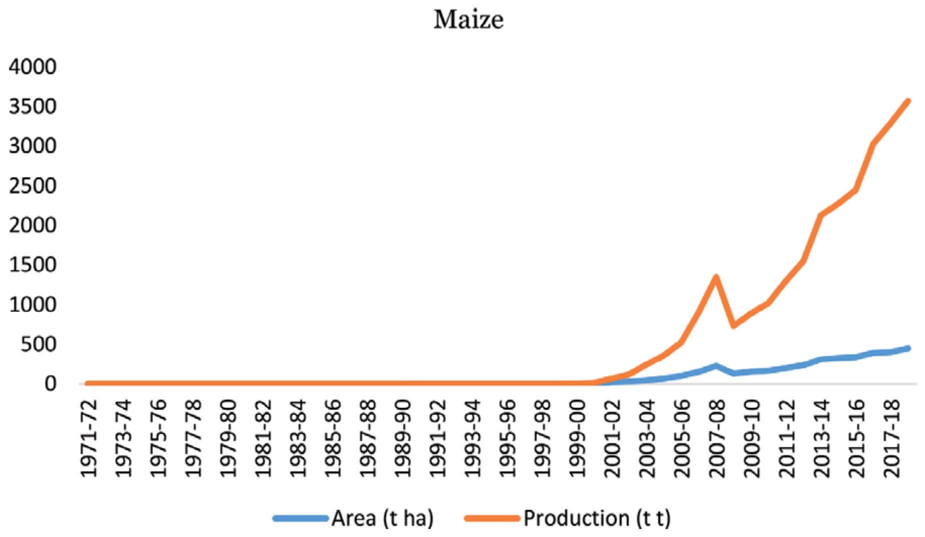

Figure 3.
Area coverage and production trend of maize. Source: BBS [4, 14].

Serial Number	Name of cultivar	Season	Yield (t ha^{-1})
1	Shuvra	Rabi	4.5–5.5
2	Khoibhutta	Rabi, Kharif	Rabi-3.5-4.0, Kharif-2.5-3.5
3	Barnali	Rabi, Kharif	Rabi-5.5-6.0, kharif-4.0-4.5
4	Mohor	Rabi, Kharif	Rabi-5.0-5.5, Kharif-3.5-4.5
5	BARI Maize-5	Rabi, Kharif	Rabi-6.5-7.5, Kharif-5.0-6.0
6	BARI Maize-6	Rabi, Kharif	Rabi-6.5-7.5, Kharif-5.0-6.0
7	BARI Maize-7	Rabi, Kharif	Rabi-6.5-7.5, Kharif-5.0-6.0
8	BARI Sweet Corn-1	Rabi	10.5
9	BARI Baby Corn-1	Rabi	1.27–1.30
10	BARI Hybrid Maize-1	Rabi, Kharif	Rabi-7.5-8.5, Kharif-6.5-7.0
11	BARI Hybrid Maize-2	Rabi, Kharif	Rabi-9.0-9.5, Kharif-7.0-7.5
12	BARI Hybrid Maize-3	Rabi, Kharif	Rabi- 10-10.5, Kharif-7.0-7.5
13	BARI Hybrid Maize-4	Rabi, Kharif	Rabi- 9.0-9.5, Kharif-7-7.5
14	BARI Hybrid Maize-5	Rabi, Kharif	Rabi- 9-10, Kharif-7.0-7.5
15	BARI Hybrid Maize-6	Rabi, Kharif	Rabi- 9.0-9.5, Kharif-7-7.5
16	BARI Hybrid Maize-7	Rabi, Kharif	Rabi- 10.0-11.0, Kharif-7-7.5
17	BARI Hybrid Maize-8	Rabi, Kharif	Rabi- 10.0-11.5, Kharif-7-7.5
18	BARI Hybrid Maize-9	Rabi, Kharif	Rabi- 11.5-12.5
19	BARI Hybrid Maize-10	Rabi, Kharif	Rabi- 10.0-11.5
20	BARI Hybrid Maize-11	Rabi, Kharif	Rabi- 10.5-11.5
21	BARI Hybrid Maize-12	Rabi	10.0–11.1
22	BARI Hybrid Maize-13	Rabi	8.1–8.9
23	BARI Hybrid Maize-14	Rabi, Kharif	Rabi- 10.84, Kharif-10.52
24	BARI Hybrid Maize-15	Rabi, Kharif	Rabi- 12.75, Kharif-12.07
25	BARI Hybrid Maize-16	Rabi	11.57
26	BARI Hybrid Maize-17	—	—

Source: Azad et al. [17]; http://www.bwmri.gov.bd/

Table 7.
Modern maize cultivars developed by Bangladesh Agricultural Research Institute.

3. Minor cereals

3.1 Barley (Bangla: Jab; *Hordeum vulgare* L.)

Barley, one of the oldest cereal crops, ranked fourth among grains behind maize, rice, and wheat. It is widely grown in marginally productive soils across the world points to the high adaptability of the genus *Hordeum* to edaphic stresses [19]. In Bangladesh, barley is a minor cereal crop grown in the small area of two Upazilas (sub-district), *viz*. Chowhali and Tarash, of Sirajganj district [20]. In 1971–1972, the coverage and total productions were only 28,700 ha and 21,300 t, respectively which decreased to 297 ha and produced 244 t in 2018 (**Figure 4**). The BARI has released 9 barley cultivars (**Table 8**), and 54 accessions of barley germplasm are also conserved at the PGRC [18]. The only barley-based cropping

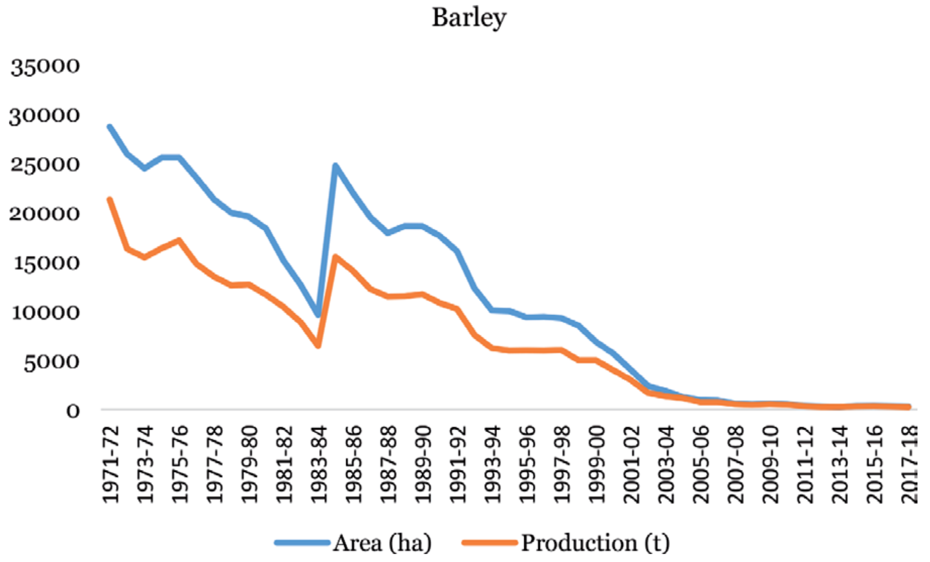

Figure 4.
Area coverage and production trend of barley. T ha thousand hectare; t t thousand metric ton. Source: FAOSTAT 2020 http://www.fao.org/faostat/en/#data/QC.

Serial Number	Name of cultivar	Year of Release	Yield (t ha^{-1})
1.	BARI Barley-1	1994	2.2–2.5
2.	BARI Barley-2	1994	2.0–3.0
3.	BARI Barley-3	2001	2.2–2.5
4.	BARI Barley-4	2001	1.75–2.0
5.	BARI Barley-5	2005	2.5–3.0
6.	BARI Barley-6	2005	2.5–2.75
7.	BARI Barley-7	2015	2.0 = 2.5
8.	BARI Barley-8	2018	2.2–2.51
9.	BARI Barley-9	2018	2.2

Source: Azad et al. [17].

Table 8.
Modern barley cultivars developed by Bangladesh Agricultural Research Institute.

pattern in Bangladesh was Barley—Fallow—Fallow, which occupied 0.0002% of the net cropped area [7].

3.2 Sorghum (Bangla: Jowar; *Sorghum bicolor* (L.) Moench)

Sorghum, one of the most drought-resistant crops that originated in equatorial Africa, grown for grain, fodder, fiber and/or biofuel, is the world's fifth-most important cereal crop after rice, wheat, maize, and barley with 57.89 m t of annual global production in 2019 <http://www.fao.org/faostat/en/#data/QC>. In 1971–1972, the coverage and total productions were 1032 ha and 745 t, respectively which decreased to only 73 ha and produced 87 t in 2018 (**Figure 5**). The only recommended sorghum cultivar available in Bangladesh is BARI Jowar-1, the PGRC (BARI) has collected and conserved 268 sorghum accessions [21].

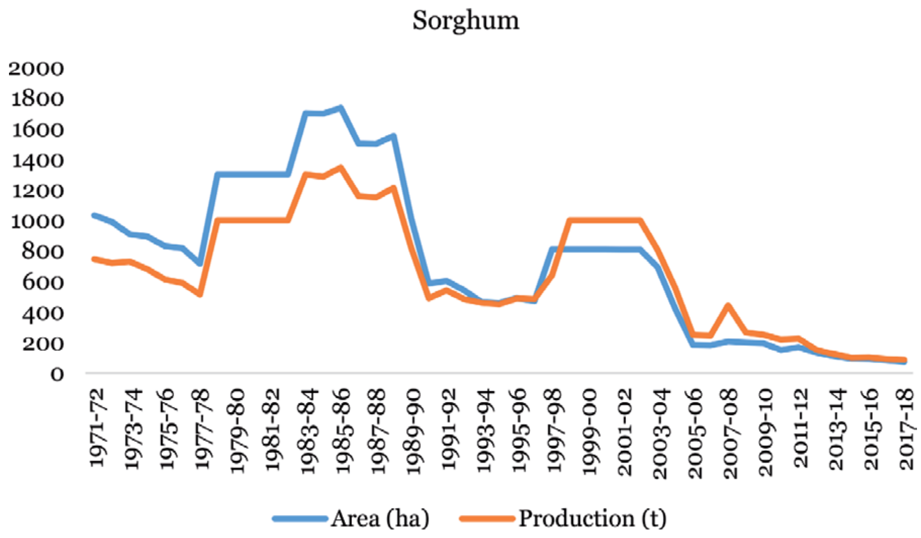

Figure 5.
Area coverage and production trend of sorghum. Source: FAOSTAT 2020 http://www.fao.org/faostat/en/#data/QC.

3.3 Pearl millet (Bangla: Bajra; *Pennisetum glaucum* (L.) R.Br.)

Pearl millet, one of the earliest domesticated millets [2], is well-adapted to poor, droughty, and infertile soils and is, therefore, a vital subsistence crop in countries surrounding the Sahara Desert and in western Africa where soils are tough and rainfall is low <www.plantsoftheworldonline.org/taxon/urn:lsid:ipni.org:names:77105978-1>. In 2007–8, the coverage and total production of pearl millet

Year	Pearl millet		Proso- and Foxtail-millet		Other Cereals		Binnidana	
	Area (ha)	Production (t)	Area (ha)	Production (t)	Area (ha)	Production (t)	Area (ha)	Production (t)
2007–2008	26.72	35	1770.44	1466	8110.12	5048		
2008–2009	26.72	35	1251.01	1100	2618.62	1697		
2009–2010	24.29	40	1214.57	1000	2024.29	2000		
2010–2011	64.78	100	1214.57	1000	2429.15	2000		
2011–2012	60.73	80	1214.57	1000	1619.43	1000		
2012–2013	56.68	80	1214.57	1000	275.30	180		
2013–2014	40.48	380	1214.57	2000	238.87	160		
2014–2015	36.44	50	1214.57	7000	12.14	90		
2015–2016	36.03	48	1214.57	1000	404.86	200		
2016–2017	30.77	40	1214.57	1000	404.86	485		
2017–2018	28.74	38	809.72	1000	—	—		
2018–2019	—	—	809.72	1000	—	—	225.10	5

Source: BBS [4, 22, 23].

Table 9.
Area coverage and production trend of some minor cereals.

in Bangladesh were only 26.72 ha and 35 t, respectively which increased to 28.7 ha and produced 38 t in 2018 (**Table 9**). However, it went completely out of cultivation in the subsequent year [4]. Only two accessions of pearl millet germplasm are conserved at the PGRC, BARI [18].

3.4 Proso millet (Bangla: Cheena; *Panicum miliaceum* L.) and foxtail millet (Bangla: Kaon; *Setaria italica* (L.) P. Beauvois)

Proso millet is rich in protein, minerals, vitamins, and micronutrients; it is gluten-free and therefore, ideal for the gluten intolerant people. The nutritive parameters of proso millet are comparable to or better than common cereals [24]. Under drought and poor soil conditions, it also gives a better yield compared to all other crops, where there is a probability of complete failure of other grain crops [25]. Foxtail millet is an underutilized, drought-tolerant crop that stands to become much more important in a potentially much warmer and dryer future environment [26]. In 2007–8, the coverage and total productions were only 1770.44 ha and 1466 t, respectively which decreased to 809.72 ha and produced 1000 t in 2019 (**Table 9**). The only cultivar of Cheena, Tushar, and four cultivars of Kaon, *viz*. Titas, BARI Kaon-2, BARI Kaon-3 and BARI Kaon-4, are released by BARI [19]. One hundred ninety-seven proso millet accessions and 515 foxtail millet accessions are also conserved at BARI [18]. Two proso millet-based cropping patterns, *viz*. Millet (Cheena) – Fallow–Fallow and Millet (Cheena) – Jute–Fallow, occupied 0.018% of the net cropped area [7]. The proso millet and foxtail millet were grown in small patches especially the char land areas in Bogura and Rangpur regions of the country [20, 27]. A recent study shows that the cultivation of proso and foxtail millets is expanding in north, north-west, central parts (in the vicinity of mighty rivers *viz*. Padma/Ganges, Brahmaputra, Jamuna and Meghna) and hilly regions of the country and provide grain yield 400–1500 kg ha^{-1} (Biswas and Biswas, unpublished data).

3.5 Other cereals (finger millet, ditch millet, rye, oat, triticale, pseudo-cereal buckwheat, quinoa, etc.)

Finger millet and ditch millet are grown on a very limited area in the districts of Kushtia and Rajshahi; others are cultivated all over Bangladesh with little inputs in poor and marginal lands including the river beds [28]. Oats and rye are extremely nutritious, with a higher fat content than most cereals and an excellent grade of dietary fiber. In 2007–8, the coverage and total productions were only 8110.12 ha and 5048 t, respectively which decreased to 404.86 ha and produced 485 t in 2017 (**Table 9**). Moreover, on cultivation data/information was available for subsequent years [4], perhaps went to out of cultivation also. A new cereal crop "*Binnidana*" was cultivated in 225.10 ha of land and produced 5 t grains in 2018–2019 [4]. A few accessions of other minor cereals germplasms *viz*. 5 accessions each of Buckwheat and Triticale, 2 accessions of Teff and 1 accession of Oat, are also conserved at the PGRC, BARI [18].

4. Constrains

Cereal (in fact rice) agriculture is synonymous with Bangladesh agriculture that plays a key role in food security and livelihood. Only 92 cropping pattern out of existing 316 was identified as an exclusive non-rice area which occupied less than 9 per cent of the net cropped area of Bangladesh [7]. The cereal agriculture, and agriculture in Bangladesh as a whole, is facing serious natural and man-made hitches that deserve special attention to this sector. The arable land is decreasing at an alarming rate (0.1% $yr.^{-1}$) due to urbanization, roads and highways, infrastructure development, etc., severe degradation of natural resources like soil, water, climate, etc., the recurrent occurrence of devastating flood and drought, and the looming threat of salinity increment in the coastal region. Further in Bangladesh condition, the global climate change and related adverse effects on agriculture are rendering the worst impacts in temperature rise, abnormal rainfalls, sea-level rise, frequency of cyclone and storm surges, the encroachment of more saline areas, aggravation of drought problem and reduction in the availability of surface and groundwater [29]. There is a substantial extent of degradation of agricultural lands caused by soil erosion (1.70 m ha), river erosion (1.70 m ha), soil fertility decline (8.00 m ha), depletion of soil organic matter (7.50 m ha), waterlogging (0.70 m ha), soil salinity (0.84 m ha), pan formation (2.82 m ha), acidification (0.06 m ha) and deforestation (0.30 m ha) [30]. Some other soil-related constraints to cereal crop production are heavy consistency, poor structure, high osmotic pressure or drought, both physical and physiological, causing a reduction in the ability of plants to absorb water and nutrients, etc. The soil health scenario becomes worsen due to imbalanced fertilization and unplanned increase in mono-crop based cropping intensity and thus, the quality agricultural land is getting scanty. A survey reported that 2% of arable land belongs to a very good type, 34% good, 39% moderate, 16% poor, and 9% very poor [30].

The quality and timely supply of agricultural inputs are other constrain for cereal crop cultivation in Bangladesh. For instance, about 18% of the entire seed requirement of the country can only be met from certified and truthfully labeled seeds of Government and private sources, and the remaining 82% comes from the seed storage of farmers' own. There are serious problems in the quality of seeds supplied by public, private, and farmers themselves [30]. The scarcity of irrigation water (and its resources) is added to another constrain for sustainable cereal production in Bangladesh and the world as well. For example, an increase in Boro growing area in Bangladesh to 6 m ha by 2050 will increase the irrigation demand to *ca*. 40 k m^3 from the current demand of *ca*. 31 k m^3; global warming may further aggravate the demand by about 3% for dry climate change scenarios [31]. Groundwater is the primary source of irrigation and supplies about 80% of the water requirement of the total irrigated area of the country [16]. There is non-regulated and excessive use of groundwater and limited effort to augment surface water. Moreover, water use efficiency is also poor at the farm level. The over-use of groundwater is most evident in a small sub-region known as the Barind Tract; this increased demand will further deplete the groundwater resources. The quality of irrigation water also comes forward as another constrain for agricultural productivity in Bangladesh because of water pollution due to the presence of arsenic, heavy metals, salts, agrochemicals, industrial wastes, etc. A countrywide campaign is, therefore, required to conserve water and use it judiciously and institute a proper land use planning system. Mandatory rainwater harvesting and water use efficiency deserve higher priority.

5. Challenges

Bangladesh, one of the highest densely populated country in the world, endures the 8th largest world population (*ca*. 164 m) which has been estimated to increase 186 and 202 m by the years 2030 and 2050, respectively [32]. One of the major challenges of cereal agriculture in Bangladesh is to produce more food, to feed this ever-increasing population. Other major challenges of cereal (crop) agriculture are to raising productivity and profitability, retaining sustainability, increasing resource-use efficiency, conserving natural resources and increasing land and water productivity, improving product quality and developing marketable production, improving post-harvest management, meeting demands for diversification and commercialization of agriculture [6]. The other emerging challenges include shrinkage of agricultural land every year due to urbanization, infrastructure development, roads, etc. The land quality is also deteriorating due to soil fertility degradation (e.g., nutrient imbalance, low organic matter, etc.), soil erosion, soil and water pollution, and increased soil salinity.

Due to climate change, sea-level rise will cause inundation of about 16% of total cropped area, displace 10% of the population, increased salinity in the coastal zone and reduce crop yields, ultimately causing loss of 2 m t of crop harvest [29]. Global warming will cause cyclones and storm surges in high frequency and volume. Due to river erosion and storm surges, moderate to severe erosion will occur in flood plains and char lands. Out of 2.85 m ha, about 1.00 m ha in the coast is affected by different degrees of salinity which will continue to increase due to climate change. About 2.32 m ha and 1.2 m ha of net cropped area are respectively severely and moderately drought-affected and the problem will further aggravate. Moreover, about 1.32 m ha and 5.05 m ha of the net cropped area are, respectively severely and moderately flood-prone that seriously hamper crop production [29]. Besides, reduced availability of surface and groundwater in the dry season due to excessive extraction of groundwater for irrigation purposes is coming up as a serious problem. The development of water-saving techniques in agriculture is a critical issue. The inadequate facilities and programs for the production and distribution of quality seeds and other inputs to the farmers are the main reason for low productivity; there is a wide yield gap between demonstration and farmers' field yield. For example, the current yield gaps between demonstration and farmers' yield for Aus, T. Aman and Boro are 2.74, 4.89 and 4.08 t ha^{-1}, respectively [29]. Thus, the challenge is to reduce the current yield gap for cereal production enhancement. The farmers' knowledge-gap in adopting modern agricultural technologies also leads to low productivity. Further, the yield ceiling of modern cultivars needs to be improved by developing super cultivars. Low quality and adulterated agricultural inputs *viz*. fertilizers and pesticides, marketed by unscrupulous traders and absence of farm gate price support for the producers are a few of several other challenges that exist in the cereal agriculture and crop subsector as well. The low level of mechanization serves as a huge impediment towards cereal production, which in turns, results in a high cost of production for these crops. The creation of adequate institutional development in the areas with poor infrastructure, research funds and facilities, and skilled manpower for the adoption of innovative agro-technologies is also an emerging challenge in the agricultural sector.

6. Prospects

Although Bangladesh faces huge constrains and challenges in achieving food and nutritional security due to its high population, diet changes, and limited room for expanding cropland and cropping intensity, Bangladesh will remain self-sufficient in rice at least to 2050 at the present rate of technological, in both cultivar and management, advancement and population growth [16]. The Intergovernmental Panel on Climate Change estimates, on contrary, reported that the rice production in Bangladesh could decline by 8 per cent and wheat by 32 per cent due to higher temperatures and changing rainfall patterns by 2050 [33]. For achieving food and nutritional security in the coming days, the following actions may be taken to increase cereal grains yield (per unit area) and production –

i. Minimize the yield gap by (i) increasing actual farmers' yield corresponding to current yield potential (Yp) levels by improving the crop management practices, *viz*. improved seed, soil, water, nutrient, pest and disease management, and (ii) maintaining or increasing the rates of progress of Yp by either adopting modern plant breeding and molecular techniques [34].

ii. Develop new cultivars with greater yield potentials and stress tolerance.

iii. Replacement of current low yielding cultivars with and other recently released high yielding hybrid, short-duration and fast-growing, drought and salt resistant cultivars. The expanded availability of modern rice and other cereal crops cultivar(s) could endure climate change impacts without yield penalties [16].

iv. New climate-smart agriculture/farming technologies e.g., climate-resilient (modern) cultivars for stress-tolerance, profitable location-specific cropping patterns, conservation agriculture, innovative cultural management to minimize yield gap, mechanization, etc., to be developed to grow four crops in a year (in the same piece of land) including three rice crops, and to bring unfavorable agro-ecosystem under productive sustainable agricultural practices.

v. A decrease in the dependence on groundwater by increasing surface water use for irrigation purposes, and replacing rice with wheat or other crops that use less water. Sustainable groundwater use in some areas combined with the use of more surface water (through rubber dam, sluice gate, flash gate and dug well) and moving some production to other less intensively cultivated areas will help meet this challenge. For example, barley is a stress-tolerant and saline adaptive crop [35]. Barley is best suitable as a Rabi (Winter; Mid-October to Mid-March) crop to cope with the saline-prone south coastal region of Bangladesh.

vi. Millets *viz*. pearl millet, foxtail millet, and proso millet, are short duration crops better adapted to dry and infertile soils with a certain degree of soil acidity and alkalinity, stress due to moisture and temperature, soils texture from heavy to sandy infertile soils, and less susceptible to disease and insect pests [36]. As climate change continues to affect the weather and rainfall patterns, the thermophilic characteristics of millets offer the advantage for subsistence farming and are likely to become an increasingly important crop for the future, especially in dry and/or char land areas.

vii. Stress-tolerant minor cereal cultivars generally possess poor yield potential; the development of high yielding cultivars would be a climate-resilient technology to secure food and nutritional security in the changing climate.

viii. Skill development of farmers, extension workers and researchers through appropriate training programmes.

ix. Promote farmer's rights through documenting farmer's indigenous innovations, farmer's creativity under plat variety and farmers' right protection act and establish a database for indigenous technologies owned and practised by the rural farming community [37].

x. Overall, the GAP (good agricultural practices) and SPS (sanitary and phytosanitary) measures will have to be popularized and promoted.

xi. Value addition to cereal grains and by-products ensures the nutritional and economic security of farmers and the economic growth of the country as a whole. For example, producing breakfast cereals, multigrain flours, bran oils, syrup, starch, health-foods, animal feed, nutraceutical/pharmaceutical products, substrates for (oyster) mushroom (*Pleurotus* spp.) production, etc.

The major cereal grains, *viz*. rice, wheat, and maize, make up a critical portion of many diets, and cereal-based foods are a major source of energy, protein, B vitamins and minerals for the world population. However, these possess a lower concentration of mineral elements (micro and macro-nutrients) which caused the hidden hunger due to micronutrients deficiency [38]. The inclusion of mineral nutrient-rich minor cereals in the everyday diet might also be helpful to meet the mineral requirements and to fight against the related problems.

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Author details

Abul Khayer Mohammad Golam Sarwar[1]* and Jiban Krishna Biswas[2]

1 Laboratory of Plant Systematics, Department of Crop Botany, Bangladesh Agricultural University, Mymensingh, Bangladesh

2 Former Director General, Bangladesh Rice Research Institute, Gazipur, Bangladesh

*Address all correspondence to: drsarwar@bau.edu.bd

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Chapter 3

Breeding Maize for Food and Nutritional Security

Ajaz A. Lone, Zahoor A. Dar, Audil Gull, Asima Gazal, Sabina Naseer, Mudasir H. Khan, Ashraf Ahangar and Asif M. Iqbal

Abstract

Maize occupies an important position in the world economy, and serves as an important source of food and feed. Together with rice and wheat, it provides at least 30 percent of the food calories to more than 4.5 billion people in 94 developing countries. Maize production is constrained by a wide range of biotic and abiotic stresses that keep afflicting maize production and productivity causing serious yield losses which bring yield levels below the potential levels. New innovations and trends in the areas of genomics, bioinformatics, and phenomics are enabling breeders with innovative tools, resources and technologies to breed superior resilient cultivars having the ability to resist the vagaries of climate and insect pest attacks. Maize has high nutritional value but is deficient in two amino acids *viz.* Lysine and Tryptophan. The various micronutrients present in maize are not sufficient to meet the nutritive demands of consumers, however the development of maize hybrids and composites with modifying nutritive value have proven to be good to meet the demands of consumers. Quality protein maize (QPM) developed by breeders have higher concentrations of lysine and tryptophan as compared to normal maize. Genetic level improvement has resulted in significant genetic gain, leading to increase in maize yield mainly on farmer's fields. Molecular tools when collaborated with conventional and traditional methodologies help in accelerating these improvement programs and are expected to enhance genetic gains and impact on marginal farmer's field. Genomic tools enable genetic dissections of complex QTL traits and promote an understanding of the physiological basis of key agronomic and stress adaptive and resistance traits. Marker-aided selection and genome-wide selection schemes are being implemented to accelerate genetic gain relating to yield, resilience, and nutritional quality. Efforts are being done worldwide by plant breeders to develop hybrids and composites of maize with high nutritive value to feed the people in future.

Keywords: food, maize, molecular breeding, Nutritional security, stress

1. Introduction

Maize or corn (*Zea mays* L.) belonging to Gramineae family is grown all over the globe as an important annual cereal crop. It is grown as staple food crop in many parts of the world and stands third leading cereal after wheat and rice [1].

Maize is globally called as queen of cereals due to its higher yield potential as compared to rest of the cereals. USA stands first in maize production which alone contributes about 35% of the world's total maize production. In India, the highest producer of maize is Uttar Pradesh, however it is grown in almost all the states in India. U.P, Bihar, Rajasthan, M.P, Punjab, Haryana, Maharashtra, Andhra Pradesh, H.P, W.B, Karnataka, and Jammu and Kashmir are major maize producing states, jointly accounting for over 95% of the national maize production [2]. For animal feed, maize is commonly used. It is commonly processed into different product categories, such as cornmeal, grits, starch, pasta, tortillas, snacks, and cereals for breakfast. Flour of maize is used to make chapatis or flat breads that used to be common dishes in a few northern states of India [3]. The phytochemical compounds obtained from maize and their health properties have recently become the main focus of studies due to increasing attention to the development of nutraceuticals. Maize a monoecious plant has differently located male and female flowers. Tassel is the male flower, and silk is the female flower. Tassel develops 2–5 days before silk that makes it protandrous in nature. The cultivated maize has six different types with each one having different characteristics and specific use, (i) Dent corn: Mostly grown in USA, called as soft maize, (ii) Flint corn: Also called hard corn and is mostly grown in India, (iii) Sweet corn: sweet in taste due to both starch and sugar present in it. It is harvest green and fetch fresh to the market, (iv) Pop corn: most popular type of corn for consumption purpose in humans. It has small sized grains with hard endosperm, (v) Flour corn: the starch present in this type is very soft and the corn shrinks on ripening (vi) Waxy corn: this corn has a soft wax-like substance which resembles tapioca starch.

Maize for livestock feed is important both as residue of crops and silage, grain and is used for extraction of oil and starch industrially. The biological value of maize reflects that it is rich source of carbohydrate, protein, iron, vitamin B, and minerals. The fresh green cobs are eaten separately as roasted or boiled or mixed with legumes. The maize plant has economic value in its every part like the grain, leaves, stalk, tassel, and cob to produce different varieties of food and non-food products.

2. Maize: a potential nutritious cerealcrop

The nutrient status of kernels in maize depends on the genotype or genetic background, management of agronomic practices, genotype-environment interaction and handling after the harvest of produce [4]. Most of the micronutrients present in widely used maize are not sufficient enough to meet nutritional demand of consumers, however the concentration of different micronutrients can be increased by developing cultivars with improved neutraceticals due to higher degrees of genetic variations in maize. This process is called biofortification [5]. Additional or complementary crop management and food science innovations may also help to enhance the nutritional effect of diets based on maize [6]. Maize researchers have developed improved nutritionally useful cultivars such as quality protein maize (QPM) rich in lysine and tryprophan [7], biofortified orange maize with provitamin-A carotenoids [8] and high-Zn-enhanced maize [9]. Through conventional breeding, higher levels of lysine and tryptophan, kernel Zn and provitamin- A have been successfully increased in maize. Due to various factors, including the availability of large genetic diversity for the target characteristics, advances in understanding key biochemical pathways for metabolite biosynthesis, analytical tools for screening germplasm for quality characteristics, and the possibilities for understanding key biochemical pathways for metabolite biosynthesis, there are now significant opportunities for more effective development of nutritionally enriched cultivars of both grain and specialty maize [10].

3. Requirements for breeding of maize

Maize is mostly grown as an energetic crop, but the use of various unique varieties is very extensive, such as high-oil maize, high-lysine maize, waxy maize, amylose maize, flint maize, white maize, popcorn and sweet maize. Unique types of traits need special attention in the selection and seed production process, as well as in the commercial production process. While breeding principles are the same for all types of maize, the approach to selection for each particular type is very much different. Due to their characteristics and genetic regulation of these characteristics, specific types of maize need special care in the handling of breeding materials during breeding processes. It is particularly associated with preventing uncontrolled pollination. Specific characteristic assessment procedures, such as estimation of popping volume and flake consistency in popcorn, determination of sugar and harvest maturity in sweet maize, determination of oil in selected samples of high-oil maize varieties, etc., are important to ensure good selection of a certain characteristic. Since the recent past, a large number of high-yielding hybrids of sweet corn, popcorn, high-oil and high-lysine, flint and white maize have been grown. The abundant genetic diversity and technical and technological possibilities required for good selection promote auspicious selection and breeding for these characteristics.

4. QPM: an alternative to normal maize

Quality protein maize (QPM) was developed in the late 1960s [11] and produces 70–100% more lysine and tryptophan than ordinary modern and traditional tropical maize varieties [12]. In addition, QPM nutritional assessment in different locations has demonstrated the consistency of the content of lysine and tryptophan within the recommended range for QPM, considering very diverse types of environmental conditions [13]. In QPM grain, the nutritional content of the protein exceeds that of cow's milk protein. In developing countries, the adoption of QPM will significantly contribute to alleviating malnutrition in maize-based economies [14]. For example, substituting normal maize in stock feeds has been found to be of economic benefit because it needs small amounts or no supplemental protein sources to balance the diet [15]. QPM cultivars may be competitive in productivity with normal maize and should demonstrate stable performance across environments, especially in terms of yield and protein quality characteristics [13]. Combining high yield with high-quality protein content in an elite maize variety has been a great challenge. QPM development faces severe biotic (diseases and pests) and abiotic (drought, heat, low soil pH, low soil nitrogen, etc.) limitations, as with normal maize. Several studies have been performed around the world to alleviate some of these limitations on breeding for QPM resistance to pests and diseases [16] and tolerance to abiotic stresses such as drought, low soil nitrogen, heat stress and combined heat and drought stress [17]. Quite a number of QPM studies have been performed on improving the nutritional performance and disease tolerance of QPM in breeding programs around the world in recent years [18]. The main research emphasis has been on growing the protein content and exploring genetic variability between QPM genotypes and normal endosperm maize varieties. More research, however, needs to be placed on the resistance of QPM varieties to certain abiotic stresses, such as heat stress, dryness and heat stress combinations, and low soil pH. In Africa, malnutrition is a persistent issue, especially in rural areas where poor people depend on staple foods and have limited access to a diverse diet. Bio-fortified crops bred for enhanced nutritional quality may mitigate nutritional deficiencies if adequate quantities are produced and consumed. The positive effect of QPM on the nutritional status of human consumption and animal feed has been shown by several studies in controlled settings [19]. In order to preserve protein content in grain, lysine or tryptophan levels should be continuously monitored during the breeding period, even if the op2op2 genotype is retained. One way to solve the problem of malnutrition in the world is the consumption of QPM varieties, especially for people who are low in resources and cannot afford other sources of protein for their families. QPM may also be used as an additional food for humans (particularly pregnant women, lactating mothers and young children) and for animal feeding. Moreover, for refugees and other people facing nutritional challenges around the world, QPM flour can also be very useful.

5. Breeding approaches for QPM

It was introduced into many breeding programs worldwide after the discovery of the nutritional benefits of the opaque-2 (op2) mutation, with a significant focus on the conversion of normal endosperm populations and inbred lines to op2 versions via a modified backcrossing-cum-recurrent selection process. At CIMMYT, QPM breeding strategies concentrate on pedigree breeding, whereby the best performing inbred lines, complementary in various characteristics, are crossed to create new segregating families. New inbred lines are formed from these segregating families [20].

5.1 Conventional and molecular breeding approaches in QPM

Pixley and Bjarnason [21] reported that the consistency of proteins was very stable across environments, while QPM varieties were less stable in protein content and endosperm modifications. Pfunde and Mutengwa [22] reported that early maturing QPM inbred lines under drought stress could be used in a breeding programme as sources of early maturation, whereas early maturing single crosses could potentially be recommended in drought-prone areas for maize growers. The stability performance of CIMMYT tropical and subtropical elite QPM hybrids across stressed and non-stressed environments was analyzed [13]. In drought conditions with wide variability in grain yield and protein content among genotypes, the stress effect was comparatively large, indicating that the content of tryptophan and lysine is most stable across stressed and non-stressed environments. While drought tolerance screening has largely been performed for QPM varieties for the vegetative to flowering stages of development, very few studies have been done on tolerance to early drought stress at the seedling level. Drought tolerance has often been hated at the seedling stage of development in that it does not offer an indicator of a genotype's yielding ability under drought stress. Clearly, therefore, the correlation parameters that could relate early drought response to late drought stress tolerance need to be further investigated.

Henry *et al.* [23] studied the molecular structure of the opaque-2 gene and found that the molecular diversity in the transcriptional activator op2 was very high relative to that of other maize transcription factors. Multiple genes have been identified to regulate the quality of amino acids. In order to monitor the levels of a protein synthesis factor associated with lysine levels, at least three loci were involved and these were mapped on chromosomes 2, 4 and 7 [24]. Via marker-assisted backcross breeding, two QPM lines (CML 180 and CML 170) were selected as donors for introgression of the op2 allele into regular maize inbreds (CM 212 and CM 145) because the crosses between the donor QPM lines and non-QPM lines showed a 41% increase in tryptophan and a 30% increase in lysine over the original hybrid lines [23]. Therefore, modified marker-assisted back cross breeding is a potential way to produce QPM variants of standard maize inbreds with suitable endosperm features that can be combined to create QPM hybrids. Using inter-simple sequence repeat (ISSR) and random amplified polymorphic DNA (RAPD) markers. Nkongolo *et al.* [25] studied the degree of genetic variation and relatedness among and within QPM and non-QPM varieties. The findings showed that the genetic difference between QPM and non-QPM varieties and within them was high, while the genetic gap among them was minimal, giving the possibility of developing improved QPM hybrids. The use of molecular markers in QPM breeding programs shortens the selection process, making it more effective across environments during the production of enhanced genotypes. It is important to remember that it is considered that the latest generation of markers such as SNPs is comparatively more efficient and cheaper than older models (SSR, RAPD).

In CIMMYT, several QPM populations, inbreds, hybrids and pools were developed through conventional conversion breeding methods that could adapt to subtropical and tropical environments and are widely used in the production of QPM cultivars in several countries in Africa, Asia, and Latin America [26]. Two measures are involved in marker-assisted introgression using backcross breeding: (1) foreground selection: targeting gene by marker, and (2) background selection: targeting uniformly distributed markers for recurrent parental genome (RPG) recovery across the genome [27]. This is an effective way to transfer particular gene(s) to an otherwise superior variety or parental lines. By foreground selection, the detection of the gene of interest becomes accurate, while background selection accelerates the rate of RPG recovery with two backcrosses [28]. Simple access to accurate gene-based or linked markers based on PCR has made MAS an effective alternative. Microsatellite or Simple Sequence Repeat (SSR) markers are often the choice for their low cost, simplicity and effectiveness among the various types of DNA sequence-based markers available. Codominant, stable, hypervariable, abundant and evenly distributed SSR markers are distributed throughout plant genomes [29]. Several thousand SSRs in maize are mapped and accessible in the public domain. The availability of sufficient linked SSRs has provided a promising choice for marker-assisted introgression of o16 to further enhance the nutritional quality attributes of grain, in particular lysine and tryptophan in endosperm protein. In this context, associated SSRs, umc1141 and umc1149, were successfully used for introgression or pyramidization of o16 alone in the genetic context of o2. The improvement of the quality of proteins (tryptophan and lysine) by o16 over normal maize is comparable to the QPM genotypes based on o2 [30]. At Guizhou Institute of Upland Food Crops, Guizhou Academy of Agricultural Sciences, China, Marker Assisted Selection (MAS) was used to improve parental lines and derived hybrids by pyramiding o2 and o16 in maize adapted to temperate regions. A half-fold increase in lysine content has been reported among pyramid progenies of o2 and o16 [31].

6. Lysine: potential source for food security

Due to breeding of modern maize hybrids for higher yields at the cost of protein, the grain composition has inadvertently trended to higher starch content [32]. In addition, as corn grain protein is deficient in some amino acids that are nutritionally important, this decline in the amount of grain protein has further decreased the grain's nutritional quality. Increasing the nutritional quality of maize grain protein, particularly by increasing the content of essential amino acids, such as lysine and tryptophan, is one approach to addressing this issue.

With regard to the nutritional needs of monogastric animals, the most restrictive amino acid in corn grain is lysine. Improving the content of lysine is therefore a primary goal for improving the quality of maize grain. Maize protein's low nutritional content is mainly affected by the amino acid composition of endosperm proteins. Corn protein has a 2.7 percent lysine content, which is slightly below the FAO recommendation for human nutrition. While the germ protein in the whole grain has a sufficient lysine content (5.4%), this is diluted by the far more abundant endosperm proteins, which have an average lysine content of only about 1.9%. This is because 60–70% of endosperm protein is made up of zeins that contain little to no residues of lysine [33]. Likewise, the lack of residues of tryptophan in zein proteins is the explanation for the low content of corn protein in tryptophan. Changing the profile of the grain protein through approaches such as zein reduction and lysine-rich protein expression could therefore significantly boost the amino acid balance. Alternatively, by elevating the free lysine level in the kernel, the lysine content of the grain could be increased.

There is overwhelming evidence available showing QPM's nutritional dominance over standard maize. Different QPM feeding studies have been performed where under-nourished children given QPM as the only source of protein showed the same growth as those given modified cow milk formula in the diet [34]. Independent research in various countries reported a 12 percent rise in weight in children eating QPM over traditional maize [35]. A study conducted in Guatemala found that the nutritional value of o2 maize is 90% of milk protein compared to 40% of regular maize in young children [11]. QPM has other nutritional advantages, i.e. a stronger leucine/isoleucine ratio and greater niacin availability, with a double increase in tryptophan and lysine and a doubling of biologically functional protein [36]. Even though QPM and normal maize have the same niacin levels, the low leucine content in QPM helps to release more tryptophan for niacin biosynthesis. Thus, pellagra is substantially reduced by QPM [26].

Several animal feed experiments were also performed to test QPM's nutritional benefits and biological superiority. It was first seen in rats where a threefold increase in growth rate was observed when fed a 90% QPM diet. Rats fed with the QPM diet weighed more and were thicker, longer, denser and stronger than ordinary maize diets [37]. The nutritional benefits of QPM have also been systematically carried out in pigs. In pigs raised on QPM, the weight gain was doubled compared to those feeding on only standard corn [38]. Pigs fed with a QPM diet alone with supplements of vitamins and minerals increased twice the rate of normal maize fed by pigs [39].

7. Provitamin-a-biofortified maize (PVABM): future food

One of PVABM's benefits is that it is cheaper than other vitamin A supplements [40]. There is a lower production cost in subsequent years after the crops have been bred and grown, given the necessary storage conditions. In addition, there is no need for additional fortification or vitamin modifications in people's diets once maize has been produced at the farm level [41]. Staple crops, such as maize, are used in rural communities to prepare various meals, so changes in nutrients can stabilize the nutrient composition within them [42]. Under smallholder farming systems, biofortification targets staple crops [43]. To improve the acceptability and accessibility of vitamin A at the household level, various maize products can be developed through PVABM. In rural communities, where maize is used for various goods, the production of PVABM can boost the local economy by people selling snacks, and can improve food security by allowing different meals to be eaten at different times, resulting in decreased VAD in children. There is no doubt that PVABM will boost the food security status of rural households and alleviate VAD, but the willingness of smallholder farmers to embrace PVABM and the acceptability of these products by consumers is a challenge before it can be integrated into smallholder farming systems. Yellow maize is commonly confused with orange maize by rural populations, which could be a major challenge given the perceptions surrounding yellow maize. Across the African continent including South Africa, PVABM has drawn attention from researchers in various fields [44]. In rural areas, where the target groups are mostly located, PVABM has the potential to alleviate VAD, hidden hunger, and boost food security. In order to fix VAD, the carotenoid content in PVABM is essential.

7.1 Carotenoids in PVABM

In the form of provitamin A, maize grain produces various forms of carotenoids [45] and are present in yellow and orange maize. The carotenoid pigments present in yellow and orange maize result from xanthophyll and carotenes, and are responsible for the endosperm color (yellow or orange). In PVABM, the most abundant carotenoids have been described as β-carotene and β-cryptoxanthin, while alpha-carotene is present in smaller capacities. The amount of carotenoids increases with the change in color [46]. Dark orange maize has higher carotenoid levels than other colored maize, but orange and dark orange maize are still not available to farmers and consumers.

8. Genomics-assisted breeding

Genomics-assisted breeding (GAB) for crop improvement initiates with identification of genomic markers linked with QTL or gene(s) related to the target trait and then the application in the breeding platform. Various GAB strategies have been used in crop improvement, including marker- assisted backcrossing (MAB), marker-assisted recurrent selection (MARS), and genomic selection (GS). Recently, speed breeding is included to the list.

8.1 Marker-assisted backcrossing and recurrent selection

Marker-assisted backcrossing (MABC) is the introgression of a genomic region (QTL or locus or gene) contributing the desired trait from a donor genotype into a breeding line or elite cultivar without linkage drag through back- crossing after multiple generations. The resultant product of MABC contains the whole genome of an elite parent with the genetic loci or QTL or gene(s) contributing to the desired phenotype from the donor parent [47]. Quantity of molecular marker used, the strength of marker association with the phenotype, undesirable linkage drags, and size of the population used for each generation of back- crossing determines the efficiency of MABC. This method has been used extensively to generate superior lines of varieties for biotic and abiotic stress tolerance. The marker-assisted recurrent selection (MARS) was introduced to counter the inefficiency of MABC in transferring multiple QTLs regulating complex traits like yield or broad-spectrum disease resistance. MARS involves the detection and selection of large QTLs or multiple genomic regions controlling complex agronomic traits within a single or across the populations and their pyramiding in a single genotype [48]. This approach makes use of the F_2 population and is most effective for cross-pollinating species. In disparity with MABC, favorable alleles may be contributed by both the parents, and the selected improved genotype becomes the chimera of their parents. The superior allele enrichment involves the phenotypic and marker effect for desired traits in the F_2 population, followed by two or multiple cycles of marker-assisted selection [49]. In the past few years, the Hyderabad situated International Maize and Wheat Improvement Center (CIMMYT) has made significant headway in the development of drought-tolerant maize inbred lines through MARS approach in their Asia Maize Drought Tolerance (AMDROUT) project.

8.2 Genomic selection and speed breeding

Genomic selection (GS) or genome-wide selection (GWS) employs large-scale DNA markers throughout the genome for developing superior germplasm lines. The genomic selection approach has the potential to express multiple QTLs/ genes which are widely distributed throughout the genome. Vigorous phenotyping is not necessary to develop a breeding population, and subsequent offspring selection is based on genotypic predictions, which combines both the genomic and pedigree data for several generations of the breeding cycle [50]. The sum of the information index with a combined effect of genome wide molecular markers called the Genomic estimated breeding value (GEBV), is the basis of recurrent selection [51]. High- density molecular markers where each QTLs is in linkage disequilibrium with a marker is necessary prerequisites for precise GEBV, and thus, for GWS. The success of GS mainly depends on the quantity and diversity of the training population (breeding lines selected for the GWS programme). The reduced number of selection events has decreased the time and cost of breeding. While breeding crops and releasing cultivars for farmers, time is a critical factor as normally it takes 3–7 years for crossing experiments, followed by long evaluation for yield, diseases and quality, and varietal release. Therefore, the approach of modulating day-light and duration for increasing the life cycle, term ‘speed breeding’, has been introduced. It shortens the breeding cycle by accelerating crop generation in glass- houses and growth chambers by providing controlled rapid growth-promoting conditions [52]. By balancing factors like photoperiod, humidity, temperature, and others we may achieve six generations per year for crops like wheat, barley, canola and chickpea [53]. Also, in the glass-house, these crops undergo only three generations in a year [53]. Early anthesis in plants was reported grown under speed breeding with fully viable mature seeds with unaffected yield between speed breeding and normal photoperiod conditions in almost all crops [52]. This programme accelerates the generations in mapping population as compared to the duration of MABC/ MARS/GWS, and accelerate the progression towards homozygosity. It has been used in all major crops (annual or biannual), and even in woody shrubs or perennial crops. Reduction of juvenile phase from 5 years to 10 months in apple and 7 to 2 years in chestnut are some of the example of the application of accelerated breeding cycle in perennial crops [54]. Rana et al., [55] has combined marker-assisted selection with speed breeding for developing salt-tolerant rice lines. Jighly et al., [56] coupled Genomic Selection with speed breeding to enhance genetic gains in allogamous plants for example tall fescue. The approach named Speed GS is gaining popularity among breeders for achieving higher genetic gain per cycle, especially for traits with low heritability.

9. Biotechnological interventions

Genetically modified (GM) or transgenic crops have modified genomes achieved through several genetic engineering techniques. Conventional plant breeding is time-consuming and enables the transfer of genetic information from closely related species, genetic engineering facilitates gene transfer across barriers from any source. With the help of established protocol for introducing gene into host species plus a rigorous selection method is needed for greater success. *Agrobacterium tumefaciens*-mediated genetic transformation is among the most reliable approaches being used for achieving stable transgenic lines. Other techniques, like particle bombardment (biolistics), sonication, and electroporation, are used for transient expression of the foreign DNA. As of now 525 transgenics in 32 crops have been commercialized, of which *Zea mays* holds the highest rank. Transgenic crop cultivation enhances agricultural productivity to about 22% leading to a 68% increase in profits [57].

10. Candidate genes

Gene cloning and isolation facilities help introgression of a target gene from any genome which is transformed into any other genome for its desired expression. Most historical example is of expression of 'Cry' gene of *Bacillus thuringiensis* for overcoming he hazards of pests and insects attack. DREB (dehydration responsive element binding) protein-encoding genes are a class of genes that are frequently isolated from one species and expressed in another for enhancing the resilience and tolerance towards different abiotic and biotic stresses. By the advancement of NGS technologies, expression and overexpression strategies also assist in illuminating the gene function, which is otherwise a useful task in covering huge genes amounts. The functional gene characterization is required to utilize the gene in developing stress tolerant plant cultivars by overexpression of candidate genes for example, T-DNA insertion lines of *Arabidopsis thaliana* have helped in understanding gene function. Overexpression of *ARGOS* genes in maize (*Zea mays* L.) leads to a reduction in sensitivity to ethylene, and transgenic plants show enhanced drought resistance as well as higher grain yield in well-watered as well as drought conditions [58]. Genome sequence information has facilitated the large-scale gene analysis, characterizing genes for their agronomic, physiochemical and other traits, genomic composition, promoter elements and expression profiling of genes towards stress which have helped in identifying candidate genes.

11. RNA interference

Also known as co-suppression, post-transcriptional gene silencing (PTGS). It is a biological process where RNA molecules inhibit gene expression or translation, by neutralizing targeted mRNA molecules. Its discovery is a breakthrough in the history of biology, and it has been widely utilized in functional genomics, reverse genetics and crop improvement [59]. RNAi pathway involves the generation of small RNAs (sRNA), which include short interfering RNA (siRNA), microRNA (miRNA), transacting siRNA (ta-siRNA) and natural-antisense siRNA (NAT-siRNA) which mediate silencing or epigenetic regulation of their target genes. Transformative RNAi has been used in several modified forms like artificial miRNA (amiRNA), artificial ta-siRNA (ata-siRNA), hairpin RNA (hpRNA), intrinsic direct repeat, 3′-untranslated region (UTR) direct repeat, terminator-less, single-stranded promoter antisense and intron delivered promoter hpRNA [60]. Significant examples include alteration of plant architecture, improvement in β-carotene and lycopene content in fruits, good shelf life and nutritional improvement like low gluten content, reduction in toxic terpenoids, biotic stress resistance against viruses, fungi, bacteria and nematodes; and abiotic stress resistance [61]. The non-transformative RNAi technique, spray induced gene silencing (SIGS), has gained widespread acceptance as it is easy to use and has low cost of application. It works by spraying plants with double-stranded (ds) RNA/siRNA and has been successfully utilized for controlling insect pests [62]. Plants sprayed with dsRNA/ sRNA targeting *DCL1* and *DCL2* of *Botrytis cinerea* showed a significant reduction in gray mold disease symptoms showing the use of this technology for the developing eco-friendly bio-fungicides. Transgenic plants are still not accepted in many countries and it is estimated that about 130 million dollars exhausted on commercializing a transgenic crop [59]. SIGS being a non-GMO approach has enormous prospective for crop improvement.

12. Gene and genome editing

Genome editing (also called gene editing) is a group of technologies that give scientists the ability to change an organism's DNA. These technologies allow genetic material to be added, removed, or altered at particular locations in the genome. Several approaches to genome editing have been developed. A recent one is known as CRISPR-Cas9, which is short for clustered regularly interspaced short palindromic repeats and CRISPR-associated protein 9. The CRISPR-Cas9 system has generated a lot of excitement in the scientific community because it is faster, cheaper, more accurate, and more efficient than other existing genome editing methods. Precise genome editing started when for the first time, it was seen that DNA binding zinc finger domains along with Fok1 endonuclease domains could cleave DNA at defined regions and act as site-specific nucleases (SSNs) [63]. Further research led to the development of transcription activator-like effector nucleases (TALENs) and clustered regularly interspaced short palindrome repeats (CRISPR)/CRISPR-associated protein 9 (Cas9). Meganu- cleases (MegaN) recognize long DNA sequences that are greater than 14 nucleotides (nt) up to 40 nt. Since they have endonuclease activity, they produce double-stranded (ds) breaks at the recognition sites [64]. CRISPR/Cas9 is easy to use and is therefore, more popular compared to other genome editing technologies [65]. CRISPR/Cas9 comprises of two components: a single-guide RNA that is customizable and Cas9 endonuclease. Protospacer adjacent motif (PAM) (5′NGG3′) is a prerequisite needed for inducing ds breaks at the targeted sites in the genome. The breaks are repaired through either homology directed repair (HoDR) or non-homologous end joining (NHEJ). Since NHEJ is error- prone, repair leads to insertions or deletions at the target site. CRISPR/Cas9 has shown promising results for crop improvement, and for several nutritional traits and biotic and abiotic stress resistance [65].

Technologies like molecular breeding and genetic manipulation help to achieve food security and resilience to various biotic and abiotic stresses. Advances in NGS technology have enabled the incorporation of genomics with various disciplines of crop breeding. Large-scale genomic markers and high-throughput genotyping have accelerated improved cultivar development in terms of cost and resources. Functional and comparative genomics have provided the platform for gene discovery and gene functional characterization. The key gene or genes regulating a molecular pathway are being genetically engineered to breed phenotypically improved crop lines. Conventional approaches together with biotechnological tools aim to increase productivity per plant and minimize yield loss at the farmer's level. The collaborative research investments in both the approaches are indispensable to food security and sustainable crop improvement.

Future thrust areas

- Discovery of trait specific novel genes from maize genomes
- Delivering superior single cross hybrids with diverse genetic base for various segments
- Thoroughly integrating marker assisted selection and doubled haploids in breeding programs
- Spearheading development of public sector events of transgenic maize
- Inventing new generation of ecofriendly and bio safe technologies for maize value chain
- Developing and popularizing high yielding, profitable and ecologically sustainable maize based farming systems
- Precision input management for higher productivity, profitability and environmental sustainability
- Popularizing resource conservation technologies in maize systems

Author details

Ajaz A. Lone*, Zahoor A. Dar, Audil Gull, Asima Gazal, Sabina Naseer,
Mudasir H. Khan, Ashraf Ahangar and Asif M. Iqbal
Sher-e-Kashmir University of Agricultural Sciences and Technology, Kashmir, India

*Address all correspondence to: ajaz999@gmail.com

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Chapter 4

Molecular and Transcriptional Regulation of Seed Development in Cereals: Present Status and Future Prospects

Anuradha Singh, Jyotirmaya Mathan, Amit Yadav,
Aakash K. Goyal and Ashok Chaudhury

Abstract

Cereals are a rich source of vitamins, minerals, carbohydrates, fats, oils and protein, making them the world's most important source of nutrition. The influence of rising global population, as well as the emergence and spread of disease, has the major impact on cereal production. To meet the demand, there is a pressing need to increase cereal production. Optimal seed development is a key agronomical trait that contributes to crop yield. The seed development and maturation is a complex process that includes not only embryo and endosperm development, but also accompanied by huge physiological, biochemical, metabolic, molecular and transcriptional changes. This chapter discusses the growth of cereal seed and highlights the novel biological insights, with a focus on transgenic and new molecular breeding, as well as biotechnological intervention strategies that have improved crop yield in two major cereal crops, primarily wheat and rice, over the last 21 years (2000–2021).

Keywords: Seed development, yield related agronomic trait, genetic, molecular and transcriptome studies

1. Introduction

Cereal seeds are the major source of starch and proteins in staple foods, animal feed, and raw materials for food and fiber-based industries all over the world [1]. Considerable efforts have been made to elucidate the molecular mechanism regulating important agronomic traits in order to improve the cereal seed production. Several agronomic traits, including grain number per spike, spike length, thousand seed weight, seed size and many others, have contributed to grain yield improvement in many cereals plants, with the development of embryo, endosperm and integuments being the most important [2]. As a result, better understanding of the genetic and molecular processes governing seed development is crucial. Here in this book chapter, we provide a comprehensive review on the ontogeny of seed development, followed by genetics, molecular and transcriptional regulation of seed development for improved crop yield.

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2. Developmental process and final structure of cereals seed

Biologically, seed is a mature fertilized ovule that consists primarily three parts: the embryo, endosperm, and seed coat (integuments) [3, 4]. The development of seed begins with double fertilization, in which one of the male gamete fertilizes with haploid egg cell to form an embryo and the other male gamete fertilizes the megagametophyte's diploid central cell to form the triploid nuclear endosperm [5]. The event of seed development, which described below can be divided into three phases: a morphogenesis and cell divisions for endosperm development (0–7 Day post anthesis, DPA), embryo development (7–15 DPA), and maturation (14 to 28 DPA), which includes embryo growth at the expense of endosperm, seed desiccation and storage materials accumulation [6].

2.1 Endosperm development

The nuclear type of endosperm development is the most common in monocot plants, particularly cereals, where initial endosperm nucleus divides repeatedly without cell wall formation, resulting in a characteristic coenocyte-stage endosperm [7, 8]. The morphogenetic event of the early stages of endosperm development was observed in wheat [9] and rice [10, 11]. The first division of the triploid endosperm nucleus, in which the daughter nuclei are separated in the central cell, without cell wall formation in subsequent mitotic divisions, results in a 256 to 512 multinucleate cell (the endosperm coenocyte) [8, 12]. The nuclei enter a 2-day mitotic hiatus, lead to the formation of interzonal phragmoplast, occurs 3 days after pollination. While much information about the regulation of phragmoplast formation and expansion remain unknown, recent evidence suggests that the mitogen-activated protein kinase cascade plays a key role in this process [13]. The development of cellularization in the coenocytic endosperm then begins with the formation of radial microtubule on all nuclear surfaces. Soon after, the microtubules from the adjacent nuclei meet, creating interzones where callose-based wall material is deposited. Further, radial microtubules that encase each nucleus undergo reorganization, anchoring the nuclei to the central cell wall while extending toward the central vacuole in a canopy of microtubules. In cereals, the endosperms become fully cellular during 6 to 8 days after pollination if this process is repeated four to five times [14, 15].

The fully developed cereal endosperm consists of four main cell types: the aleurone layer, transfer cells, starchy endosperm, and cells of the embryo-surrounding region [16]. The former two cells, i.e. Aleurone layer, transfer cells remain alive at the end of cereal seed development, while later two including starchy endosperm, and cells of the embryo-surrounding have undergone programmed cell death (PCD) with characteristic DNA laddering and organelle degradation [17].

The cereal endosperm has attracted attention from researchers because of its economic importance, and much insight has accumulated about the genes underlying the accumulation of storage products such as proteins and starch. Additionally, the endosperm protects the embryo from atmospheric oxygen that eventually leads to the formation of hydroperoxides and cell death [18] and critical cross-talk between abscisic acid (ABA) and gibberellin (GA) regulating seed development, size, dormancy or storage breakdown during germination are also the results of endosperm—embryo interactions [19, 20]. Considerably less is known about the genes that regulate the developmental biology of these cell types, which is the topic of this section. Cell fate specification in cereal endosperm is believed to occur by positional signaling at an early developmental stage [12]. For simplicity, each cell type is described separately below, although cell fate specification occurs simultaneously with the cellularization process described above. How this integration occurs is unknown, but elucidation of the molecular controls for each of the four cell types should lay the foundation for understanding the genetic specification of the entire endosperm body plan.

2.2 Starchy endosperm

Starchy endosperms, which accumulate starch and storage proteins, encoded by transcripts that are expressed differentially in these cells, make up the largest body of cell in the endosperm [21]. There are two types of starchy endosperm present in the cereal crop. The first, and most important, is the inner cells of cell files that remain after endosperm cellularization is complete. The second source of starchy endosperm cells is the inner daughter cells of aleurone cells that divide periclinally. These cells redifferentiate to become starchy endosperm cells and likely are the source of the so-called subaleurone cells found adjacent to the aleurone layer in the starchy endosperm in all cereals. Several collections of mutants such as *dek* (defective kernel) [22], and *Dee-D1* (DEFECTIVE ENDOSPERM-D1) [23], physically located on the long arm of chromosome 1D involved in the genetic control of endosperm development in wheat. The absence of *Dee-D1* in the genome of hexaploid wheat leads to a decrease in the number of grains and thousand grain weights. Similarly, DWARF AND RUNTISH SPIKELET1 (DRUS1) and DRUS2 [24] and EMBRYONIC FLOWER2a (OsEMF2a), a zinc-finger containing component of polycomb repressive complex 2 impaired endosperm development in rice [25].

2.3 Aleurone

The aleurone layer covers the perimeter of the endosperm with the exception of the transfer cell region. Wheat have one layer of aleurone cells, while rice has one to several layers, functions in seed germination by mobilizing starch and storage protein reserves in the starchy endosperm through the production of hydrolases (α-amylase), glucanases, and proteinases after hormone (gibberellic acid) stimulation from the embryo [26]. In the mature grain of cereals, the aleurone layer consists of an estimated 250,000 aleurone cells derived by an estimated 17 rounds of anticlinal divisions. Toward the end of seed maturation, a specialized developmental program confers desiccation tolerance to the aleurone cells, allowing them to survive the maturation process. *Several mutants such as, Crinkly4* (*Cr4*), a receptor like kinase protein [27], *Supernumerary aleurone layer1* (*Sal1*), homolog of the human *Charged vesicular body protein/Chromatin modulating protein1* gene [28], Defective seed5 (des5), bZIP zinc finger transcription factor RISBZ1 and the DOF zinc finger transcription factor RPBF regulate both storage protein biosynthesis and the differentiation of the aleurone [29].

2.4 Transfer cells

Transfer cells develop in the basal endosperm over the main vascular tissue of the maternal plant, where they facilitate solute (mainly of amino acids, sucrose, and monosaccharides), transfer across the plasmalemma between the symplastic (maternal plant) and apoplastic (endosperm) compartments [30]. However, sucrose is not delivered in this form to transfer cell; instead, it is converted into monosaccharide glucose and fructose through the major activity of cell-wall invertase, offering a mechanism for controlling cell division and even cell differentiation in developing kernels [31].

In cereals, the *miniature1 (mn1)* mutant and *GRAIN INCOMPLETE FILLING1* (*GIF1*) which encodes a cell-wall invertase, exclusively expressed in transfer cells, have significant smaller grains, implying that invertase contributes to create a sucrose concentration gradient in the apoplastic gap between the pedicel and the endosperm by hydrolyzing sucrose to glucose and fructose [32, 33]. Furthermore, in developing *mn1* kernels, the abundance of auxin and transcript of YUCCA genes was drastically reduced, implying that sugar level influence auxin level in seed, which in turn regulates specific aspects of seed developments [34].

Several groups of transcripts, for instance, OsPR602 and OsPR9a in rice and Endosperm 1 (*END1*) in barley have been shown to be expressed preferentially in endosperm transfer cells during the early stages of grain filling [35]. Further, an orthologues gene from *Triticum durum* (TdPR60) and *Triticum aestivum* (TaPR60), a small cysteine-rich protein with a hydrophobic signal peptide, predicted to interact with several protein, which are involved in the regulation of regulation of secretion and degradation of signal peptides in other organisms [36].

2.5 The embryo-surrounding region

The embryo-surrounding region (ESR) lines the cavity of the endosperm in which the embryo develops and has been studied most extensively in maize. The exact role of the ESR is unknown, but possible functions include a role in embryo nutrition, the establishment of a physical barrier between the embryo and the endosperm during seed development, and providing a zone for communication between the embryo and the endosperm. The ESR development is under the control of CLAVATA3, a peptide hormone with the conserved domain composed on 12 to 14 amino acids, regulates embryo and endosperm development, cotyledon establishment, and pollen wall formation in Arabidopsis [37], while root and stem development in wheat plants [38].

2.6 Seed coat development

The seed coat (also known as testa) is made up of two structures covering the nucellus [39], while the single integuments ovules can be found in members of certain families. The seed coat provides a mechanical shield protecting the embryo and the endosperm from the environment, but it also regulates phloem unloading of assimilates in growing seeds [40], fluid and gas exchanges with the environment, and seed dormancy and germination [41]. Generally, seed coat development and maturation precede that of filial tissues. In cereals, after an initial phase of cell division during the first two days after flowering (DAF), pericarp differentiation involves cell elongation along the longitudinal axis between 3 and 10 DAF coupled to PCD, and it coincides with the cellularization of the endosperm [42]. PCD in the pericarp may contribute to redistribution of nutrients, relaxation of physical constraints of the maternal tissue to allow inner growth of the filial tissue, and the re-activation, together with PCD in the nucellus and the nucellar projections, of post-phloem transport functions to allow passage of solutes [42]. Crosstalk among embryo, endosperm, and seed coat appears to be complex, but gene networks that coordinate development of these three seed compartments are being elucidated [41, 43].

3. Genetic regulation of seed development for improved yield

Seed yield is a quantitative trait that is influenced by the genetics and environment. It is usually determined by plant height, number of primary and secondary branches, plant density, date of flowering, number of panicle per plant, number of seed per panicle, seed size including seed length and seed width, and finally seed weight [44, 45]. The last two traits, i.e. seed number and weight, were found to be trade-off [46], but recent evidence from studies in wheat suggests that increasing one yield component without reducing the other is possible [47]. The grain number has maintained higher phenotypic plasticity throughout domestication events when compared with grain weight, which enables crop to effectively respond to resource availability during early reproductive stages [46]. The critical periods for determination of grain number and weight are also generally considered separated by the developmental stage of anthesis (flowering), although Ugarte et al. [48] found that grain weight was affected by pre-anthesis environmental conditions in other cereals including wheat. The genotype × environment interaction for grain yield is likely strong in winter wheat [49] and rice [50].

To explore candidate genes underlying yield related traits, GWAS were conducted to identify underlying loci for each phenotype. Association mapping has been used to successfully discover significant marker–trait associations in cereal crops including rice [51–54] and wheat [55–58]. A large number of well-characterized QTLs such as GW2, GIF1, qSW5, GS3 and qGL7 in rice [59–63] and more than 40 QTL including TaGW2 [64–66] associated with kernel morphological traits such as kernel length, kernel width, kernel thickness, kernel length/width ratio, kernel length/thickness ratio, kernel width/thickness ratio, flag leaf width, length and area have been recently identified and mapped in wheat [67–70]. A variety of QTLs regulating seed size have been identified in other crop species, but they have yet to be functionally characterized [47, 71]. The additional genetic approaches on key agronomic traits for improved yield are presented in **Table 1**.

Cereal Crop	Traits	Gene/QTL/Markers	References
Wheat	1000-grain weight	qTgw.nwipb-4DS; qTgw.nwipb-6AL	[72]
		wsnp_Ex_c32624_41252144, BS00021705_51	[73]
	Grain yield, TKW, spike weight, spike length	rs36032, rs4772, rs736, rs50187, rs59282	[74]
	Heading and flowering dates	RAC875_c41145_189, Excalibur_c60164_137, RAC875_c50422_299, Ppd-D1, Vrn-B1, Vrn-D1	[75]
	Grain weight and grain number	TaGW2-6A, Rht-B1, Vrn-D1a	[56]
Rice	Yield associated loci	qSN8 and qSPB1	[76]
	Heading date	Ghd8/OsHAP3H	[77, 78]
	Panicle trait	DENSE AND ERECT PANICLE 1 (DEP1)	[79, 80]
	Grain length and yield	OsLG3	[81]
	Heading date and yield potential	Hd1, Ghd7, and DTH7	[82]
	Grain yield and quality traits	qPH1/OsGA20ox2, qDF3/OsMADS50, PL, QDg1, qGW-5b, grb7–2, qGL3/GS3, Amy6/Wx gene and OsNAS3	[83]

Table 1.
Genetic approaches for improved seed yield in cereal crops.

4. Molecular regulation of seed development for improved yield

Overexpression, targeted mutagenesis and mutation breeding are examples of recent biotechnological strategies that have been used to manage seed development for increased yield. The activity of ADP-glucose pyrophosphorylase (AGPase), starch synthase (SS) includes granule bound starch synthase (GBSS) and soluble starch synthase (SSS), starch branching enzyme (SBE), debranching enzyme (DBE), and amylase catalyzes the synthesis and accumulation of endosperm storage components, primarily starch, in cereal crops [84–87]. AGPase catalyzes the first committed step of starch biosynthesis, namely the conversion of Glc-1-P and ATP to ADP-glucose and pyrophosphate (PPi). Through a new –1,4-linkage, the glucose moiety from ADP-glucose is transferred to the non-reducing end of the -glucan receptor of existing chains of amylose and amylopectin [86]. In addition few transporters and transcription factors also play an important role in the regulation of the biosynthesis of starch [88, 89]. Modification of these enzymes has the drastic effect on different aspects of starch such as composition, and finally grain yield and summarized in **Table 2**.

Gene	Crop	Mechanism	Function/phenotypes	References
AGPase	Wheat/Rice	Over expression +Chemical mutagens	Enhanced ADP-glucose pyrophosphorylase activity in endosperm and seed yield	[90–93]
GBSS	Wheat	Combining null alleles	Low amylose and lower yield	[94]
SSI,SSII/SSIII	Wheat/Rice	RNAi silencing	Reduced SSI enzyme activity with novel starch structure	[95]
SSSIIIa	Rice	Chemical mutagen	High amylose	[96]
BEIIa	Wheat/ Durum wheat	RNAi silencing TILLING	High amylose and resistant starch	[97–99]
ISA	Rice	RNAi silencing	Alters the physicochemical properties of starch	[100]
AMY	Wheat	Overexpression	Increased the soluble carbohydrate (mainly sucrose) in dry seed	[101]
OsbZIP58	Rice	Overexpression	Regulates the expression of starch biosynthetic genes in rice endosperm	[102]

Table 2.
Molecular approaches for improved seed yield in cereal crops.

5. Transcriptional regulation of seed development for improved yield

In the context of seed development, genotype-specific and stage-dependent temporal shifts in gene expression profile have been reported in the aleurone, embryo and endosperm, and other cell-type of maturing seeds, potentially leading to seed phenotypic differences [103, 104]. Transcriptomic studies in several plant systems has led to the identification of transcriptional programs and regulatory networks underlying molecular functions associated with cellular activities in endosperm [105, 106], starch metabolism [107], seed storage substances and high molecular weight glutenin genes [108–110], grain quality (glycemic index) [111], post-transcriptional regulations occurs at the end of seed development [17] and programming of seed developmental and maturation processes, and elucidation of the underlying functional transitions (**Table 3**) [103].

Cereal Crop	Traits	Transcription factor/gene	References
Wheat	Grain number per spike	*TaTEF-7A*	[112]
	Endosperm specific transcription factor	bHLH (seven tissue-specific bHLH TF clusters were identified according to their expression patterns in endosperm, aleurone, seedlings, heading-stage spikes, flag leaves, shoots and roots).	[113]
	Starch biosynthesis	bZIP (TabZIP 151, TabZIP121, TabZIP69.1, howing moderate negative to moderate positive correlation with GBSSI and SBEIIb, respectively	[89]
	Embryo and endosperm specific transcriptome	Identification of genes underlying macromolecules biosynthesis (starch, protein, lipid, protein translation)	[17]
		ABA mediated transcriptional mechanisms controlling seed maturation	[103]
		Identification of key genes for processing quality	[105]
Rice	Seed germination, grain size and yield	*OsSPMS1* (Spermine Synthase)	[114]
	Fatty acid metabolism	*OsACOT Acyl- CoA thioesterase*	[115]
	Panicle branching	miR156 targeting OsSPL13, OsSPL14 and OsSPL16	[116]
		[117]	
	Seed setting	*LOW SEED SETTING RATE1* (*LSSR1*), regulates the seed setting rate by facilitating rice fertilization.	[118]
	Metabolism of sugars, fatty acids, amino acids, and phytosterols	Mutation on *OsSBEIIb*	[119]
	Transcriptome analysis of colored rice	Flavonoid biosynthetic pathway	[120]
	Accumulation of seed storage substance	NF-YC12	[121]
	Regulation of grain size	OsPIL15, targeting purine permease gene OsPUP7	[122]
	Early seed development	*MADS78* and *MADS79*	[123]
	Plant architecture, longer panicles, more grain number and yield	*OsNAC2*	[124]
	Leaf angle, grain size and seed quality	OsmiR1848 regulating OsCYP51C expression and mediates BR biosynthesis	[125]

Table 3.
Transcriptional approaches for improved seed yield in cereal crops.

In rice, Nie et al. [15], identified 12 classes of endosperm-specific genes, including transcription factor, stress/defense, seed storage protein (SSP), carbohydrate and energy metabolism, seed maturation, protein metabolism, lipid metabolism, transport, cell wall related, hormone related, signal transduction, and one unclassified category. In addition, several cis-regulator elements were found in the promoter region of endosperm-specific expressed genes including, AACA box, ACGT box, GCN4 motif (TGA (G/C) TCA), the prolamin box (P box: AAAG), SKN-1 *cis*-element, RY repeat (CATGCATG) [29], ABA responsive element (ABRE) motif, and transfer cell-specific motif TATCTCTATCT (C/A) from aleurone cell [126]. These elements may play an important role in regulating the temporal and spatial expression genes in endosperm development.

Based on the cis-element, the corresponding transcription factor were also determined. For example, the MYB protein specifically binds to the AACA box, and the GNC4 motif is bounded by transcription factors of the Opaque2-like basic leucine zipper (bZIP) activators (rice RISBZ1), ABRE motif by bZIP transcription factors, the P box by plant-specific DNA binding with one finger (DOF) zinc-finger transcription factors (rice RPBF), and FUSCA3 (FUS3) recognizes the RY repeats [29, 127, 128]. In addition, synergy between RPBF and RISBZ1 has been implicated in mediating the regulatory networks essential for seed development by binding to the GCN4 motif to trans-activate the expression of seed storage proteins in rice [29, 129]. Recently, Grimberg et al. [130] identified an oat endosperm homolog of WRINKLED1 transcription factor (*AsWRI1*), which when expressed under the control of endosperm-specific HMW1Dx5 promoter, causes substantial alterations in carbon allocation in wheat grains, including lower seed weight and a wrinkled seed phenotype.

Polyamines such as putresceine, Spermidine (Spd), and Spermine (Spm) have been implicated in regulation of spikelets postanthesis development [131]. Exogenous Spd and Spm are applied to rice panicles to improve grain filling and grain weight in inferior spikelets [132]. Furthermore, the concentrations of Spd and Spm are related to rice grain size. The *OsSPMS1* gene is involved in the conversion of Spd to Spm, as well as the production of 1-aminocyclopropane-1-carboxylic acid (ACC) and ethylene. Manipulation of the *OsSPMS1* gene has a significant impact on a variety of traits, including plant height, grain size, seed germination, and yield production [133]. More importantly, knockout of *OsSPMS1* increases grain production in a high-yield variety, implying that *OsSPMS1* is a key target gene for rice yield improvement [114].

During plant reproductive growth, cell-to-cell communication via receptor-like kinases (RLKs) regulates a wide range of biological processes. FLORALORGANNUMBER1 (FON1), a potential ortholog of CLAVATA1 (CLV1), interacts with the putative ligand FON2/FON4, a CLV3-related protein, to maintain the inflorescence meristem [134]. The orthologous *Catharanthus roseus* RLK1-like (CrRLK1L) subfamily has a putative carbohydrate binding malectin-like domain and is involved in a variety of biological processes [135], including male–female interactions mediated by the synergid-expressed genes FERONIA (FER), DWARF AND RUNTISH SPIKELET1 (DRUS1), and DRUS2. These two proteins, which operate as essential regulators, control reproductive growth in rice in a redundant manner by suppressing cell death and influencing sugar use [24]. Evidence has been presented in my laboratory which demonstrates that endogenous repression of *CCA1* gene under the control of *TOC1* promoter resulted in improved morphological traits: increased number of tillers/panicle, thousand seed weight, seed size; whereas, over-expression leads to diminution in morphological traits: decreased number of tillers/panicle, thousand seed weight, seed size as compared to the wild type in *Agrobacterium*-mediated genetically transformed T1 and T2 transgenic progeny plants of rice variety Taipei 309 [136].

6. Conclusions and future prospects

Seed development is a multi-step process that includes the production of an embryo and endosperm. The synthesis and accumulation of storage product in the seed is controlled by genetics, molecular and transcriptional regulation, which is critical for maximum yield. For instance, seed yield improvement can be achieved directly under genetic control by selecting and applying markers, QTL linked to agronomic and physiological traits, and improved grain yield potential. Intensive use of molecular tools such as Genetic engineering, Gene silencing and Genome editing together with increase access of system biology tools would provide researchers to gain a better understanding of the pathways and genes that control seed size and number, resulting greater yield as shown in **Figure 1**. It is envisaged that a more detailed investigation is urgently required for understanding of metabolic control of seed development, storage, product partitioning, epigenetic controls, phytohormone regulation and their interplay would appear to be sufficient to solve global food security challenges faced by the world in future.

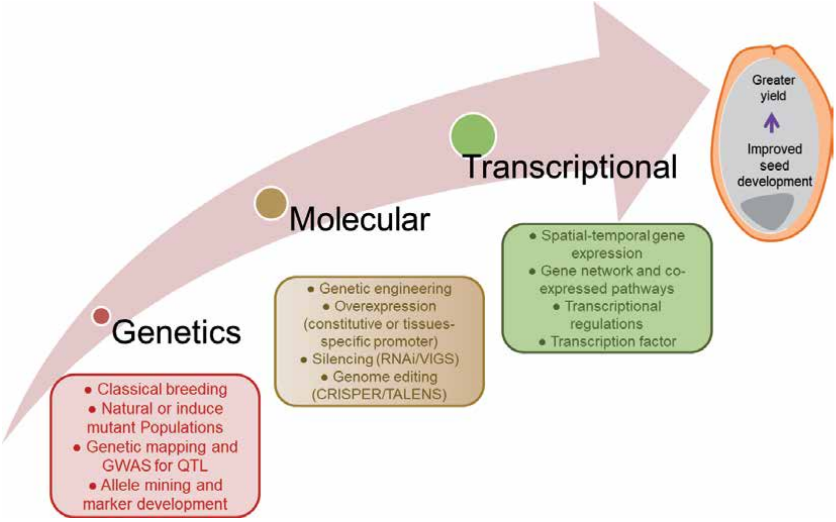

Figure 1.
Summary of Molecular Approaches for Regulation of Seed Development through Plant Breeding & Genetics, Genetic Engineering & Genome Editing and at Transcriptional Levels.

Author details

Anuradha Singh[1,5], Jyotirmaya Mathan[2], Amit Yadav[3], Aakash K. Goyal[4]
and Ashok Chaudhury[5]*

1 Department of Plant, Soil and Microbial Sciences, Michigan State University, East Lansing, USA

2 National Institute of Plant Genome Research, Aruna Asaf Ali Marg, New Delhi, India

3 Zuckerberg Institute for Water Research (ZIWR), Ben-Gurion University of the Negev, Israel

4 RYAN Cultivation Inc., Nisku, Alberta, Canada

5 Plant Molecular Laboratory, Department of Bio and Nano Technology, Bio and Nano Technology Centre, Guru Jambheshwar University of Science and Technology, Hisar, Haryana, India

*Address all correspondence to: ashokchaudhury@hotmail.com

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Section 2

Nutrition

Chapter 5

Benefits of Barley Grain in Animal and Human Diets

Ana Badea and Champa Wijekoon

Abstract

Barley (*Hordeum vulgare* L) is one of the major cereal grains grown in temperate countries and ranked globally as the fourth largest grain crop. Currently, it is produced in more than 100 countries around the world with a global production of approximatively 159 million tonnes and 51 million hectares in 2019. The production and value-added barley products impact breweries, food processors, feed mills, and livestock operations. Barley grain is used primarily as an energy and protein source in beef cattle diets and as a malt source for alcoholic beverages, especially in the beer industry. Also, barley is used in bread, soups, stews, and health products since the barley grain is rich in several health-boosting components. As such, barley is high in protein, fibre, vitamins and natural bioactive antioxidants such as phenolics and lipids. However the studies of bioactive and nutritional properties of barley and the utilization of the crop as a functional food in animal and human diet is still limited. The work herein provides a review covering world production, end-use and processing, nutritional attributes, and will advocate its potential as a functional food for animal and human health and its role in preventing some chronic diseases.

Keywords: barley, feed, functional ingredients, food, health benefits, malt

1. Introduction

Barley (*Hordeum vulgare* L) was domesticated in approximately 10,000 BC and is considered one of the oldest cultivated grains [1]. While the Fertile Crescent is widely accepted as the center of origin through the years, there were numerous debates, for example, regarding the number of times and locations [2–5] that barley was domesticated, the number of wild barley populations descended from [6, 7] and so on. Relatively recent, comparative genomic analysis of 6,000-year-old barley grains, found in a cave in the Judean Desert, and modern Israeli landraces showed close affinity and supported the previously proposed location, Jordan Valley, as the origin of the domesticated barley [8]. Moreover, the availability of additional barley reference genomes such as those recently reported by [9] may also help elucidate some of these controversies [10].

Currently, barley ranks fourth in both quantities produced and in the area cultivated for cereal crops globally. It was presumably first used as human food but evolved primarily into a feed, malting and brewing grain, in part due to the rise in prominence of wheat and rice [11]. Due to its ability to be cultivated in a wide range of climates, the crop is essential in places in the world where food security is an issue [12]. Moreover, barley has also been used as a principal food source in places where other cereals are more challenging to grow [13].

Barley is classified as spring or winter type, two-row or six-row, hulled or hulless, and malting or feed by end-use (**Figure 1**). Based on grain composition, barley is further classified as normal, waxy or high amylose starch types, high lysine, high beta-glucan, and proanthocyanidin-free types [14]. It has been shown that both genetics and environment could affect the overall metabolite composition of the barley and subsequent malt [15]. For example, [16] demonstrated a direct association between barley genotype and beer flavour, independent of the malt quality traits.

One of the most genetically diverse cereal grains, barley, is also considered a model plant in research allowing advances in plant genetics, plant physiology, plant pathology, plant biochemistry, and plant biotechnology [17]. Genetic diversity provides an ample opportunity to identify and breed barley varieties for specific end-uses for processors.

Barley is used as feed in ruminant, swine, poultry, and aquaculture production. As reported by [18] compared to feed grain corn, besides offering greater protein, barley grain is also richer in methionine, lysine, cysteine, and tryptophan. Moreover, compared to corn, due to its more rapid starch fermentation rate, barley provides a more simultaneous release of energy and nitrogen, consequently improving the microbial nutrient assimilation. The benefits of using fermented barley grain in the diets of broilers were also demonstrated. Fermented barley is

Figure 1.
Examples of different types of barley: two-row (upper left), six-row (upper right), hulled (bottom left) and hulless (bottom right). Source: authors' personal photo collection.

considered a valuable functional ingredient that can improve performance, breast meat quality, and intestinal health of birds [19].

Nowadays, human health and well-being are foremost. Therefore balanced nutrition and diet are receiving more and more attention. In this context, functional foods are much sought. Beyond meeting basic nutrients, these foods also provide additional health benefits by promoting and combating chronic diseases [20]. Thus, barley grain is gaining renewed attention worldwide due to the richness in functional ingredients. In particular, the nutritional composition meets the needs of a diet high in protein, fibre and vitamins, and low in fat and sugar [21]. The increase in the use of barley and malt in processed foods is mainly due to its natural antioxidants and the unique soluble fibre beta-glucan [22]. Barley is rich in groups of bioactive compounds, including phenolics and lipids, that have potential health benefits [23]. The epidemiological studies have shown that long-term consumption of diets rich in barley flour can offer protection against the development of hyperlipidemia, diabetes, and atherosclerosis [24]. The phenolic compounds found in barley, such as cinnamic acid derivatives and benzoic, proanthocyanidins, flavonols, flavanones, and flavones, could have beneficial effects, antioxidative and antitumor, decreasing blood lipids and hypoglycemic, on human health [22, 25]. In addition, the consumption of barley is an important source of macro- and micro-nutrients that is needed in the typical human diet and has beneficial effects against the development of illnesses such as cardiovascular disease, diabetes, and cancer [26].

2. Barley production

Barley is very versatile and has adapted well throughout its evolution. Its high prevalence is likely due to its high adaptability to a variety of climates, including cold and drought, and its adaptability to poor soil conditions compared to wheat. Much of the world's barley is produced in the regions where cereals such as maize and rice cannot grow well [27].

To date, barley is produced by more than 100 countries around the world [28]. In 2019, the global barley production was approximatively equal to 159 million tonnes (M t), after rice (755 M t), wheat (765 M t), and corn (1,148 M t). From 1961 to 2019, the average global production was 142 M t, with the highest production of 178 M t recorded in 1990 (**Figure 2**). In 2019, Europe accounted for more than 60% of the global barley produced, followed by Asia (16%) and North and Central America (9%) (**Figure 3**). Among the European barley producers, the Russian Federation, France, and Germany have exceeded, on average, 10% each for the past ten years. Australia and Canada follow them at 8.9% and 8.4%, respectively (**Table 1**).

United Kingdom of Great Britain and Northern Ireland; Source: prepared based on data from [28].

In 2019, the total area harvested for barley was 51 million hectares (M ha) and ranked fourth after rice (162 M ha), corn (197 M ha) and wheat (216 M ha). Over the past six decades, barley maintained its position in the global top five most cultivated cereal crops, and its harvested area ranged from 50 to 80 M ha, with the highest reached in 1979 at nearly 84 M ha (**Figure 4**).

In 2019, barley yield was 3.1 tonnes per hectares (t/ha) and ranked fourth after wheat (3.5 t/ha), rice (4.7 t/ha), and corn (5.8 t/ha). The average yield of the top cereal crops has been continuously increasing since 1961. During this period, barley yield averaged 1.8 t/ha in the '60s and '70s, 2.2 t/ha in the '80s and '90s, and 2.7 t/ha since the 2000s. In 2016, it broke the 3 t/ha barrier, with the highest yield reached in 2019 at 3.1 t/ha (**Figure 5**).

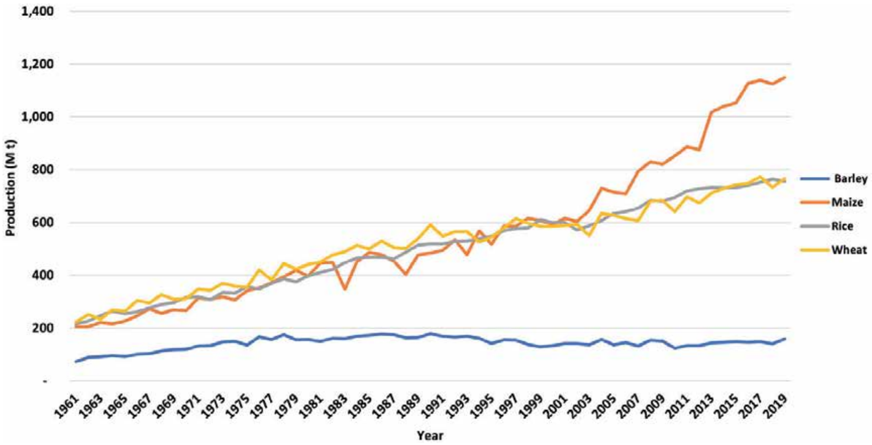
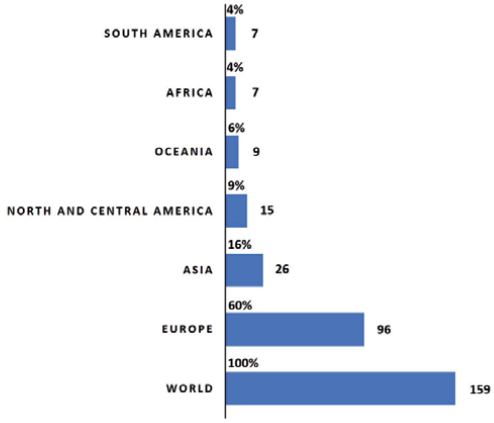


Figure 2.
Global top cereal crops production (M t), 1961–2019. Source: prepared based on data from [28].



EUROPE includes the Russian Federation
OCEANIA includes Australia, New Zealand and South Pacific Islands

Figure 3.
Global barley production (M t) by region, 2019. Source: prepared based on data from [28].

3. End-use and processing of barley grain

Different barley classes often differ in physical and compositional characteristics and accordingly have different processing properties and end-use quality. Overall, worldwide barley has three primary uses: malting, feed, and food (**Figure 6**). In most countries, the majority portion of the barley is used as animal feed, particularly for cattle and pigs, and the use of barley as human food is more limited [13]. Although feed is the main use of barley, in many instances, more value comes from the crop if it is used for malting and production of beverages such as beer and whiskey [12]. However, barley is still considered a major staple food in several regions such as some areas of North Africa and the Near East, in highlands of Central Asia, the Horn of Africa, the Andean countries and the Baltic States, which are characterized by harsh living conditions. In 2016, per capita consumption was reported to be the highest in North Africa, with Morocco at 41 kg/person, Ethiopia and Syria at 15 kg each [30]. By contrast, very little barley is used as human food in developed countries. Overall, in 2016, the global per capita food use of barley was estimated at 1 kg/person compared to 17 kg of maize, 54 kg of rice and 67 kg of wheat. However,

Country	Year										Average
	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	
Russian Federation	8.3	16.9	13.9	15.3	20.4	17.5	17.9	20.6	16.9	20.4	**16.8**
France	10.1	8.7	11.3	10.3	11.7	13.0	10.4	12.0	11.0	13.5	**11.2**
Germany	10.3	8.7	10.3	10.3	11.5	11.6	10.7	10.8	9.5	11.5	**10.5**
Australia	7.8	7.9	8.2	7.4	9.1	8.6	8.9	13.5	9.2	8.8	**8.9**
Canada	7.6	7.8	8.0	10.2	7.1	8.2	8.8	7.8	8.3	10.3	**8.4**
Ukraine	8.4	9.0	6.9	7.5	9.0	8.2	9.4	8.2	7.3	8.9	**8.3**
Spain	8.1	8.2	5.9	10.0	6.9	6.7	9.1	5.7	9.5	7.7	**7.8**
Turkey	7.2	7.6	7.1	7.9	6.3	8.0	6.7	7.1	7.0	7.6	**7.3**
United Kingdom	5.2	5.4	5.5	7.0	6.9	7.3	6.6	7.1	6.5	8.0	**6.6**
Argentina	2.9	4.0	5.1	4.7	2.9	2.9	4.9	3.7	5.0	5.1	**4.1**

Table 1.
Global top barley producers (M t), 2010–2019.

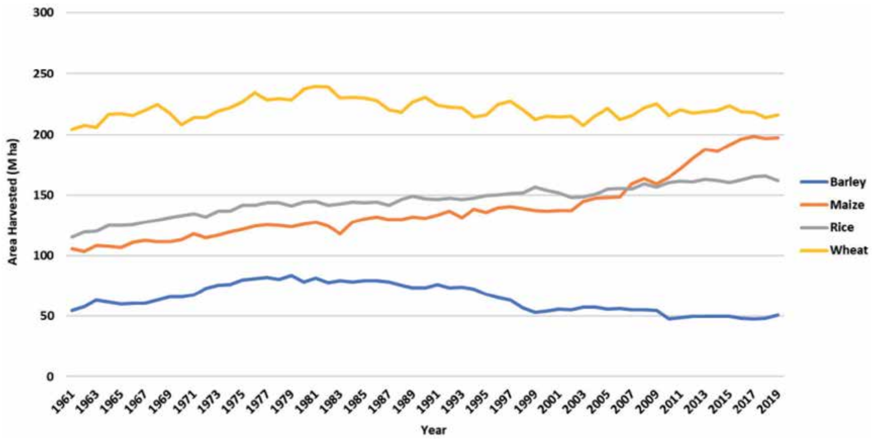


Figure 4.
Global top cereal crops area harvested (M ha), 1961–2019. Source: prepared based on data from [28].

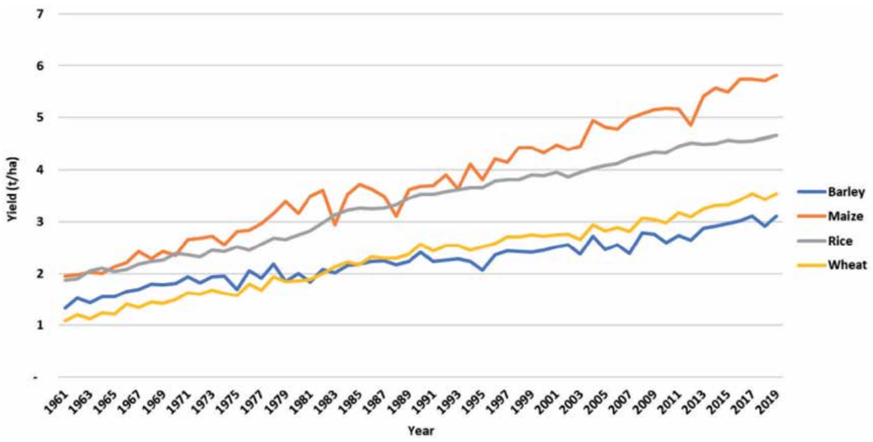


Figure 5.
Global top cereal crops grain yield (t/ha), 1961–2019. Source: prepared based on data from [28].

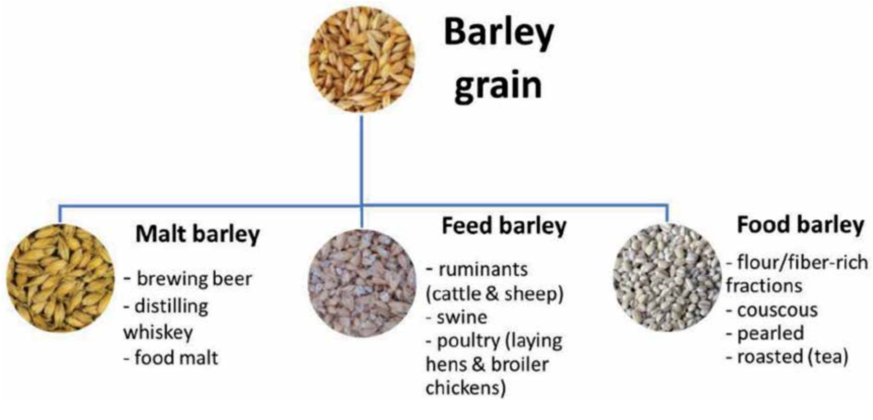


Figure 6.
Main end-uses of barley grain, worldwide. Source: elaborated from [29].

there is renewed interest throughout the world in barley food because of its nutritional value [14]. During the past decade, of the total global barley consumption, about 65% is used as feed, followed by industrial at about 20%, which includes

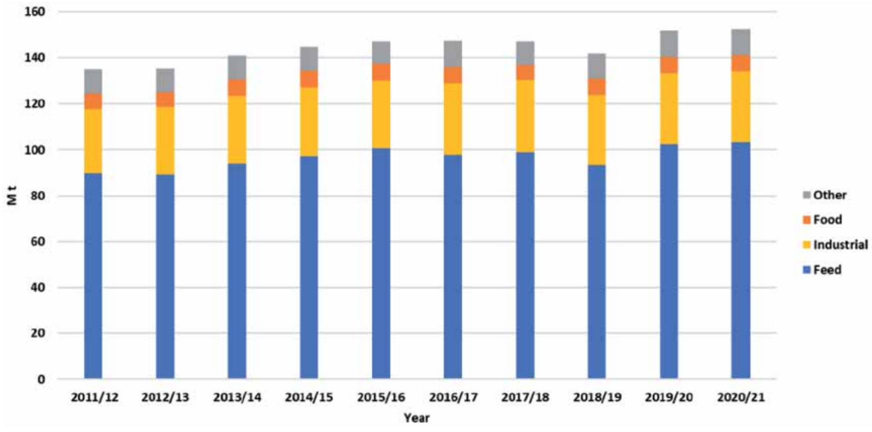


Figure 7.
Global consumption of barley grain by end-uses (M t), 2011–2020. Source: prepared based on data from [31].

malting. A smaller percentage is used for food (5%) as well as some for other uses (7%) (**Figure 7**).

The processing (e.g. rolling, grinding, flaking) improves the digestibility of barley grain. For example, whole barley grain is 15 to 30% less digestible than the same barley grain when dry rolled [32]. Studies showed that the barley starch is readily degradable for ruminants without gelatinization, unlike corn that requires steam-flaking to make starch available by breaking down the protein that surrounds starch granules within the endosperm [33].

After the inedible outer shell has been removed during processing, the barley grain is considered a healthy whole grain. The more commonly available pearled barley is not a whole grain because the fibre-containing bran has been removed [34]. Despite that, pearled barley still has a high beta-glucan content (**Figure 8**). When assessing the content and distribution of beta-glucan of low and high beta-glucan barley genotypes, [36] found that the highest content was in the subaleurone

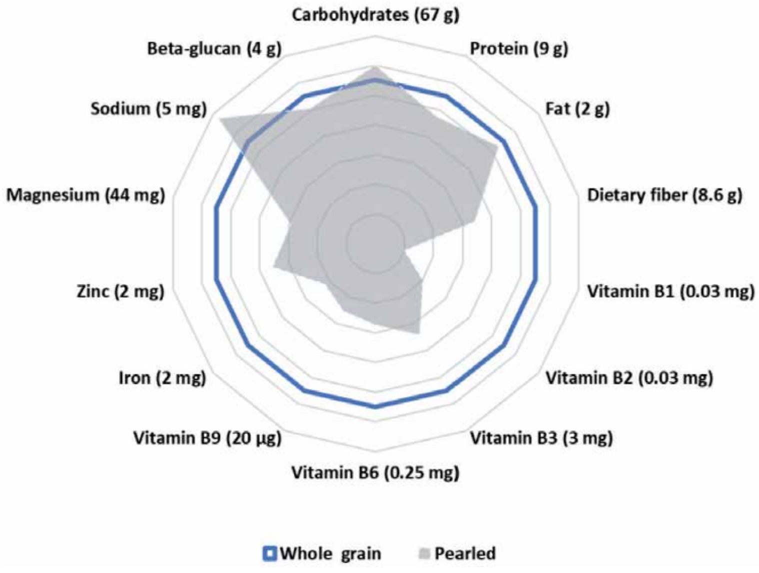


Figure 8.
Nutritional profiles of pearled barley vs. whole grain. Source: prepared based on data from [35].

region, in the case of low beta-glucan barleys, while in the high beta-glucan ones, it was distributed more evenly throughout the endosperm.

A significant high-value use of barley is in producing malt as a raw material for the brewing and distilling industries. In short, the malted barley is barley grains that have been made to germinate and then stopped from further germination by drying. The process comprises five stages: barley grading and cleaning, steeping, germination, kilning and malt cleaning and grading. To obtain 100 kg of malt approximately 120 to 130 kg of screened barley are necessary, depending on grain quality and purity. The average ratio used is 1.267 [37]. The contribution of barley to beer flavour is primarily developed through the malting process, as well as its macro-chemical contribution to brewing [38]. Barley malt provides saccharides, proteins, free amino nitrogen, and enzymes that facilitate fermentation reactions in brewing, and the malt quality traits can influence the flavour of the beer [39].

4. Nutritional attributes of barley grain

The nutrient composition of barley grain varies with the cultivar, environment, and processing [34]. In the last two decades, we have seen a rediscovery of food preparations with barley with a significant increase of use and may be due to recently developed barley varieties that are rich in nutrient composition [39]. The composition and nutritional attributes of barley as food and feed are described below.

4.1 Carbohydrates and fiber

Barley starch content is nearly 20% lower than that of wheat or corn grain [14]. It has been reported that hulled or hulless regular varieties have higher starch contents than hulled or hulless waxy barley grain cultivars. For example, the waxy or regular barley is determined by the composition of amylose to amylopectin levels. Thus, regular barley typically has a ratio of amylose to amylopectin of 1:3, whereas waxy barley contains higher amylopectin levels (up to 100%) [34].

Beta-glucan is one of the non-starch water-soluble fiber in barley grain. The beta-glucan content varies in different barley varieties from 2 and 11% in dry grain [40]. For example, 1.2 to 6.7% in hulled varieties and 4.6 to 7.3% for regular versus waxy barley, and hulless varieties ranging from 2.8 to 7.3% DM (non-waxy) and 4.8 to 16.9% DM (waxy) [34]. The water-insoluble fibre in barley is comprised of lignin and other non-starch polysaccharides, such as cellulose and hemicellulose, that are concentrated in the hull of the grain. The total fibre contents are different between hulled (13.2 to 27.0 vs. 19.6 to 22.6% DM; regular vs. waxy) and hulless (9.4 to 20.2 vs. 12.6 to 33.4% DM, regular vs. waxy) barley varieties concentrated in the endosperm cell walls. It is considered that due to the hull, barley grain provides greater dietary fibre than wheat or corn, and a larger portion of the fibre is in an insoluble form [41].

4.2 Proteins and amino acids

Barley grain protein content is an important quality factor determining grain end-use value [42]. Prolamins are a class of storage proteins that account for up to 70% of the total protein in barley, however, the amino acid composition of prolamins is characterized by high levels of glutamine, proline and low amounts of essential amino acids such as lysine, threonine and tryptophan [43]. A recent study on the comparative proteomics analysis between the six-row and two-row barley cultivars indicated that 20 proteins were differentially abundant between the two cultivars [44]. Variation in the abundances of hordoindoline proteins was one of the key differences between them, and the authors suggested that the type of hordoindoline proteins may contribute to the differences between the seed hardness of these two cultivars.

In a 2018 survey, conducted in Western Canada, where barley plays a prominent role as a source of feed for both ruminants and monogastric farm animals, it was found that the average crude protein content is higher than the average found in corn, rye, and oats [45]. Earlier, [34] also reported that barley has 4% higher protein content than corn grain. Also, [46] investigated the grain protein concentration and harvestable protein under future climate conditions on a large collection of barley accessions and reported that despite the increase in grain protein concentration (5% at elevated temperature and 29% at elevated CO_2), the decrease in grain yield under the predicted future climate conditions resulted in 23% less harvestable protein. However, variation in the reponse of the barley accessions tested was observed and could be exploited.

4.3 Vitamins

Vitamins in barley include B1, B2, B3, E and gamma-aminobutyric acid, which may vary based on the cultivars. For example, it was shown that vitamins B1 and B2 were the most variable within a barley collection from Tibet, China [47]. Vitamin B1 was present as the highest proportion, followed by B2 and E, while B3 was present as the lowest proportion in the collection. The content in gamma-aminobutyric acid was also highly variable. Moreover, it was found that the content of vitamins B1, B2 and C, and proteins increased notably after germination [48].

4.4 Phenolic compounds

Barley is a good source of phenolic compounds, which can be found free as well as bound to fibre [49]. Phenolic compounds in barley include monophenol, phenolic acids, flavonoids and other polyphenols [22]. The flavanols, such as catechin, procyanidins and prodelphinidins, are the main compounds in the free phenolic fraction of barley grain, while phenolic acids, such as ferulic, coumaric and vanillic acids, are major constituents of the bound phenolic fraction [49–51]. However, ferulic acid is the most abundant hydroxycinnamic acid found in barley and accounts for up to 90% of total polyphenols [52]. Flavanols, anthocyanins, and proanthocyanidins (polymers of flavonoids) are the major types of flavonoids found in barley grains (**Table 2**). Flavanols are located in the pericarp of barley grains, while anthocyanins are water-soluble vacuolar pigments mainly present in the pericarp or the aleurone layers of barley grain, causing purple or blue hues of kernel colour [61]. Anthocyanins in barley include cyanidin, cyanidin 3-glucoside, delphinidin, pelargonidin, pelargonidin glycosides, and petunidin 3-glucoside [60]. It was reported that the bran-rich fraction of barley grain contained the most flavonoid content, whereas the hull fraction did not contain any significant flavonoid content [62]. Out of major proanthocyanidins in barley, prodelphinidin B3 (90–197 μg/g) accounted for the majority of proanthocyanidins, whereas procyanidin C2 (5–19 μg/g) was reported to be present only in minor quantities [63]. In the malting process, the green malt had the highest antioxidant activity (79.80%) and total phenolic content (122.43 mg/100 g) than those of barley and malt [64]. For example, carotenoid (1.71 μg/g), (+)-catechin (69.06 mg/100 g), 1,2-dihydroxybenzene (37.21 mg/100 g), quercetin (30.78 mg/100 g) and isorhamnetin (22.44 mg/100 g) contents were higher in green malt.

Phenolic acids	Free form (μg/g)	Conjugated form (μg/g)	Bound form (μg/g)	Health benefit	Reference
p-Hydrobenzoic acid	Not determined	5.8–26.7	0.5–5.4	Anticarcinogenic effects	[53]
2,4-Dihydroxybenzoic acid	0.04–2.62	6.8–61.8	11.1–74.4		
Vanillic acid	1.45–4.71	8.9–30.2	0.5–7.5	Anti-inflammatory effect and neuroprotection	[54, 55]
Syringic acid	0.45–3.74	2.2–10.0	0.0–3.0	Antioxidant, antimicrobial, anti-inflammatory, antiendotoxic, neuro and hepatoprotective activities	[56]
Sinapic acid	Not determined	12.4–24.4	8.9–17.8	Exhibit antioxidant, anti-inflammatory, anticancer, antimutagenic, antiglycemic, neuroprotective, and antibacterial activities	[57]
Ferulic acid	1.32–5.87	21.7–42.5	104.3–365.4	Anti-inflammatory, antidiabetic, anticancer, antiapoptotic, antiaging, hepatoprotective, neuroprotective, radioprotective, pulmonary protective, hypotensive effect, and antiatherogenic effect	[58]
p-Coumaric acid	0.57–7.01	1.7–13.1	2.7–109.7	Protective role against heart diseases	[59]
o-Coumaric acid	0.27–1.31	1.2–3.2	2.7–4.7		

Source: elaborated from [60].

Table 2.
Composition of the total, free, conjugated, and bound phenolic acids in barley, and their health benefits.

4.5 Lipids

Barley lipids include fatty acids, phytosterols and tocols (**Table 3**). A recent study comparing Irish barley varieties showed that linoleic acid is one of the most abundant unsaturated fatty acid, while phytosterols vary, beta-sitosterol being the most abundant sterol, and alpha-tocotrienol is the most abundant tocol homologue [72].

Compound	Mean	Health benefit	Reference
Tocols (µg/g)	61.49	Protection against toxins, neurological diseases like Alzheimer's disease, diabetes, and modulating degenerative diseases such as cancer and cardiovascular diseases	[60, 65]
Beta-Tocopherol	0.22		
Delta-Tocotrienol	1.01		
Unsaturated fatty acids (mg/100 g)	1505.32	Reduce the cardiovascular risk by decreasing the low density lipoprotein-cholesterol level	[66, 67]
Sterols (mg/100 g)	71.24	Cholesterol lowering effect	[68]
Flavones (µg/g)	11.81	Decrease endothelial dysfunction, lower blood pressure and cholesterol, and modulate energy metabolism	[69]
Apigenin-6-C-arabinoside-8-C-glucoside	1.53		
Apigenin-7-O-glucoside	0.38		
Anthocyanin (µg/g)	4.82	Antioxidant, lower risk of myocardial infarction, and cardiovascular disease related mortality	[70, 71]
Pelargonodin- rutinoside	0.41		
Malvidin-rutinoside-hexoside-pentoside	0.11		
Delphinidin glucoside	0.16		
Pelargonodin-malonylglucoseide	0.09		
Cyanidin-malonylglucoside	0.45		
Peonidin-malonylglucoside derivative	0.10		
Petunidin malonylglucoside	0.07		
Peonidin- rutinoside	0.23		
Peonidin- hexoside-pentoside	0.23		
Delphinidin- rutinoside	0.05		
Cyanidin-dimalonylglucoside	0.68		
Delphinidin-dimalonylglucoside	0.06		
Unknown (peonidin glucuronide derivative)	1.44		

Source: elaborated from [49, 72].

Table 3.
Mean values of lipids (tocols, unsaturated fatty acids and sterols), flavones, and anthocyanin compounds present in barley.

Tocopherols and tocotrienols (Vitamin E), also called tocols, are known to have several chemical and physiological properties in barley [49]. Besides, [73] showed that the total lipid content and fatty acid composition varies with the barley variety and decreases during the malting process. However, a study showed that barley lipids contained 18.53% palmitic, 19.94% oleic and 51.74% linoleic acids while malt oil contained 17.33% palmitic, 15.62% oleic and 56.56% linoleic acids, and linoleic acid content increased during the malting process while oleic and palmitic acid content decreased [64].

5. Potential of barley as a functional food for animal and human health

The human lifestyle, including diet composition and the pattern of physical activities, have undergone a major shift since the last millennium. In recent years, it has been well documented that healthy eating practices, maintaining a normal body weight, controlled blood pressure, and regular physical activity could prevent up to 80% of coronary heart disease, 90% of type-2 diabetes and one-third of all cancers [74]. Consumers are becoming more aware of the relationship between diet and disease, and there is an ongoing shift from animal-derived to plant-based meals. Thus, globally, more effort in developing novel, healthier, more nutritious and fortified functional foods is invested nowadays. Likewise, continuous efforts are made to ensure the health and well-being of animals raised for food since this is a critical component of providing safe food products. For example, use of bioactive compounds are encouraged since they have similar proprieties as withdrawn antibiotic growth promoters [75]. Additionally, [76] demonstrated the transfer efficiency of tocotrienols from barley into egg yolk when offered as a dietary supplement and signalled the possibility of developing hen's eggs that are nutritionally-enriched in specific health-promoting tocotrienols.

Barley, which recently is seeing renewed interest, is a versatile crop used both for human nutrition and as an animal feed for energy and nutrients [11, 17] due to its high content of biologically active constituents such as dietary fibre, especially beta-glucan, tocols, including tocopherols and tocotrienols, and phenolic compounds.

5.1 Benefits of barley as an animal feed

The nutritional quality of barley grain fed to animals is traditionally defined by energy content [77]. Accurate and rapid evaluation of the energy content of barley is key to ensure the optimum nutrient content of the barley as an animal feed. Usually, barley is fed to beef cows when they graze poor-quality pastures to increase the energy content of their diet [34]. Beef cattle could be fed barley either as whole or processed, with the last one providing greater animal performance. Barley is also considered suitable for inclusion in the diet of all types and ages of poultry, with older birds being more able to utilize barley than younger chicks. Inclusion of whole barley grain in broiler diets has been reported and may be cost-effective due to limited processing required [78]. Barley has been suggested to be included in the diets of horses, rabbits, and fish to provide energy and nutrients. However, the level of inclusion may need to take into consideration the digestive physiology of the animal and its ability to digest fibre [34].

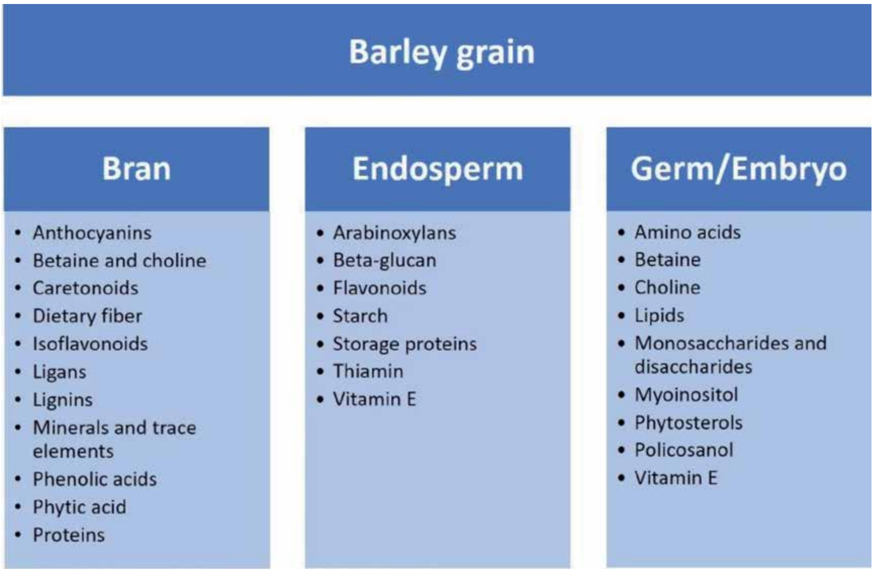
High levels of insoluble dietary fibre can increase fecal bulk due to its high water holding capacity [79]. In animal nutrition, high-amylose barley is associated with enzymatic resistance to digestion in swine and poultry, contributing to slower glucose release and prolonged satiety. In addition, increased amylopectin is associated with faster digestion of starch to glucose, which may result in higher feed intake due to rapid rises in insulin [34].

While it was demonstrated earlier that the use of fermented barley is a valuable functional ingredient for broilers diets [19], recently it was shown that feeding fermented barley can also be a possible nutritional strategy for managing nursery pigs without in-feed antimicrobial growth promoters [80]. It has been suggested that feeding high-barley diets to finisher pigs may improve pork quality attributes compared with feeding corn since barley has lower fat and linoleic acid content than corn, resulting in firmer and whiter pork fat, increasing its contrast with myoglobin and thus enhancing the visual appeal of loin marbling [81].

5.2 Health benefits of barley for humans

Barley can be breakfast, lunch, or dinner. However, it surpasses the meals since it has unique advantages. The renewed interest in barley grain is mainly due to its unique soluble fibre beta-glucan and antioxidant phytochemicals (**Figure 9**).

The effectiveness of barley beta-glucan in barley food products in lowering blood cholesterol [83–87] and glycemic index [88–91] has been reported in numerous studies. Therefore, foods containing substantial levels of barley beta-glucan are considered functional foods, and in several countries, they are permitted to carry health claims. So far, barley health claims have been approved by the US Food



Bran
- Anthocyanins
- Betaine and choline
- Caretonoids
- Dietary fiber
- Isoflavonoids
- Ligans
- Lignins
- Minerals and trace elements
- Phenolic acids
- Phytic acid
- Proteins

Endosperm
- Arabinoxylans
- Beta-glucan
- Flavonoids
- Starch
- Storage proteins
- Thiamin
- Vitamin E

Germ/Embryo
- Amino acids
- Betaine
- Choline
- Lipids
- Monosaccharides and disaccharides
- Myoinositol
- Phytosterols
- Policosanol
- Vitamin E

Figure 9.
Barley grain anatomy and the distribution of the key biologically-active phytochemicals within the barley grain. Source: elaborated from [82].

and Drug Administration (FDA) (2006), European Food Safety Authority (EFSA) (2011), Health Canada (2012), and more recently by Food Standards Australia and New Zealand (FSANZ) (2017) [92–95].

Besides health-benefiting beta-glucan, barley contains phytochemicals in varying concentrations, usually determined by genotypic or environmental factors or the interaction of both factors [60]. These phytochemicals in barley may exist in free, conjugated, or bound forms, categorized into several major classes, including phenolic acids, flavonoids, lignans, tocols, phytosterols, and folates [96]. Tocols are components.

of plant oils that provide benefits such as protection against toxins, neurological diseases like Alzheimer's disease, and diabetes [60]. For example, barley is a rich source of tocols, including tocopherols and tocotrienols. When assessing the grains of 16 feed/food barley genotypes, it was found that on average, the total tocols were 69.8 μg/g, with tocotrienols being the most abundant averaging 53.10 μg/g, while tocopherols were averaging only 16.69 μg/g (**Figure 10**). The genotype was found to significantly affect the content of all individual tocols, combined tocopherols, combined tocotrienols, and total tocols for those barley genotypes [97]. In addition to their antioxidant properties known to reduce serum low-density lipoprotein cholesterol [98, 99], the tocol content of cereals such as barley can confer health benefits, including modulating degenerative diseases such as cancer and cardiovascular diseases [65]. Also, [67] suggested that alpha-tocotrienol and polyunsaturated fatty acids are hypocholesterolemic components in barley oil. Furthermore, studies indicate that a high intake of alpha-tocopherol decreases lipid peroxidation and platelet aggregation, functioning as a potent anti-inflammatory agent [49, 100]. Recent studies showed a significant correlation between phenolic components and antioxidation especially suggesting that coloured barley grains are rich in phenolic compounds with antioxidant capacity [22, 49]. It was also reported by [101] that the free and bound phenolic extracts in the blue hulless barley grains have an equivalent proportion in the total phenol and co-exist in two forms. The bound forms of barley grain phenols contribute to the antioxidative and antiproliferative

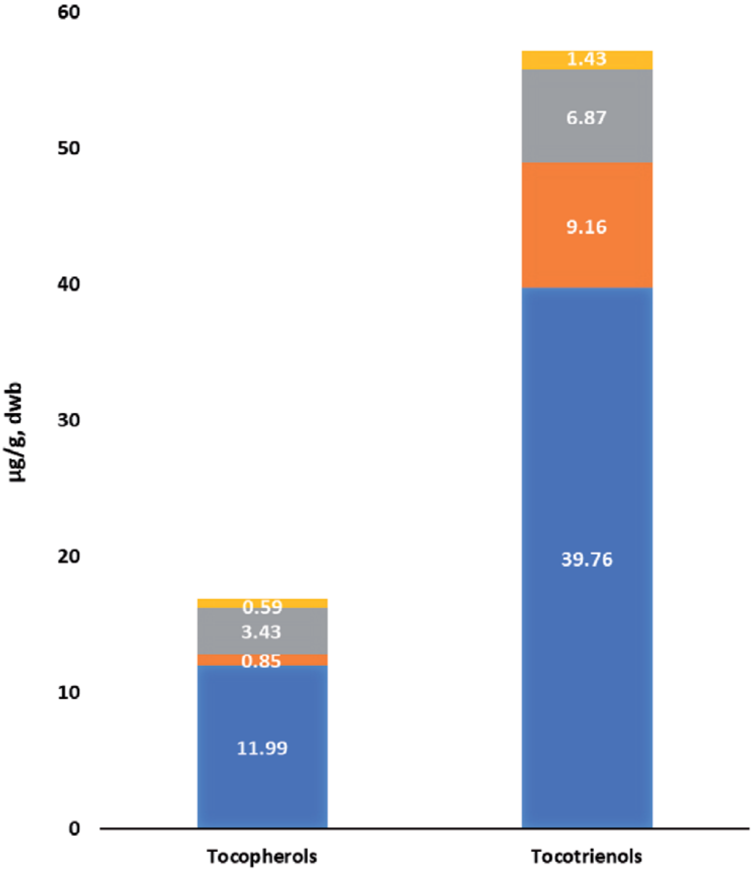


Figure 10.
Average of individual and total tocopherols and tocotrienols in the barley whole grain. Source: prepared based on data from [97].

activity against cancer cells in the human liver. Their high concentration in barley may be responsible for its usefulness in controlling certain diseases [21, 60]. For instance, a phenolic acid named ferulic acid in barley has a wide range of health benefits, including anti-inflammatory, therapeutic usage, antidiabetic, anticancer, antiapoptotic, antiageing, hepatoprotective, neuroprotective, radioprotective, pulmonary protective, hypotensive effect, and antiatherogenic [58, 102]. Coumaric acid has anti-inflammatory, anticancer, antimicrobial and antioxidant effects, and by decreasing low-density lipoprotein peroxidation, coumaric acid has a protective role against heart diseases [59, 103]. Vanillic acid is considered a bioactive molecule for treating inflammatory diseases [54, 55]. In addition, sinapic acid can attenuate various chemically induced toxicities [57], whereas syringic acid shows a wide range of therapeutic applications in preventing diabetes, cardiovascular diseases, cancer and cerebral ischemia [56].

Studies have consistently shown that regular consumption of barley whole grain reduces the risk of developing chronic heart diseases, cancer, and gallstones [60, 104–106]. Based on an recent pre-clinical study, it was demonstrated that life-long barley intake could positively contribute to healthy ageing [107]. It was found that barley intake prolonged the lifespan, delayed locomotor atrophy, reduced loss of balancing ability and spatial recognition and significantly increased the particle sizes of high-density lipoprotein cholesterol, which is associated with a reduced risk of total stroke.

6. Conclusion

Barley is one of the first cultivated crops, globally grown in diverse soil conditions and in areas where other crops cannot be easily cultivated. Although the crop is primarily grown as an animal feed and as a source of malt for alcoholic beverages, more and more it is included as a component of various foods due to the health benefits attributed mostly to dietary fibre, lipids, vitamins and antioxidant phytochemicals. These components are broadly distributed in barley and play an important role as substrates in the biosynthesis of various metabolic compounds and influence the flavour, taste, and colour of foods. Nutritional attributes of barley contribute to the prevention of numerous metabolite disorders providing antioxidant, anti-carcinogenic, anti-inflammatory, and cardio- and neuro-protective effects. Overall, having barley in animal and human diets showed beneficial effects against the development of chronic illnesses.

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Conflict of interest

The authors declare no conflict of interest.

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Author details

Ana Badea[1]* and Champa Wijekoon[2]

1 Agriculture and Agri-Food Canada, Brandon Research and Development Centre, Brandon, Canada

2 Agriculture and Agri-Food Canada, Morden Research and Development Centre, Canadian Centre for Agri-food Research in Health and Medicine, Winnipeg, Canada

*Address all correspondence to: ana.badea@canada.ca

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Chapter 6

Cereal Grain: A Vehicle for Improved Healthy Living

Timilehin David Oluwajuyitan, Oseni Kadiri,
Babawande Adeboye Origbemisoye, Oladapo Fisoye Fagbohun,
Ruth Nkemjika Ukejeh, Oyekemi Popoola
and Babatunde Olawoye

Abstract

The increasing population of the world, emergence, and prominence of diseases coupled with side effects of drugs has led to the search of non-toxic, healthy foods products. Cereal grains are a stable food consumed by a large population of the world, containing an array of nutritional and bioactive compounds such as dietary fiber, protein, carbohydrate, vitamins, minerals, β-glucan, lignans, phytosterol, phenolics among others. These compounds proffer beyond basic nutritional needs as they also provide health benefits on consumption such asantioxidants, antidiabetics, antihypertension, antihyperlipidemic/anti-cholesterol, antimicrobial and anticancer with no side effects. Cereal grains canbe processed into divers of food products, singly or as multigrain food products in other to increases the bioavailability of its nutrients or bioactive compounds. Its by-products can further be used to enriched human diets or serve as animal feeds. Hence, this review addresses the needs for more processing, value additions and consumption of cereal grain as a vehicle to improved healthy livings.

Keywords: Cereal grains, processing, food applications, health benefits

1. Introduction

Cereals are grass-like crops cultivated for its grains consumption which comprises of endoderm, germ and sperm. The world top seven (7) most important cereal includes maize, wheat, rice, barley, sorghum, oats, and rye. Globally, world production of cereals grain varies from maize (1, 116.34), wheat (764.49), rice (495.78), barley (156.41), sorghum (57.97), oat (22.83) to rye (12.17) million metric tons, and these accounts for over 60% of the world food consumption [1]. Over the years, research has shown that consumers of food products are more concerns about diet and diseases relationship rather than satisfying abdominal emptiness [2, 3]. Cereal grains contain an array of nutritional and bioactive compounds such as dietary fiber, protein, carbohydrate, vitamins, minerals, β-glucan, lignans, phytosterol, phenolics among others [4]. These compounds have been shown to exhibits a positive effect on diseases management and improved healthy living.

Epidemiological studies have shown that constant intake of cereal grains rich in dietary fiber protects the human body from cardiovascular diseases such as hypertension and diabetes [5–7]. Likewise, studies conducted in the United States shows that consumer of cereal whole grains are at 20–40% reduced risk of cardiovascular diseases compared with non-consumer across all age group [8–10]. Jensen et al. [11] reported on a 14 years' research over 42, 850 male subjects aged between 40 and less than 80 years. They concluded that consumption of cereals wholegrains is attributed subjects' healthier lifestyle compared with other non-consumer subjects'. Therefore, this review focus on the dietary constituent, processing and applications of cereal grains as a vehicle for improved healthy living.

2. Global production of cereal grains

Cereals grains generally have been ofadvantage to humanity for decades [12]. Rice, wheat, and maize are the three major cereal crops in China (**Table 1**), and they play a key role in global cereal production (**Table 2**). China, with 565,754 hectares cropped by far the largest cereal areas in the world, followed by the USA which accounted for 328,474 hectares while other countries have cereal areas between 228,844 hectares (Canada) and 130,882 hectares (Kazakhstan) for India [14]. Cereal production in 2017 increased to about 2977.0 million tons, with China having over 617 million tons [15], which contributed to more than 40% of the global cereal production, while a sharp decline was observed in 2018, 2019 and 2020 as shown in **Figure 1**. The sharp decline observed was due to the reduced yield prospects for maize in the United States of America (USA) and in Ukraine, meager rains that

Countries	Metric tons in millions			World percentage
	2018	2019	2020	
China	610.04	613.7	669.49	20.75
India	259.6	263.14	273.5	10.53
Russian Federation	130.8	109.12	126	4.4
Brazil	226.34	242.07	246.63	3.96

Source: FAOSTAT [13], Food and Agriculture Organization of the United Nations.

Table 1.
Countries with high cereal production.

Cereal	Metric tons in millions	Country with the highest production (FAO, 2018)
Corn	1116.3	United States
Wheat	764.49	China
Rice (milled)	495.78	China
Barley	156.41	Russia
Sorghum	57.97	United States
Oats	22.83	Russia
Rye	12.17	Germany

Source: FAOSTAT [13], Food and Agriculture Organization of the United Nations.

Table 2.
Global production of cereal grains.

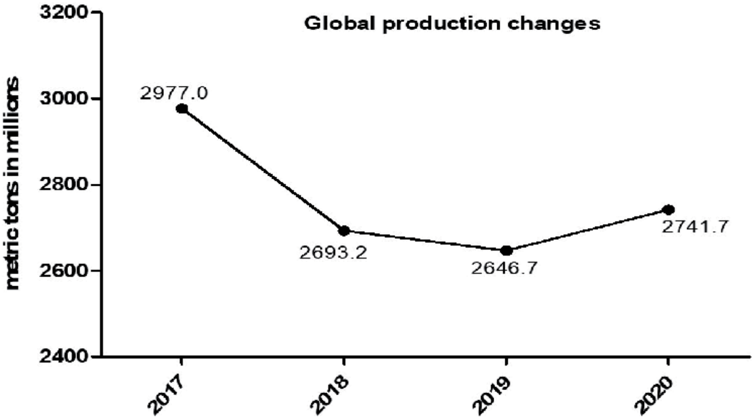

Figure 1.
Global production changes.

reduced yield expectations in Argentina, Brazil and Kazakhstan, which in turn affected the increase made to the production in the Russian Federation [16]. While rice production worsened in Bangladesh and Viet Nam due to the weather. Moving forward, the FAO has projectedthat the global average of cereal yields to increase by 1.1% per year (slower than the 1.9% seen in the previous decade), driven by advances in biotechnology, structural changes towards larger farms, and improved cultivation practices.

3. Dietary and nutrition composition of cereal grains

Cereals belong to the grass family, Gramineae. They are edible grains or seeds grown in several countries of the world. Some typical examples include oats, rye, maize, sorghum, barley and millet. Rice and wheat account for over 50% of the world's cereal production.

Cereals are a major and important aspect of the diets of the populace of both the developing and developed countries worldwide. Even with the food diversity prevalent in our present now, cereals remain an important contributor to the dietary pattern. Cereals are known to be a good source of food nutrients such as protein, carbohydrate, as well as having a range of micronutrients such as vitamins E, vitamins B, zinc, magnesium and iron.

Breakfast cereals and white bread are typical examples of fortified cereal products which are vital nutritional food products for children and adults, although there is the need to reduce the sodium levels of this processed foods product. Lignans and other types of bioactive compounds, which can improve health, have been reported in cereals and there are on-going researches on identifying other bioactive substances in underutilized cereals, their importance and bioavailability. Most studies have associated the health benefits accrued to cereal grains to its fiber contents, micronutrients, bioactive and resistant starch content. Several cereal products are usually fortified with a range of B complex vitamins, vitamin C, vitamin D, iron, vitamin E, zinc and beta-carotene [17]. The regular consumption of cereals, most especially whole grains have been deduced as having a role in halting the development of chronic diseases such as diabetics, colorectal cancer and coronary heart diseases though the precise mechanism is not yet fully understood. Whole pseudo-cereal grains such as quinoa, amaranth, and buckwheat are rich in bioactive compounds like vitamins, trace element, phenolic acids, flavonoids, and fatty acids with knownabilities to prevent the onset of many degenerative diseases [18].

4. Processing techniques/methods of cereal grains

Cereals are been processed in different ways due to their specific characteristics and purpose. Their processing comprises an important part of the food production chain, but it is a complex procedure. The most common cereal processes include dry milling (wheat and rye), pearling (rice, oat, and barley), wet milling (corn and wheat), and malting (barley, corn, and wheat) [19]. However, certain general principles applied to most of them. Cereals undergo several processing stages between harvest, storage and consumption. Processing methods of cereal grains can be divided into two different methods, primary and secondary processing method. Primary processing includes cleaning and grading, hulling, milling and drying while the secondary process is the storage of the cereal grains for further processing.

4.1 Primary processing

4.1.1 Cleaning and grading

The first stage in cleaning is threshing, i.e. the removal of grains from the rest of the plant. It involves four different operations: Separating the grain from the panicle; sorting the grain from the straw; graded according to size; winnowing the chaff from the grain. Before cereal processing, the grains should be dried to 10–15% moisture before storage to avoid spoilage of the cereal grains.

4.1.2 Hulling

Grains have an unpalatable huskthat needs to be removed before processing. There are different kinds of de-hulling machines designed for this purpose, depending on the type of cereal grains.

4.1.3 Milling

This can be achieved using any of these cereal grains mill; Plate mill, hammer mill and roller mill. The type of mill to be used depends on the cereal grains. Roller mills are majorly used industrially due to its high cost and maintenance while hammer mill and plate mill can be used at home and all business scale level.

4.1.4 Drying

Before storage, the cereals grains should be dried to 10–15% moisture to avoid spoilage of the cereal grains.

4.2 Secondary processing

4.2.1 Storage

Dried grains are stored in much quantity until required for processing. The grains should be inspected regularly for signs of spoilage and the moisture content tested. If the grain has picked up moisture, it should be re-dried.

5. Cereal grains products and by-products

Cereal grains products are a staple in the diets of many cultures around the world forming the basic and essential supply of nutrients to humans as well as animals. Nutrients provided by cereal grain products include carbohydrate (as an energy source), minerals such as magnesium, phosphorus and zinc, proteins, vitamins, especially the B Vitamins (niacin, riboflavin, and thiamine) and fiber. Cereal grain products are extensive and are derived using indigenous as well as technologically enhanced procedures [20]. Cereal grains products include a wide range of products which are made out of grains such as quinoa, maize, rice, sorghum, rye, barley, millet and oats.

5.1 Products and by-products from Rice

Majorly, rice is consumed in cooked form. In addition to rice being eaten in the cooked form, lots of products and by-products are available as a consequence of its prevalent functional properties and less sensitivity to allergens. A major product from rice is rice flour, which is gluten-free and is used to make rice noodles, rice crackers, dumplings, bread, rice paper, breakfast cereals, pancakes, baby foods, cakes, waffles and wrappers for egg rolls. Other products include rice milk, puffed rice, rice starch, bran oil, vinegar and alcoholic beverages comprising rice beer and wine [20]. By-products from rice include rice bran, rice husk as well as rice straw which serves as feed for animals [21].

5.1.1 Rice noodles

Extruded and flat rice are noodles made out of rice flour that has been wet milled. They are consumed alongside soups and dishes. In Thailand, Japan and Chinese, it is called" senmee", "harusame" and "mi fen" respectively.

5.1.2 Rice flour dumplings and cakes

Dumpling is a ball of dough that is wrapped around a filling. Several methods are used in its preparation, including baking, frying, steaming, boiling or simmering and are found in a lot of world cuisines. In Asia, sweet dumplings and cakes from rice flour are readily available to buy in stores and stalls. Rice cake is a sticky, dense meal that is well known in parts of East Asia.

5.1.3 Rice alcoholic beverages

Rice beer is a major beverage produced from rice. It is produced by first boiling rice and then inoculating with some amount of yeast and the resulting mixture fermented for a few days. Sake (rice wine) is also a Japanese alcoholic beverage made from rice [22].

5.1.4 Rice starch

Rice starch is employed as a thickener in sauces, desserts as well as baby foods. Sweet syrup can also be made using rice starch.

5.1.5 Rice bread

A good replacement for other cereal flour containing gluten is rice bread, which is consumed as an alternative source for people that are allergic to other types of flour.

5.2 Products and by-products from wheat

5.2.1 Whole wheat

Whole wheat flour has none of its constituents (bran, endosperm and germ) removed. The Middle East and Southern Europeans commonly consume decorticated and pounded type of wheat. Pounded wheat is usually considered to possess a higher nutritional value at the same time having better retention of nutrients present in the aleurone layer in addition to its germ. Artificial or natural dehydration is usually carried on decorticated wheat grains [23]. Whole wheat lowers the possible adverse outcome of metabolic syndrome. Consumption of whole wheat has also been reported to support beneficial bodyweight [24]. It has a favourable nutrient profile as effective sources of magnesium, dietary fibre, pantothenic acid, copper and manganese. However, whole wheat is considered as one of the major causes of allergies in foods [25].

5.2.2 Wheat flour

The flour that is gotten when wheat (endosperm only) is ground into finer particles is called wheat flour. Depending on the gluten value, they are classified as weak/soft flour or hard/strong. Weak/soft denotes flour with low gluten value, while hard/strong flour denotes flour with high gluten value. Bread flour, cake flour and all-purpose flour are majorly the types of wheat flour consumed. Others include self-rising flour, pastry flour, gluten flour, durum flour and fortified flour. In most homes across the world, wheat flour is the most significant ingredient used in baking. It forms the framework of the majority of commercially available baked goods and pasta [26].

5.2.3 Durum flour

A by-product that is employed in the production of semolina, another form of pasta, durum bread and American noodles is durum flour which is gotten from durum wheat. Durum wheat falls under the category of hard wheat.

5.2.4 Semolina

Semolina is gotten from durum wheat that has been coarsely ground. Pasta with high protein value and are of great importance including spaghetti in addition to macaroni are made from semolina.

5.2.5 Wheat noodles

In most African countries, noodles made from wheat dominate about 30–40% of the cereal-based diet [27]. White noodles coated with salt are generally consumed in Japan White noodles coated with salt are generally consumed in Japan [27]. Noodles from wheat are produced from soft or hard wheat flour. It can also be produced from wheat flour that is intermediate between soft and hard wheat flour.

5.2.6 Spaghetti and macaroni

Spaghetti is a type of pasta made in the shape of long thin strings while macaroni is pasta usually in the form of short tubes.

5.3 Products and by-products from sorghum

Sorghum grains are utilized by lots of food industries for the production of flour, starch and alcohols which results in many by-products. By-products obtained from sorghum grains include sorghum wine, sorghum gluten meal, sorghum germ meal, sorghum distillers dried grains and solubles, sorghum brewers' grains, malted sorghum sprouts and sorghum bran [28]. Sorghum is also consumed in fermented forms. Fermented forms of sorghum include Injera, Nasha, Ting, Asida, Kisra, HumulurKhamir [29]. Sorghum wine is a by-product obtained from the fermentation of indigenous sorghum liquor. It is known as kaoliang in China.

5.4 Products and by-products from millet

Millet is usually dehulled and made to pass through several treatments before consumption to enhance their edibility and sensory attributes Millet is usually dehulled and made to pass through several treatments before consumption to enhance their edibility and sensory attributes [30]. The small nature of millet has relegated its use to products that are solely flour-based because of the difficulty in decortication. Several treatments for millet grains have however observed to improve its decortication [31]. Alcoholic beverages, distilled liquors and different types of meals are prepared from millet. Candied puffs called Awaokoshi in Japan are made from millet. In some parts of the world, sorghum flour is mixed with millet flour to produce a type of flatbread usually rolled by hand. Millet porridge is an indigenous meal eaten in China, Russia and Germany. A Vietnam snack is known as banh-da-ke also comprises of millet as a major ingredient.

5.5 Products and by-products from barley

Flour, flakes, grits, starch, malt and beverages are commercial products gotten from barley grain. Animals are mostly fed with whole grains of barley. Food products from barley are rich sources of minerals, fiber, proteins and B Vitamins. Pearled barley or pot is made by removing the outer layers of barley grain by the process of abrasion. Porridge and filing for pies are made from pearl or pot barley. They also serve as an alternative to potatoes, pasta, in addition to rice. Barley flour is used to produce bread, noodles, cakes, flatbreads, cookies and extruded snacks [32]. Sweeteners and binders are made from barley starch. Barley starch is also used besides with barley malt to produce beer. The primary use of barley is in the production of malt used in brewing, alcoholic and non-alcoholic beverages. Bakeries and distilling industries also utilize barley malt [33].

6. Diseases prevention/Management of Cereal Grains Products

Several cereal grains product has been developed and used in the prevention and management of diseases which includes diabetes, hypertension, inflammation and stroke.

Diabetes: Diabetes is a metabolic disease associated with high blood glucose level (hyperglycemia) usually treated using expensive synthetic drugs. Recently, scientific research focuses on the prevention and management of diabetes using cereal grains food products with high resistant starch, and low glycemic index (GI). Hefni et al. [34] developed a low GI cereal-based bread fortified with legume kernels in sourdough fermentation. Developed bread samples resulted in the reduction of high blood sugar level (>250 mmol/dL) to normal (<100 mmol/dL) after 90 min of consumption in human subject aged between 29 and 62 years, at Linnaeus University, Kalmar, Sweden. Likewise, Olagunju et al. [34] developed a whole wheat multigrain bread with significant *in-vivo* α-amylase and α-glucosidase inhibitory activities which slow down the rates of metabolism of blood glucose level in experimental animals. Hence, developed whole wheat multigrain bread may serve as a potential food product for the management of diabetes.

Hypertension: It is also known as high blood pressure and its onset is associated with a high-risk factor of other cardiovascular diseases. Epidemiological studies have shown that consumption of diet from cereals grains such as oat, barley, rice and rye can reduce blood pressure [35, 36]. He et al. [37] conducted a meta-analysis on consumption cereal grains fiber and found a significant reduction in high blood pressure of subjects. Clinical evidence has also shown that constant consumption of cereal whole grains (oat fiber) in less than 9 weeks by 88 human subjects significantly reduced subject blood pressure [38, 39]. Recently, Odebode et al. [40] developed a dough meal samples enriched with cereal fiber (rice bran). Developed products exhibit antihypertensive potentials in experimental animals fed for four weeks which is attributed to a high content of high-density lipoprotein in developed dough meal.

Inflammation: Inflammations refers to the autoimmune ability to fight against germs and diseases. Cereal grains such as maize contains an anti-inflammatory compound called *Ferulic acids*. This derivative is responsible for the production of macrophages which plays a crucial role in the secretion of mediators such as pro-inflammatory and inflammatory cytokines. Productions of these compounds prevent the body against chronic diseases which includes cancer, atherosclerosis, diabetes, among others [41–43].

Stroke: Stroke is a cerebrovascular disorder due to shortage of blood (oxygen) reaching the brain which could results in difficulties in walking, talking, and body paralysis. Scientific evidence has shown that the consumption of cereal grains exhibits possible potentials of risk reduction against stroke [9, 10, 43–45]. Mozaffarian et al. [9] conducted a cross-sectional analysis of over 8 years on both male and female stroke subject, aged 65 and above based on cereals grain fiber consumption. The results show that higher consumption of cereal grains fiber is associated with lower risk and recovery of the partial and total cerebrovascular disorder. In the same vein, Fung et al. [46] analyzed the correlation between dietary consumption pattern and stroke in women between 40 and 60 years of age for 14 years. Calculated dietary pattern score shows that subject with higher consumption of processed animal protein and full fats are at higher risk of stroke compared with subjects with higher consumption of cereal grains fiber, fruits and vegetables.

7. Summary and future applications of cereal grains products

Human populace exposed to a series of health complications due to urbanization and industrialization. Synthetic drugs used in the management of these health challenges are linked with side effects, thereby instigating the application of plants in disease management. Cereal grains are food crops with immeasurable nutritional and functional benefits. Regular consumption could enhance better dietary lifestyle and healthy living. Nevertheless, the development of varieties of novel cereal grain food products, encapsulation, and application of cereal grain bioactive compounds in nanotechnology will further reduce menace caused by a widespread of diseases on human populace.

Author details

Timilehin David Oluwajuyitan[1], Oseni Kadiri[2]*,
Babawande Adeboye Origbemisoye[1], Oladapo Fisoye Fagbohun[3],
Ruth Nkemjika Ukejeh[4], Oyekemi Popoola[5] and Babatunde Olawoye[5]

1 Department of Food Science and Technology, Federal University of Technology Akure, Nigeria

2 Department of Biochemistry, Edo State University Uzairue, Edo State, Nigeria

3 Department of Biomedical Engineering, First Technical University, Ibadan, Oyo State, Nigeria

4 Department of Food Science and Technology, Obafemi Awolowo University, Ile Ife, Nigeria

5 Department of Food Science and Technology, First Technical University, Ibadan, Oyo State, Nigeria

*Address all correspondence to: kadirioseni@yahoo.com

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Chapter 7

Millets Cereal Grains: Nutritional Composition and Utilisation in Sub-Saharan Africa

Shonisani Eugenia Ramashia, Mpho E. Mashau
and Oluwatoyin O. Onipe

Abstract

Millets are small to medium size cereal grain crops that are cultivated throughout the tropics and subtropical region. The grains are used for food and fodder for feeding animals around the globe. Millets have great economic, health importance, gluten-free, have low glycemic index and are known as "nutra–cereals". The grains are mostly utilised as a food source by population with lower socio-economic factors which are traditional consumers in the farm and village levels. They are rich sources of carbohydrates, protein, crude fibre, phytochemicals, minerals, and vitamins. They are processed by using different traditional processes such as soaking, germination, malting, fermentation, milling or grinding, cooking, roasting and popping. Millet grains/ flours are utilised and consumed as flat breads, biscuits, snacks, beverages, porridges, *chapati*, *dosa*, pastas. There is a need to produce new value-added products from millets which is underutilised crop to improve food security and prevent micronutrients deficiencies.

Keywords: Millets, cereal grains, nutritional composition, health benefits, utilisation

1. Introduction

Millets are cereal crops that belong to the family *Gramineae* and they are small-seeded species [1–3]. Most millets belong to the tribe *Panicoideae* apart from finger millet and teff that belong to the tribe *Eragrostideae* [4–6]. The grains are available in some parts of African countries and they are cheap [7]. They differ from each other by their appearance, grains quality, taste, morphological and biochemical behavior [8]. They are widely grown around the world for food and fodder and are staple food in the West, East, Central and Great Lakes region of Africa as well as in Asia and India [9–11]. The word millet has been derived from the French word "mille" which means thousand, a handful of millet has been referred to contain thousands of grains [12]. Millets are classified with maize and sorghum in the grass sub-family *Panicoideae* [3, 8]. They are the 6th most important cereal grain crop in the world agricultural production after wheat, maize, sorghum, rice, and barley that are regarded as the major economic grains in the world [13–15]. Millets are resistant to pests and diseases as compared to other cereal grains [1, 13]. They are major food sources for millions of people, especially those who live in hot, dry areas of the world, adapt to harsh environment especially drought conditions. Millets are one of the cereal grain crops that are drought-tolerant and have short growing season [15, 16]. They grow well on poorly fertilised and dry soils with short rainfall periods [1, 17]. The grains are cultivated between February and August while harvested in June or January [18]. About 55–60% of worldwide produced millet grains are cultivated in the sub-Saharan Africa including Ethiopia, Kenya, Malawi, Nigeria, Tanzania, Uganda, Zambia, and Zimbabwe (**Table 1**). Major types of cultivated millet species varieties are finger millet (*Eleusine coracana*), pearl millet (*Pennisetum glaucum)*, Japanese banyard millet (*Ecchinochloa frumentacea*); foxtail millet *(Setaria italica)* and proso or white millet *(Panicum miliaceum)* [20, 21].

The millet grains are gluten-free, non-acid forming, easy to digest, low glycemic index and healthy food diet for people with celiac disease – common disease caused by cereal protein ingestion [1, 2, 19, 22]. Other gluten-free cereal grains are maize, brown rice and sorghum while barley, wheat and rye are gluten rich cereal grains [4]. **Table 2** and **Figure 1** show the major cultivated millet species in the world. Millets are globally grown in different regions from East to West and they are called in different names around the globe which indicate their specific originality such as foxtail millet as Italian millet, proso as French millet and barnyard as Japanese millet [25]. Finger millet originated in East Africa while white fonio (*Digitaria exilis*), black fonio (*Digitaria iburua*) and pearl millet originated in West Africa [26]. **Table 3** shows various characteristics of millet species and their functions are shown in **Table 4**.

Countries	Yearly production (in tonnes)				
	2015	2016	2017	2018	2019
Angola	43746	42000	70000	69854	51054
Benin	21640	25182	24717	26143	25000
Botswana	555	1264	1099	2462	902
Burkina Faso	946184	905071	828234	1189079	970176
Burundi	9970	10019	9955	9891	9827
Cameroon	95810	99015	101101	103186	105271
Central African Republic	10000	10000	10000	10000	10000
Chad	592124	725677	660175	756616	717621
Congo	13197	13595	13896	14197	14499
Côte d’Ivoire	55200	58300	61600	65000	65000
Democratic Republic of the Congo	43776	41006	40887	40908	40930
Ethiopia	1036444	1017059	1030823	1035630	1125958
Gambia	73420	65073	52000	38000	35000
Ghana	157369	159017	163484	181564	190000
Guinea	224587	238177	241714	214747	223220
Guinea-Bissau	14000	14000	16177	18000	20000
Kenya	99000	54000	54000	72000	135000
Malawi	33512	19510	35121	31315	34479
Mali	1864301	1806559	1492650	1840321	1878527
Mauritania	2790	3145	3277	3247	3218
Morocco	4953	4564	4312	4104	3928
Mozambique	10916	21000	21000	19869	12832

Countries	**Yearly production (in tonnes)**				
	2015	**2016**	**2017**	**2018**	**2019**
Namibia	42494	19428	57644	83515	18700
Niger	3404813	3886079	3790028	3856344	3270453
Nigeria	1485387	1552576	1500000	2119000	2000000
Rwanda	4960	5021	5083	5140	5195
Senegal	749874	493340	875484	897574	807044
Sierra Leone	44000	38000	39000	38000	38000
South Africa	6243	5950	5683	5424	5160
South Sudan	8000	6000	5000	5000	5000
Sudan	486000	1449000	878000	2647000	1133000
Togo	38664	23838	26044	26082	26806
Uganda	236484	193461	211050	238558	243104
Zambia	31967	29972	32566	32278	24843
Zimbabwe	17672	27461	62157	38964	35000

Source: [19].

Table 1.
Millet production in sub Saharan Africa in thousands per tons from 2015 to 2019.

Common name	**Tribes/genus and species**	**References**
Finger millet/*ragi/mandua/nagli/nachani/kurakkan/mufhoho*	*Eleusine coracana*	[2, 20]
Teff	*Eragrostis tef*	[4]
White fonio (*acha*)	*Digitaria exilis*	[22, 23]
Black fonio (*iburu*)	*Digitaria iburua*	
Barnyard millet/*banti/kudiraivali sawan/shama*	*Echinochloa frumentacea*	[1, 2, 24]
Proso millet/*panivaragu/kutki/cheena*	*Panicum miliaceum*	[13, 20]
Kodo millet/*haraka/varagu/kodra/ditch*	*Paspalum scrobiculatum*	[13, 15]
Foxtail millet/*navane/tenia/kauni/kakun*	*Setaria italic*	[2, 13]
Pearl millet/*bajra/cambu/saije/cattail*	*Pennisetum glaucum*	[15, 20]

Table 2.
Major cultivated millet species.

2. Nutritional composition of millet species

Some nutritional values of millets are similar to that of wheat and rice. Millets are staple food for many African countries; however, they are low in macro nutrients such as protein and fat but rich in vitamins and minerals [7]. Millets are a good source of magnesium which reduces the severity of asthma, frequency of migraines, lowers high blood pressure and reduces the risk of heart attacks. These nutrients play important roles in human nutrition [27]. The grains are also a good source of diet for growing children and expectant mothers [28]. They are a good source of phytochemicals such as polyphenols, tannins, and phytic acid which helps to lower cholesterol and reduces cancer risk, high blood pressure, heart disease and diabetes

Figure 1.
Cultivated millet species. A = Foxtail millet; B = Pearl millet; C = Proso millet; D = Banyard millet; E = Teff millet and F = Kodo millet. Source: [25].

Millet	Colour	Shape	Size	Origin
Foxtail millet	Pale yellow to red	Ovoid	2 mm long	China
Finger millet	Light to dark brown	Spherical	1–2 mm in diameter	East Central Africa (Uganda)
Proso millet	White cream, yellow, orange	Spherical oval	3 mm long/ 2 mm diameter	Central and eastern Asia
Pearl millet	White, grey, pale yellow, brown, or purple.	Ovoid	3–4 mm in length	Tropical West Africa (Sahel)
Kodo millet	Blackish to dark brown	Elliptical and oval	1.2 to 9.5 μm long	Mainly in India also in west Africa
Little millet	Grey to straw white	Elliptical and oval	1.8 to 1.9 mm long	Southeast Asia
Banyard millet	White	Tiny round	2–3 mm long	Mainly Japan and India

Source: [18].

Table 3.
Various characteristics of millet species.

[21, 27]. Other potential health benefits and medical function of millets are increasing in time span of gastric emptying and provides roughage to gastro intestine. Millet is also known as an alkaline forming food. Alkaline based diet is often recommended to get better optimal health and prevent illness/ diseases [7, 29].

Table 5 shows the nutritional composition of some millet's species. They have higher amount of minerals such as magnesium, manganese, phosphorus, iron, copper, and potassium when compared with corn, sorghum, and wheat [1, 8, 30]. The main nutrients in millets are starch, protein, lipid, dietary fibre, vitamins, and minerals as shown in **Table 6**. When comparing millet with other cereals, millet contains 75% of carbohydrates and is low in fat (2–5%) content than maize, rice, and sorghum [1, 2, 8]. Other potential health benefits of millets are the development and repair of body tissue, the prevention of gallstones, protection against breast cancer and protection against postmenopausal complications and the reduction of chances of childhood cancer [1, 2]. Millets contain 65–75% of complex

Millet	**Functions**
Finger millet	It prevents tissue damage and stimulates the wound healing process in diabetic rats. Prevents cardiovascular disease by reducing plasma triglycerides in hyperlipidemic rats.
Proso millet	Gluten-free and can prevent humans from celiac disease. Helpful in reducing the risk of type 2 diabetes in humans due to a low glycemic index.
Foxtail millet	It prevents colorectal cancer in mice models. Reduces cholesterol level & have an antidiabetic effect on impaired glucose tolerance persons. Capable of attenuating acute ethanol-induced hepatic injury in mice.
Pearl millet	Prevention of celiac disease in humans due to gluten-free property. Stimulates the immune system to prevent the Shigella-induced pathogenicity in the mice model.
Banyard millet	Acts as an inhibitor of cancer by inducing apoptotic cell death in HT-29 human colon cancer cell line. Its phenolic content inhibits the protein glycation and glycoxidation, which plays a crucial role in the progression of diabetes.
Little millet	Prevents from modern metabolic disorders due to the presence of polyphenols.
Kodo millet	Reduce glycemic index and prevents diabetes in the human female model, also have antioxidant activities.

Source: [25].

Table 4.
Functions of millet species.

Mineral contents (mg/ kg)	**Millet**	**Wheat**	**Maize**	**Rice**	**Sorghum**
Phosphorus	2400	1170	990	1030	350
Potassium	2200	1550	1200	1500	240
Magnesium	1000	250	470	350	188
Calcium	100	170	60	60	27
Sodium	None	20	10	20	5
Zinc	34	8	5	17	3
Iron	48	12	11	12	11
Manganese	7	5	NA	9	1
Source: [30]					
Nutrient compositions (g/100 g)					
Protein	7–12	11.6–11.8	8.1–10.5	6.8–7	7.9
Fat	2–5	1.5–2.0	3.8–4.6	0.5–1	2.8
Minerals	1.0–2.3	1.5–1.8	1.2	0.6	1.6
Dietary fibre	15–20	2.0–12.6	2.8–13.4	4.1	2.3–12.8
Carbohydrates	65–75	71.0–71.2	73.0	78.2–79.0	73.0
Vitamins (mg/100 g)					
Riboflavin	0.25	0.17	0.20	0.06	0.15
Thiamine	0.59	0.45	0.38	0.06	0.38
Niacin	3.2	5.5	3.6	1.9	4.3

NA – not applicable.
Sources: [1, 14, 27, 30–32].

Table 5.
Nutritional composition of whole grains (at 12% moisture).

Contents	Foxtail millet	Kodo millet	Barnyard millet	Pearl millet
Proximate composition (g)				
Moisture	11.2	12.8	11.9	12.4
Protein	11.50–12.3	9.8	6.2	11.6–11.8
Fat	2.38–4.3	1.3	2.2	4.8–5.0
Minerals	0.47–3.3	2.6	4.4	2.2–2.3
Dietary fiber	2.5–8.5	2.47	1.98	11.3
Carbohydrates	60.9–75.2	65.9–66.6	65.5	67–67.5
Energy (kcal)	331	309	307	361–363
Minerals (mg)				
Phosphorus	290	188	280	296
Potassium	250	144	—	307
Magnesium	81	147–228	82	137
Calcium	31	27	20–22	42
Sodium	4.6	4.6	—	10.9
Zinc	2.4	0.7	3.0	3.1
Iron	2.8	0.5–5.0	5.0–18.6	8.0
Manganese	0.60	1.10–3.3	0.96	1.15
Copper	2.4	1.60	0.60	1.06

Sources: [1, 13, 31].

Table 6.
Proximate composition and mineral contents of some millet species.

Phenolic compound	Foxtail millet	Kodo millet	Barnyard millet	Pearl millet
Hydroxybenzoic acid and derivatives				
Methyl vanillate	—	—	—	19.8
Protocatechuic acid	10.2	39.7	—	11.8
p-Hydroxybenzoic acid	5.63	10.5	—	22
Vanillic	22.1	4.01	—	16.3, 7.08
Syringic	93.1	—	—	17.3
Gentisic acid	21.5	—	—	96.3
Hydroxycinnamic acid and derivatives				
Caffeic acid	34	276	—	21.3
p-Coumaric acid	848	767	—	268.9
Trans-ferulic acid	631	1844	—	637
Cis-ferulic acid	101	100	—	81.5
8,8′-Aryl ferulic acid	19.6	94.8	—	—
5,5′-Di ferulic acid	62.2	173	—	57
Flavonoids	169	173	—	71

Source: [27].

Table 7.
Phenolic compound content (μg/g defatted meal) of some millet species.

carbohydrates, 5.6–12% protein, fat, 2–5%, 15–20% crude fibre and 2.5–3.5% minerals.

Millets are rich source of antioxidant activity such as phenolic compounds that contains phenolic acids, flavonoids, and tannins. Phenolic acids are sub-divided into hydroxybenzoic acids, hydroxycinnamic acids, hydroxyphenylacetic acids and hydroxyphenylpropanoic acids (**Table 7**). The phenolic compounds of millets phenols are reported to have antioxidant, anti-mutagenic, anti-oestrogenic, anti-inflammatory, antiviral effects, and platelet aggregation inhibitory activity [18]. The antioxidant activities of foxtail and proso millets are high because of their high total carotenoid and tocopherol content which range from 78 to 366 and 1.3–4.0 mg/100 g. The grain has good nutritional value however it is mostly consumed by traditional consumers in a tribal community. Its products are scarce in the urban areas as compared to rice ready-to-eat products [7, 29]. The major challenge with millet grains is that the commercial industrial method of processing the grains are not well-known or developed as compared to other cereal grains [29].

3. Processing and utilisation of millet grains/flours

Processing is a technology which is used to convert the cereal grains into an edible form of food products. Millet grains are prepared using modern and traditional technologies such as soaking, germination, malting, fermentation, milling or grinding, cooking, roasting, compositing flour, fortification, irradiation and popping or puffing mostly widely used in rural areas [13, 33, 34]. Traditionally, millet grains are spread and dried in the sun for a period of one week and are stored inside the bags for future use or processing. The grains can be stored for 5 to 10 years. These processes improve the consumption, nutritional composition, and sensory attributes of food products. Various studies has been conducted and the researchers have tried to produced millets products like puffed, popped, flaked, extruded and

Current	**Emerging**
Foods • Flours and meals (Africa and India) • Dumplings, porridges, and gruels (Africa and India) • Rice (Africa and India) • Couscous (Africa) • Malt (Africa and India)	Foods • Gluten-free baked products (USA) • Ready-to-eat breakfast cereals (USA) • Noodles (Japan) • Instant porridges (Africa) • Instant infant foods (South Africa) • Expanded snack foods (Africa)
Beverages • Non-alcoholic fermented beverages (Africa, Europe, and Asia) • Cloudy opaque beers (Africa and Asia) • Spirits (China)	Beverages • Lager beers and stouts (Africa, USA and Australia)
Animal feeds • Processed cattle feed (USA and South America) • Bird food (Asia and Africa) • Poultry feed (Australia)	Animal feeds • Formulated dog food (South Africa)
Industrial uses • Starch (USA and Africa)	Industrial uses • Bioethanol from starch (USA)

Source: [35].

Table 8.
Current and emerging uses of millets in the world.

Uses	References
Traditional opaque beer, Busa	[36]
Bread, porridge, soup, cake, beer and distilled liquors	[37]
Light and thick porridge; Beer called *pito*	[9]
Weaning and infant food preparations, dumpling, porridge and roti	[38]
Food products: *mathri, sevain, kachari, kachauri, laddu, cheela, cheela,* biscuits and *halwa*	[39]
Polenta, couscous, medicinal herb, folk remedy for leprosy, liver diseases, measles. Pneumonia and smallpox	[40]
Flour- based foods such as *roti, mudde* and *ambli*	[1, 41]

Table 9.
Uses of millets.

roller dried products; fermented, malted and composite flours; weaning foods. Some of the recent studies are promising to produce popped and milled products [7]. Current and emerging food products produced from millet grains/ flours are shown in **Tables 8** and **9**.

Traditional processing of millet products has received poor scientific applications especially in the developing countries and the use of the modern processing technology has been restricted which can help to produce commercialised products in a large industrial volume [13, 42]. The development of value-added and convenient food products in urban areas may be a possible solution for promoting consumption of millets products. Most of the research have been conducted on the development of composite flour and extruded products which also increase the availability of millet products in the urban areas [1, 43]. Presently, food scientists are more interested in neglected small grains such as finger millet to reduce food shortage and hunger in the developing countries such as Nigeria, Uganda, Kenya, Tanzania, and South Africa. People who are living in the developing countries have limited access to animal food products so it is better to consume healthy millet foods that are rich in minerals and vitamin B complex. Animal food products contain high amount of minerals such as iron and zinc [44–46].

4. Traditional millet-based products

Millet grains/flours are consumed as flat bread, porridge, roasted and alcoholic and non-alcoholic beverages. They are utilised to bake different baked products (cookies, biscuits, bread and muffins) and weaning food. Composite flours are utilised to make chappati, puti and *murukul*, supplementary foods for feeding babies or infants. Some traditional products produced from millets are *burfi*, *baddis*, *halwa* and *papad.* They are also utilised to replace commonly used cereals in local community dishes like *idli*, *dos*a, *puttu*, *adai* [27], *khichdi*, millet ball "*fura*" and *tuwo*. Other products that are produced from millet grains/ flours are traditional foods and beverages such as snack, fast foods, millet wine roti, bread (fermented or unfermented), porridge and millet powder [7]. **Table 10** shows the most common indigenous millet based fermented food and beverage products produced around the world in which liquid drink is the most popular product and microorganisms associated with each product.

Products	Microorganisms	Regions
Busa (liquid drink)	*Lactobacillus, Sacchromyces*	Egypt
Chikokivana (Alcoholic beverage)	*Sacchromyces cerevisiae*	Zimbabwe
*Dalaki (*thick porridge)	Unknown	Nigeria
Doro (colloidal, thick, alcoholic drink)	Yeast and bacteria	Zimbabwe
Bogobe (solid dough)	*Lactobacillus* sp., yeast	Botswana and Ghana
Kenkey (solid dough)	*Lactobacillus sp., yeast*	Botswana and Ghana
Kwanu-Zaki (liquid drink)	LAB, Yeast	Nigeria
Ogi (liquid porridge)	*Lactobacillus* sp., *Aerobacter*	Nigeria
Merissa (alcoholic drink)	*Sacchromyces*	Sudan
Mahewu (liquid porridge)	*Lactobacillus delbrukii, L. bulgarius, Streptococcus lactis*	East African Countries
Munkoyo (liquid drink)	Unknown	Africa
Uji (porridge as staple foods)	*Leuconostoc mesenterodes*	Uganda, Tanganyika
Other fermented products		
Traditional opaque beer (*Kaffir* beer) and *Isidudu Imbila* (fermented thin porridge)		South Africa
Commercial brewing, opaque beer, *mangisi (*sweet–sour non-alcoholic drink).		Zimbabwe
Nasha or *madida* (thin porridge).		Sudan/Kenya

Sources: [47–51].

Table 10.
Most common indigenous millet-based fermented foods and beverages.

5. Non-alcoholic beverage products

Some other non-alcoholic beverage products that are produced form different millet species include *appalu, samaipayasam* and *korramurukulu. Appalu* is a food product made from pearl millet and Bengal gram flours. The mixed dough is divided into small balls and flattened into round shape. The dough is fried in a hot cooking pan, then fried and served hot with some vegetables or meat. *Samaipayasam* is a little millet which is also known as *samai* and it means little millet while *payasam* means *kheer*. The food product is prepared by milling roasted groundnuts into fine powder or flour. Little millet is added to boiling water while stirring constantly. After stirring, the jaggery solution is mixed and cooked for a few minutes on low temperature and served hot. Any millet can be used to make this recipe instead of little millet. *Korramurukulu* is prepared from foxtail millet and Bengal gram flour. The mixed dough is placed by using hand extruder and *murukulu* extruded is deep-fried until they turn brown [26]. Millet flour can be utilised to produce breakfast meals that are also known as gruels such as "*og*i" and "*akamu*". They can be consumed with various animal and vegetable products like meat and leafy vegetables that can nourish the human body by providing good nutritional value [52].

6. Conclusion

In general, this book chapter covered the nutritional composition of millets, processing and utilisation of millets grains or flour into traditional based products and non-alcoholic beverages. Different types of millet such as pearl millet, proso millet, kodo millet, finger millet, foxtail millet and little millet) are currently being utilised for different purposes (bread, cookies, muffins, chapatti and biscuit. The availability of gluten free value-added millet products globally may help mitigate the incidence of celiac disease and obesity. Therefore, there is a need for commercialisation and development of value-added gluten-free food products from millets.

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Author details

Shonisani Eugenia Ramashia*, Mpho E. Mashau and Oluwatoyin O. Onipe
Department of Food Science and Technology, School of Agriculture, University of Venda, Thohoyandou, Limpopo Province, South Africa

*Address all correspondence to: Shonisani.ramashia@univen.ac.za

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Section 3

Biotic and Abiotic Stresses

Chapter 8

Building Stress Resilience of Cereals under Future Climatic Scenarios: 'The Case of Maize, Wheat, Rice and Sorghum'

Clemence Muitire, Casper Kamutando and Martin Moyo

Abstract

World population is projected to reach 10 billion by 2050 and the phenomenon is expected to cause a surge in demand for food, feed and industrial raw materials. Cereals (i.e., carbohydrate-rich grain crops) are the most widely grown and consumed crops worldwide. All cereals combined provide approximately 56% and 50% of global energy and protein needs, respectively. Maize, wheat, rice, barley and sorghum are the most produced and consumed cereals, globally. These are widely grown across the world from the tropics to the temperate regions. Although efforts are being done by governments, research organizations and academic institutions to increase productivity of these important crops, huge yield deficits still exist. Climate induced biotic (e.g., pests and diseases) as well as abiotic stresses (especially; heat and drought) are widely regarded as the key yield-constraining factors of most cereal crops. Given the contribution of cereals in global food and nutrition security, improvements in productivity of cereal production systems is mandatory if livelihoods are to be guaranteed. This chapter discusses the global production and utilization of four of the major global cereals, limiting factors to their productivity and possible solutions to the production constraints.

Keywords: cereals, cereal production, cereal utilization, constraints to production, sustainable solutions to constraints

1. Introduction

With the ever-increasing world population (expected to reach 10 billion by 2050) [1, 2] and the changes in human dietary structure, global food demand is projected to keep increasing. All cereals combined, account for approximately 56% and 50% of global energy and protein needs, respectively, making them a major source of calories and protein for the human populace directly through human consumption and indirectly via consumption of cereal fed animals and animal products [3, 4]. The term "cereals" refers to members of the *Graminae* family which are cultivated for their edible seeds [3, 5]. The group consists of nine crop species: wheat (*Triticum*), rye (*Secale*), barley (*Hordeum*), oat (*Avena*), rice (*Oryza*), millet (*Pennisetum*), corn (*Zea*), sorghum (*Sorghum*) and triticale a hybrid of wheat and rye [3]. A variety of cereals are produced worldwide in different climates and production systems ranging from the tropics to the temperate regions. The five major cereals on the global scale, in-terms of area under production and yield are; maize (*Zea mays*), rice (*Oryza sativa*), wheat (*Triticum aestivum*), barley (*Hordeum vulgare*), and sorghum (*Sorghum bicolor*) [4, 6]. Combined, these five crops contributes to about 50% of world food [7].

Although huge strides have been made in agricultural research and development (R and D) to increase crop productivity and efficiency of food production systems, global food deficits are still in existence [6]. In 2019, approximately 690 million were reportedly food-insecure with most of the affected people found in African and Asian countries [8]. Given the importance of cereals in the human diet, increasing their production will significantly improve current and future global food and nutrition security. To meet the projected high demand for food, food production should at least double by 2050 [8]. In particular, cereal production need to be increased by 60 to 110% by 2050 to meetup with the expected high demand for human consumption, livestock feed and industrial purposes needs [2].

Although cereals are notably important in global food and nutrition security, productivity of these crops is continually being hampered by biotic (e.g., pests and diseases) and abiotic (particularly; heat and drought) stresses [9]. These reduce crop yield and quality in field and post-harvest during storage [10]. The magnitude of the impact of these constraints on cereal productivity and yield quality however depends on crop species and variety, the extent and length of the stress on the crop, and the developmental stage at which the stress occur [11, 12]. If comparisons are made, global crop losses due to abiotic stresses are higher than those caused by biotic stresses [13].

If current and future food and nutrition security is to be guaranteed, cereal productivity should be increased to match food, feed and industrial demand [14]. This is done by increasing the efficiency of the cereal production systems, reducing the impact of biotic and abiotic stresses on cereals and policy changes. In addition, genetic crop improvement using both, the conventional and molecular breeding technologies, is also widely known as an important adaptation strategy for crops under the future predicted socio-climatic scenarios.

2. Global cereal production and utilization

2.1 Global cereal production

Cereals in their broad category are historically the major type of crops produced and traded across the world for food, feed and industrial uses [8]. In 2019, a global total of 2 719 million tonnes of cereals were harvested on 6,006 million ha of land [15]. This represents 60% and 50% of global food production on all cropped land, respectively. Of all the cereals produced in 2019, Africa accounted for 46.9%, Asia 49.1%, Europe 3.7%, the Americas 0.3% and Oceania 0.1% [15]. For decades, global leaders in cereal production are the United States of America, China and India [2]. However, different individual cereals are produced in large quantities in different regions of the world with the distribution driven by the prevailing climatic conditions, soil types, and general preference by local consumers. For instance, sorghum is widely produced and consumed in Africa while rice is widely produced and consumed in Asia [16]. Cereals including wheat, maize, rice and sorghum (*see* **Figure 1**) have a global cropping area of almost 700 million ha and together, they supply approximately 50% of the world's caloric intake [17]. At the global scale, wheat is the most important food security crop with a production of 750 Mtonnes on about 220 Mha in 2017 [11], followed by maize, rice, barley and

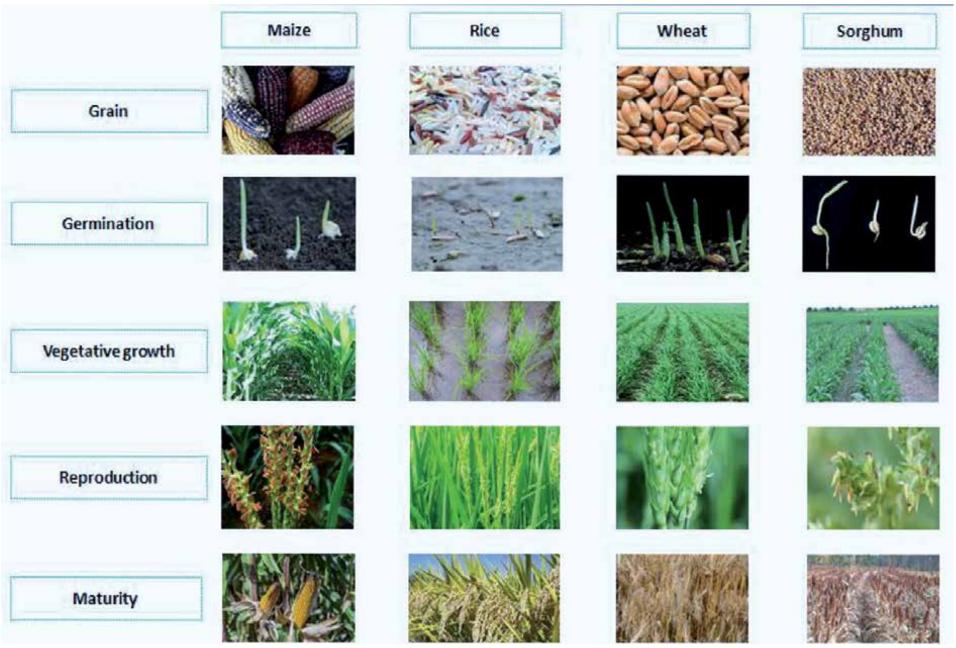

Figure 1.
Major cereals produced for food and feed on the global scale.

sorghum [8]. These are the major cereals produced across the world for human consumption and industrial utilization [7].

Global production of cereals is projected to increase as new crop production technologies are discovered and old ones being improved. The increase is projected to be 13% between 2015 and 2027 [18]. This projected increase in global production is attributed to the expected increase in production area and yield per area [18]. In 2020, global cereal production was expected to reach a record high of 2 742 million tonnes, which is an increase of 1.3% from the production in 2019 [2]. Area under wheat and maize are projected to increase by 1.4% and 3.2% respectively while other coarse grain cereals such as sorghum and barley are expected to increase by 2.4% by 2027 [18]. Global yields for wheat, maize and rice are projected to increase by 9%, 10% and 12% respectively between 2015 and 2027 [18].

In Africa and Asia, sorghum is a primarily produced as a subsistence crop using open pollinated varieties with low or no inputs and thus the productivity is usually very low, averaging 1.2 t/ha [19]. Production of sorghum in these regions is declining due to lack of established markets, consumer preferences and social pressure [19]. However, this decline in production is expected to be offset by increased production in the developed world, where demand is projected to increase as modern high yielding sorghum hybrids are becoming popular.

2.2 Global cereal utilization

The main uses for cereals are as food for human consumption in assorted whole grain and processed products, as stockfeed for animals such as pigs, cattle and poultry, and as raw materials for industrial production of chemicals and other non-food products. Given the importance of cereals as staple crops and the discrepancy between consumption and production in many countries, increase in cereal production can significantly reduce prevalence of undernourishment and hunger, thereby improving food and nutrition security on the global scale.

2.2.1 Human food uses

All major cereals are generally prospective sources of food for consumption by both humans and animals for energy and general nutrition [20, 21]. Cereals are nutritionally rich with very high starch content to meet human and animal energy needs [20], some harbor proteins, but in low quantities [22], but they are limited for most of the important micronutrients for a healthy being such as zinc, iron [23], and some vitamins [24], although nutritional levels vary between crop species and varieties. The most important cereals worldwide are rice, wheat, maize, barley, and sorghum [21]. Due to the ever increasing human population, demand for cereals is expected to increase [21, 25]. The increasing demand for food weighs mainly on cereals such wheat, rice and maize which are some of the most important global sources for energy and nutrition.

In terms of total global cereal consumption, wheat provides 41% of the calories and 50% of the proteins [26]. In developing countries, it provides about 18% of daily caloric needs as compared to 19% of globally and 21% in high income countries [26]. It is usually ground to different flour types according to the rate of extraction and the flour is used to produce a wide range of products such as different bread types, cakes, biscuits, breakfast cereals, noodles, pies, pastries, bran, and alcoholic beverages [12]. Traditionally, wheat was not a crop of economic importance in some regions such as sub-Saharan Africa (SSA) but, it is now gaining popularity, especially in the urban areas [11].

Sorghum is mostly important as a food crop in the tropics and subtropics, particularly in Africa and Asia, where it is grown as a yield bank although it is now losing its popularity to maize. Like wheat, sorghum is mainly consumed after processing into flour and is used for baking and brewing purposes [19]. The flour which comes in different colors due to different grain colors (i.e., red, yellow and white) is used in baking and cooking. Sorghum colored four is now being considered as an alternative to using artificial food coloring products in production of cakes (velvet cake) [27]. Sorghum leaf sheaths can be used to produce an orange/red food dye that comes from its high content of antioxidants [27]. Its nutritional value and preference over wheat is that it is gluten free and has high content of several antioxidants and micronutrients that offer health benefits to humans [19]. Although sorghum is gaining importance as a nutritionally-rich food crop, its consumption in the developing world is declining [19]. In order to offset this narrative, the benefits of growing and consuming sorghum need to be effectively communicated in the developing world [19].

Maize is one of the most important food crops worldwide [16]. It is of great importance as a food and nutrition crop in SSA where more than 300 million people depend on it as their staple [16, 28]. Of all the major cereals, maize is eaten is several dishes and preparations more than all of them. For instance, the physiologically immature maize cobs are roasted or boiled and consumed as a snack, dry maize grain can swell and burst when heated to produce popcorn (i.e., a popular snack food), dry milling of maize grain produces maize meal, corn flour, and corn oil [16, 28]. Maize flour is used to make porridges, soups, pastes and for baking [29]. Various alcoholic and non-alcoholic beverages are prepared from maize flour [16]. Maize also produces a syrup which is used as a sweetener in food production [16]. Global maize consumption is projected to increase by 16% by 2027 and the increase is expected to be highest in the developing countries [18].

Rice is the principle food crop for more than 50% of the world's population [30, 31]. Ninety percent of the global rice is consumed in Asia where nearly 2.4 billion depends on it as a staple [2]. It provides two thirds of all calories to Asians who eat rice-based diets [2]. On a global level, rice contributes about 19% and

13% of the calories and proteins, respectively [26]. Rice consumption is on the rise particularly among urban populations in traditionally non-rice eating regions such SSA and this is expected to accentuate the global rice demand [32]. The bulk of the rice produced worldwide is consumed in the form of rice kernels, rice noodles and other rice-based value-added products such as breakfast cereals, gluten-free rice pasta, rice flakes and crackers [32].

2.2.2 Livestock feed uses

Maize, wheat, rice, and sorghum are primarily grown for human consumption, but they are also extensively used directly as animal feed or as inputs in the production of livestock feed [33]. Approximately 30% of global cereal production goes toward production of livestock feeds and this uses about 40% of global arable land [33]. This has led to some global debates on the competition between livestock and humans for land and other resources required in the production of crops for animal feed [33, 34]. Due to their high starch content, animal feed formulation predominantly comprises cereal grains or their by-products as energy sources [34]. Traditionally, cereal grains and straw were used to feed animals directly, but, with the advent of modern stockfeed formulations these crops are being used as ingredients in the manufacture of commercial rations especially for beef and dairy cattle, pigs, and poultry [35]. Cereals are used for animal feed in different ways. Maize, wheat and sorghum grains can be directly fed to livestock such as poultry and cattle (beef and dairy) [36] or can be processed and used as ingredients in production of feed. The stover can be used as dry grazing material or harvested for feeding [36, 37], whole plants (maize and sorghum) can be harvested for silage and fed to animals after ensiling [36]. Demand for cereals for livestock feed production is expected to increase as demand for animal products is increasing in many parts of the world [33]. The projected increase in demand for animal products is driven by human population growth, rising incomes and urbanization [33] and dietary preference towards western diets.

Maize is the major cereal used as livestock feed directly or as an ingredient in livestock feed production for swine, poultry, and cattle [36]. In the U.S, approximately 42.9% of maize grain is fed to livestock and poultry while only 11.2% is used for human consumption [36]. In Pakistan and some Asian countries, maize is the second most important cereal in the production of livestock feed, where the cereal component of poultry feed is composed of 40% maize, 40% rice by-products, 18% wheat and 2% sorghum [35]. In Africa, maize grain is mainly used for human consumption, while animals particularly cattle, is fed on dry maize fodder in winter. In some East and Southern African countries such as Ethiopia and Tanzania, dual-purpose maize varieties with increased fodder quantity combined with high grain yield are preferred by some rural farmers [38].

Wheat is usually not used in commercial stockfeed formulations. Its use in poultry feed formulations in Pakistan does not exceed 15% due to its negative effect on egg laying [35]. The same goes to rice, in which milled rice is not directly incorporated into livestock and poultry rations, but its by-products such as rice bran, rice tips, rice polish are utilized for commercial poultry and livestock feeds [35]. Use of rice straw as a source of feed for ruminant animals is limited due to high polysaccharides, lignin and silica content which reduce degradability by ruminal microorganisms [37]. However, it is still used for animal feed in some southeast Asian countries such as Thailand and Indonesia where rice straw is abundant due to high rice production [37]. Sorghum grains are widely used in production of poultry feeds. After harvesting, sorghum stover is used as a dry fodder just like other cereals. Sorghum stover represents up to 50% of the total value of the crop and its value and contribution to feed and food security increases in drought years [35]. Sorghum is an important crop that serves multiple purposes as human food, animal feed and bioenergy production. It is also planted as a forage crop for livestock and the straw can be used as a ruminant feed component or construction material [12].

2.2.3 Industrial uses

Besides being used for food and feed, cereals are also used in industry as inputs and raw materials for the manufacture of a range of chemicals and other food and non-food products. Sorghum and maize are used in the brewery industry to manufacture alcoholic drinks by fermentation [16, 39]. Distillation and fermentation of cereal grains produce solvents and acids for instance ethyl alcohol, butyl alcohol, propyl alcohols, acetaldehyde, acetic acid, acetone, lactic acid, citric acid glycerol and whisky [16]. Cereal straw and starches are used to improve the quality of recycled paper. Cornstarch obtained from the wet milling process is used for food, textile and paper sizing adhesives [16]. Cereal grain residues and straw dehulling are used in the production of energy in anaerobic biogas digesters. The gas produced from cereals has high methane, making it suitable to for use in internal combustion engines or to drive turbines for power generation. Corn syrup from wet milling of maize is used as a natural sweetener [16]. Currently, the major industrial use of cereals is in production of bioenergy. Cereals, especially maize [16], wheat [39], and sorghum [28] are used for ethanol (ethyl alcohol) production. This is the same type of alcohol found in alcoholic beverages, and is most often used as a motor fuel, mainly as a biofuel additive for gasoline [16]. Increasing demand for ethanol production and the anticipated expansion of the industry has resulted in increased maize prices and has provided incentives to increasing maize acreage [28, 36]. Production of bioenergy crops offers opportunities for agriculture to be part of the solution for global energy challenges and mitigation of climate change impacts [19].

3. Major current and emerging constraints to cereal production

The historical and current importance of cereals in the human diet clearly shows that global food supply and human nutrition are anchored on cereal production [2]. Major constraints to global cereal production can be broadly grouped into biotic and abiotic factors [9]. These are continually reducing potential yield and crop quality during production and post-harvest despite efforts to increase food supply to meet demand [10]. The magnitude of the impact of these constraints on cereal productivity and yield quality depend on the crop species and variety, the extent and length of the stress factor on the crop, and the developmental stage at-which the stress affects the crop [11, 12]. If comparisons are made, crop losses due to abiotic stresses are higher than losses effected biotic stresses [13]. A lot of scientific studies have been done to understand the physiological and molecular response of plants to different biotic and abiotic stresses that limit grain yield production yet huge yield gaps still exist between optimal and stressful conditions. More studies are therefore paramount if future food and nutrition security is to be guaranteed.

3.1 Climate change

While some of the constraints, for instance, extremely low temperatures, flooding and some specific pests and diseases usually exhibit regional importance, some of the stresses, of-note; drought (water scarcity), heat (extremely high temperatures) and some pests and diseases have global significance and require global cooperation to reduce their impact. Climate change is the most critical environmental challenge currently facing humanity [40, 41]. It has brought with it extremes of weather events such as extremely high temperatures, a shift in rainfall patterns, uneven and unpredictable rainfall and increased frequency of dry spells [9, 40]. Because of these climatic factors, usually, food deficit on one region can be compensated by surpluses from another region. However, if climate-induced droughts and temperature increases continue, whole regions will be rendered inhospitable to crop production resulting in global food deficits [40]. Climate change effects on crop production are not uniformly distributed across all regions. It is expected to have far reaching impacts on the global production of maize, rice and wheat, especially in the developing countries [6]. Climate change could have catastrophic effects on cereal production with an expected 20% reduction in wheat and maize production in Africa alone [6]. Globally, it is estimated that higher temperatures and a shift in precipitation trends observed since 1980, have lowered yields of wheat by 5.5% and maize by 3.8%, below what could have been had the climate remained stable [42]. Climate change is expected to bring further increases in temperature, rising sea levels, more intense biotic stress (i.e., pests and diseases) incidences, emergence of new pests and diseases, water shortages, extreme weather events and loss of biodiversity [30].

3.2 Main climate-induced abiotic stresses

3.2.1 Drought

Globally, the major abiotic stresses impacting cereal production are droughts (water scarcity) [12, 40], extremely high temperatures (heat stress) [43], and poor soil fertility [4]. In the history of global crop production, drought has always been regarded as one of the major cause of poor crop yields [40, 42]. Droughts can occur in virtually all climatic regions [44]. Frequency of droughts is expected to intensify in most parts of the world due to climate change which could make cereal production exceedingly challenging in the future [45]. The effects of droughts are being exacerbated by the increase in global temperatures, the shift in rainfall patterns, and declining availability of irrigation water [40, 45]. Water is essential for plant growth and functioning as it is involved in various physiological, chemical and metabolic activities in the plant [46, 47]. As a result, water scarcity leads to reduced tissue dehydration, damage to the photosynthetic apparatus [26], plant growth and development and in extreme cases, total plant failure [48]. Drought can reduce nutrient uptake by reduced root growth and it can also aggravate effects of pests and diseases in the case of sorghum [49]. Sensitivity to moisture deficit stress depends on crop type (i.e., species or variety), the duration and extent of the stress and the developmental stage at which the stress strikes out but, for most cereals, including the relatively drought tolerant sorghum, water deficit conditions are most devastating if they occur during the reproductive stage [49, 50]. Yield losses due to water deficit stress conditions are more imperative if they occur during the reproductive stage [51]. Different crops have different physical and physiological traits that confer tolerance to drought and these include, presence of a highly efficient rooting system for water uptake such as the one in sorghum whereas some crop demonstrate ability to quickly recover after occurrence of the stress [52]. Studies to develop and/or identify drought tolerant crop species and varieties therefore mainly focus on reproductive traits such as a small anthesis-silking interval (ASI) in maize [16, 52].

In developing countries, 60% of all crop production is done under irrigation [51]. Declining availability of irrigation water due to over-exploitation of ground water resources, competition with other crops, restrictive government policies and deterioration of irrigation infrastructure [46], constitute several production challenges in the developing world. Drought consistently decrease maize yield due to water deficiency and concurrent heat, with greater yield loss for rainfed maize in wetter areas [4].

Wheat is very sensitive to moisture stress with the reproductive growth stage more sensitive than the vegetative stage [11, 26]. In the developing countries, approximately 50.4% of wheat yield is lost as a result of droughts [46]. In the wheat growth cycle, tillering is more sensitive to moisture stress compared to pre-anthesis [50], while water stress during the anthesis and post-anthesis stages is most devastating [47]. Studies have shown that wheat exposed to moisture stress throughout its growth stages had reduced plant growth rate, total dry matter, 1000-grain weight and grain yield [48]. In some studies, water stress increased grain protein content, however, with a serious yield penalty [43].

Moisture deficit stress affects all growth stages of maize growth and development [13, 16]. In some studies, moisture deficit stress reduced the development and growth of all maize hybrids at different stages and had a negative effect on grain yield. However, the period from one week before silking to two weeks after silking is the most sensitive stage [16]. Moisture stress during this period can lead to delayed silking, abortion of ovules, kernels and ears, low pollen production and viability [13]. Moisture deficit stress delay silking more than it delays pollen shedding in maize, resulting in increased ASI [53]. This lack of synchrony in male and female flowering is the main reason underlying maize yield loss under drought stress since ASI is directly correlated to kernel setting, number of kernels formed and cob filling [53].

Although sorghum is reputed for its ability to tolerate both intermittent and terminal water deficit stress, drought is still mentioned as a major factor limiting its production [53, 54]. Despite its drought tolerance abilities, long-term and severe drought stress can still be devastating to sorghum grain yield [49]. Due to its natural tolerance to mild droughts, it is a preferred crop when long dry periods are expected in the growing season or in naturally dry environments, especially in the tropics and sub-tropics, where it is grown as a yield assurance crop [49, 55]. Drought tolerance in sorghum is conferred by the ability of its root system to deeply penetrate the soil which allows high water uptake capacity [54], and the adaptation of its photosynthetic apparatus to withstand drought stress [52]. Drought reduces yield by up to 27, 27 and 12% respectively if it occurs during the early boot, heading and early grain filling stages [49]. Yield reductions are because of reduced number of panicles, seeds per panicle and seed weight [49].

The predominantly rice-growing areas in Asia are often threatened by severe abiotic stresses of-which the most common is drought [56]. Lowland rainfed rice ecosystems (about 25% of global rice areas) are drastically affected by drought stress due to unpredictable, insufficient, and uneven rainfall during the growing period [56]. Losses influenced by drought in rain-fed rice in Thailand are estimated to be as high as 45% [57]. The intensity of water-deficit stress depends on the duration and frequency of the stress [58]. Rice is most susceptible to drought stress particularly if stress coincides with the irreversible reproductive processes [59]. Rice is greatly susceptible to water deficit stress due to its small root system, rapid stomatal closure and little circular wax during mild stress [60].

3.2.2 Heat/extremely high temperature stress

Heat stress is one of the major abiotic stress limiting crop productivity worldwide [45, 60]. Many studies on the effects of high temperatures (heat stress) on crop productivity did not sufficiently separate the effects of heat stress from those of moisture stress [61]. This is because high air temperatures are highly correlated to high evapotranspiration, hence, low soil moisture content [62], therefore, studies are usually done on combined heat and drought stress. However, there is a possibility of determining the effects of heat stress divorced from the effects of moisture stress since heat stress impact on crop yield through physiological pathways different from those affected by moisture stress conditions [61]. High temperature stress causes a myriad of plant morpho-anatomical, physiological, and biochemical changes that affect the plant's capacity to produce yield [49, 63]. Heat stress affects all stages of the plant growth from germination to maturity resulting in yield threatening shifts to phenological developments [64]. However, the magnitude of the effects largely depends on plant species, varietal type and the growth stage [60, 63]. During germination, heat stress slows down or totally inhibit growth, during the vegetative stage it reduces photosynthesis and respiration capacity, affects water relations, and membrane stability [60, 63], while at reproductive phase, it reduces yield, mainly by reducing pollen production and viability [65]. In response to heat stress, plants produce a variety of stress-related proteins and reactive oxygen species (ROS) [61]. Some plants withstands heat stress by maintaining membrane stability, scavenging for ROS as well as production of antioxidants [61]. Heat stress incidences are mostly rampant in the tropics and sub-tropics and in the low altitude areas. However, on a global level, an estimated average surface temperature increase of 0.2 °C per decade in the next 30 years is expected [40]. This climate change-induced temperature increase is expected to be accompanied by increased frequencies of extreme weather events drastically reducing crop yields in general [66].

Heat stress has devastating results on maize production if the daily maximum temperatures exceed 30 °C [67]. These findings support the projections that the increasing seasonal temperatures will further lead to declines in maize yields as climate induced temperature changes continue [68]. Heat stress has greater impact on maize productivity compared to drought stress [69]. In a study conducted in the US Corn Belt, irrigated maize did not respond to heat stress and this demonstrated that good agronomic management and sufficient water supply can solve heat stress in maize production [62]. In East and Southern Africa, heat stress, as it occurs alone or in combination with drought stress, is projected to become an increasing constraint to maize productivity in those regions [65]. Heat stress in maize is associated with shortened life cycle, reduced light interception, increased respiration, reduced photosynthesis and increased pollen sterility [65].

Heat stress was identified as the most devastating abiotic stress limiting wheat production in developing countries [46]. Climate induced temperature increases are estimated to reduce wheat production in developing countries by 20–30% [70]. Heat stress during the anthesis and grain filling period accelerates maturity and significantly reduce grain size, weight, and yield [46]. For every 1 °C rise of temperature, global wheat production is predicted to decline by 6% [71]. In China, wheat yield reductions of up to 10% is estimated for each 1 °C temperature increase during the growing season [72]. Climate induced temperature increases are expected to reduce wheat production in developing countries by 29% [73]. Wheat farming systems in south and west Asia as well as in north Africa are projected to suffer most from heat stress and water scarcity due to climate change [26].

3.3 Main biotic factors

Biotic stresses are ravaging cereals globally as much as the abiotic factors [46]. These type of stresses rapidly evolve hence they are very difficult to manage. For instance, crop varieties developed as tolerant/resistant to certain pests and diseases are rendered susceptible within a short time when a new strain of a pathogen comes up [74]. Biotic factors include insect pests and diseases and weeds and all these significantly reduce crop yield through physical damage to plant tissue, physiological and biochemical effects. Climate change (global warming) [75] and increase in international grain trade has brought with it waves of new crop pest and disease epidemics such as the migratory locusts in the east and southern Africa (ESA).

3.3.1 Diseases

Yield losses due to diseases can reach 100% as in the case of rice blast [76]. Plant disease can cause significant yield losses if they occur during any of the plant growth stages but major damage occurs if the pathogens attack during certain critical and weak stages such as the seedling stage in rice production [76]. Diseases of economic importance in cereal production are those caused by fungal, bacterial and viral pathogens, but importance varies with regions. This is because the aggressivity and virulence of some pests and diseases depends on the prevailing climate, presence of natural enemies, type of crops cultivated, and the availability of their wild types. Pests and diseases that are native and not significant in other regions could be great threats to crop productivity in other regions. For example, the fall armyworm (FAW; *Spodoptera frugipeda*) is a native insect pest of cereals in north and south America where the pest is not is really a yield constrain, but in Africa, where it only emerged in 2016, FAW was reported to cause yield loses of 100% in some instances [77].

Diseases of economic importance in global maize production are turcicum leaf blight (*Exserohilum turcicum*), grey leaf spot (*Cercospora zeae-maydis*), maize streak virus disease, leaf rusts (*Puccinia sorghi*) and maize lethal necrosis (MLN) caused by a combination of maize chlorotic mottle virus (MCMV) and the sugarcane mosaic virus (SCMV), as well as ear rots (several fungal pathogens) [74]. Among all diseases that constrain global wheat production, three rusts caused by *Puccinia triticina* (Leaf rust), *P. striiiformis* (yellow rust) and *P. graminis* (stem rust), and the most feared Ug99 race of wheat stem rust caused by the fungus *Puccia graminis* Pers. F. sp. *tritici* Eriks. And E. Henn [76–79] are the most damaging and aggressive, worldwide. Of all biotic factors that constrain rice production, disease is the most important factor [74]. In rice production systems, disease occurrence is high in upland rainfed rice production systems compared to lowland systems (Ithisham). The major diseases of rice are bacterial blight (*Xanthomonas oryzaepypv. Oryzae* (Xoo)), sheath blight (*Rhizoctonia solani*), rice blast (*Pyricularia grisea*), rice yellow mottle virus disease, sheath rots (a combination of fungal and viral infections) and brown spot (*Bipolaris oryzae*) [76]. Bacterial diseases mostly occurs in the tropical and temperate regions of the world, but incidences are common in irrigated crops and in rainfed fields, especially when heavy rains will be coupled with strong winds.

Common diseases of sorghum are; anthracnose (*Colletotrichum graminicola*), charcoal rot (*Macrophomina phaseolina*), gray leaf spot (*Cercospora sorghi*), rough spot (*Ascochyta sorghi*), smut (Covered Kernel) (*Sporisorium sorghi*) and zonate leaf spot (*Gloeocercospora sorgh*).

3.3.2 Insect pests

Like in any other crop, insect pests cause yield losses in cereals by chewing tissues (e.g., FAW), boring into stems and leaves (e.g., maize stalk borer), sucking plant saps (such as aphids), and transmitting plant disease pathogens (e.g., white flies) [76]. Postharvest insect pests [e.g., maize weevil (*Sitophilus zeamais*) and the larger grain borer (*Prostephanus truncates*)] cause substantial yield losses of up to

40% of global maize grain [80]. Modelling studies have shown that the yield lost as a result of insect pests in the world's three most important crops (i.e., wheat, rice and maize) will increase by 10–25% per 1 °C increase in temperature [81]. Insect pest of economic importance to rice production depends on the region [82]. They are grouped into root and stem feeders, stem borers, gall midges, defoliators, leaf and planthoppers, and panicle feeders all of-which significantly constraining global wheat production [83]. The rice plant is vulnerable to insect attack throughout its growth cycle [82]. Of all the insects that can attack the wheat crop, it is the wheat stem sawfly and Russia wheat aphids, that cause significant economic losses in SSA [11]. The United States of America (USA) is the world's top maize producer of maize. In that country, maize production is limited by four key insect pests which are; corn earworm (*H. zea*), European corn borer (*O. nubilalis*), northern corn rootworm (*Diabrotica barberi* Smith and Lawrence and the western corn rootworm (*Diabrotica virgifera virgifera* LeConte) [75]. With global climate change, effects of these insect pests on maize production is expected to increase [75]. In SSA, maize stem borers (*Busiola fusca*), fall armyworm (*Spodopetera frugiperda*) [84] and migratory locusts (*Locusta migratoria*) [85], are of economic importance in cereal production. FAW is a recent insect pest in ESA, being reported first in 2016 [86]. It has over 100 hosts including cereals such as maize, sorghum, rice and wheat [84]. Stem bores are a serious threat to maize production in the humid forest and mid-altitude agro-ecologies of western central Africa [16]. In Africa where most of the world sorghum is produced, 42 sorghum panicle feeding insect pests have been identified as serious pests including the recently introduced FAW [87]. Most of these insect pests also feed on other crops such as maize [87].

4. Increasing the resilience of cereal production systems

4.1 Breeding for stress tolerance/resistance

Crop improvement for tolerance/resistance to biotic and abiotic stresses is regarded as the most sustainable and cost effective strategy that can be used to combat the current and the future food supply–demand discrepancies (**Figure 2**) [40]. Through plant breeding, many crop pest and disease challenges [89] and yield losses due to heat and drought stress factors [65] have been solved in Africa. Biotic stresses are quickly changing due to natural evolutions and climate-induced causes making new crop varieties quickly obsolete. Modern breeding strategies such as the doubled haploid technology, mutation breeding and genomic selection are being used to develop new varieties quickly, particularly in maize hybrid production [14]. Wheat improvement programs targeting drought and heat tolerance in rainfed lowland rice production systems are using marker-assisted selection (MAS) and rapid generation advance techniques to produce new rice varieties [57].

The climate change-induced abiotic stresses (especially, heat and drought) and biotic stresses (i.e., pests and diseases) are the major factors projected to continue constraining cereal production, especially in the developing countries. Stress tolerance/resistance can be: (i) identified among crop genotypes; (ii) improved in relatively tolerant/resistant genotypes; and, (iii) introduced into non-tolerant crop types [90]. Identification of stress resistance/tolerance in crop genotypes is one of the major ways to control crop pests and diseases and reduce the impact of abiotic stresses through crop improvement. For instance, sorghum genotypes tolerant to witchweed in Zimbabwe were identified which could be grown in areas prone to witchweed infestations [91]. The breeding techniques of screening genotypes for stress tolerance/resistance is also being used in identifying maize,

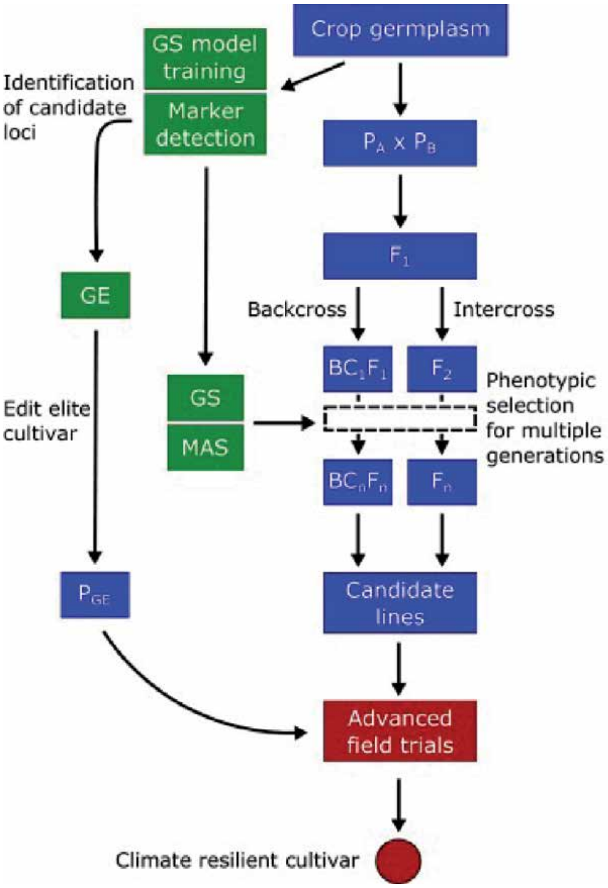

Figure 2.
Genomics-assisted breeding scheme for developing climate resilient cultivars. Steps for developing candidate lines from the initial crop germplasm pool and a selected parental cross (PA x PB) or genome edited elite cultivar (PGE) are shown in blue. Genomic methods assisting the conventional backcrossing (BC1F1 to BCnFn) and intercrossing (F2 to Fn) approaches are shown in green. In a final step, shown in red, genome edited cultivars and candidate lines selected from the successive generations of backcrosses or intercrosses are tested for broad viability in advanced multi-environment field trials to select novel climate resilient cultivars. Abbreviations: genomic selection (GS), marker-assisted selection (MAS), genome editing (GE), breeding generations resulting from intercrosses (F1 to Fn), breeding generations resulting from backcrossing to a parental cultivar (BC1F1 to BCnFn) (Adapted from Scheben et al. [88]).

wheat and sorghum genotypes with tolerance to heat, drought and combined heat and drought stress conditions [42, 52]. In breeding for stress tolerance, traits that confer either stress escape or stress avoidance are selected for but selecting for yield under these stress factors is also known to be effective [43]. For drought tolerance, crops (e.g., maize) with an efficient root system for water uptake, high water use efficiency, a canopy that loses less water, and high grain yield under stressful environments are selected for [43]. Stress resistance or tolerance can be outsourced from exotic genepools and can be introduced into local elite genotypes.

Development of new drought resistant rice varieties is the objective of rainfed lowland rice breeding programs in Asia. In ESA, breeding efforts for drought and heat stress tolerance [65] are being combined with tolerance to low soil nutrients (phosphorous and nitrogen for maize) [92], for maize, wheat, sorghum and rice [43]. Many studies on the effects of heat stress and drought on cereal production have combined since they are closely related [61]. Some studies estimated a 13% decrease in maize yields by a projected 2% increase in temperature while a 20%

increase in intra-seasonal variability reduced maize yields by only 4.2% [65]. These studies highlight the need to incorporate heat tolerance as well as increased drought tolerance into maize germplasm in order to offset these predicted yield losses [65]. The international Center for Maize and Wheat Improvement (CIMMYT) has been leading for decades, in breeding for drought and heat stress tolerance in maize, both in the tropical and subtropical regions [65]. However, relatively less effort has been devoted to breeding specifically for heat stress tolerance in maize. Short season varieties use drought avoidance [13].

Breeding efforts for disease and pest tolerance in cereals have successfully solved some of the biotic constraints to cereal production. Genetically modified (GM) maize varieties resistant to pests of the lepidopteran family such as FAW and the stem borers are being successfully grown in some countries such as the U.S and in South Africa [93]. Breeding crops to resist abiotic and biotic stresses should not compromise other desirable traits of the crops such as high yield and quality. Modern sorghum varieties are a blend of the desirable characteristics of both white and colored sorghum to provide consumers with colored sorghum with higher antioxidants levels while being suitable for farming through resistance to molds, bird and insect pest damage [27]. In SSA, breeding of cereals has also produced high yielding and stable maize hybrids with good post-harvest qualities [16].

4.2 Agronomic practices

Understanding the nature of the stress and crop response to abiotic and biotic stresses allows the farmer to employ agronomic practices that effectively reduce the impact of the stress on crop yield [42]. Agricultural practices that conserve soil moisture or use of varieties that has high water use efficiency will reduce the impact of climate-induced droughts and heat stress on crop production. Agricultural practices such as proper crop rotations, proper fertilizer application, proper planting time, proper tillage practices, good varietal selection, optimum seed rate, effective weed management, proper soil nutrient management and sufficient water supply have been reported to mitigate both abiotic and biotic stresses in cereal production [42]. In Zimbabwean smallholder farming systems, maize damage from FAW was significantly reduced by frequent weeding, zero and minimum tillage [94]. Effective weed control directly and indirectly controls crop pests and diseases and the impact of drought under rainfed lowland rice production systems [76]. At farm level, cereal productivity could be increased by prioritizing adoption of new and improved agricultural technologies [95].

Techniques such as conservation agriculture (minimum soil tillage, mulching, and crop rotations) are effective in conserving soil moisture in moisture deficit areas, especially in small and medium-scale farms [41, 87]. Irrigation with good quality water eliminates drought stress in crop production. High maize yield can be maintained in areas with insufficient precipitation by appropriate irrigation [4]. However, drip irrigation combined with mulching was shown to reduce water loss by 45% compared to sprinkler irrigation in some farming systems [96]. Proper weed control reduces water deficit stresses in cereal production since weeds directly compete with crops for available moisture [76].

5. Conclusion

Cereals are important as human food, animal feed and industrial raw materials. Their production is under threat from climate-induced stresses such as high temperatures, droughts, pests and diseases. Climate change is projected to continue

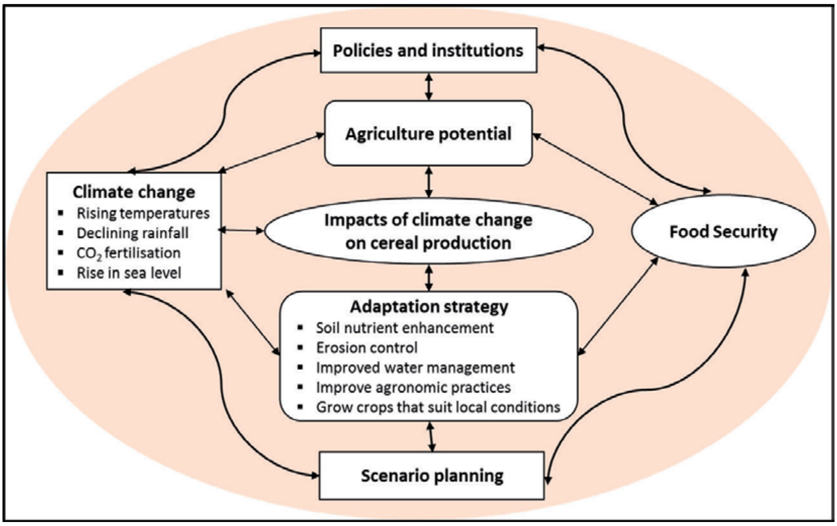

Figure 3.
Methodological flowchart for climate change, cereal yield and food security (Adapted from Nhamo et al. [97]).

threatening crop production and if it continues at the current rate, many regions of the world will be inhospitable to crop production. If future food and nutrition security is to be guaranteed, investments in crop breeding and efficient crop production systems are needed. Crop breeding produces crop varieties suitable for growth in stressful environments. Proper agronomic practices such as proper tillage, planting dates, water management, nutrition management, pests and disease management, coupled with appropriate crop genetics, together with holistic policies at institutional, governmental or regional levels (**Figure 3**), can offset any climate related yield losses expected in the future.

Author details

Clemence Muitire[1], Casper Kamutando[2]* and Martin Moyo[3]

1 Department of Soil and Environmental Science, University of Manitoba, Canada

2 Department of Plant Production Sciences and Technologies, University of Zimbwabwe, Zimbabwe

3 International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Zimbabwe

*Address all correspondence to: kamutandocn@gmail.com

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Chapter 9

Management of False Smut Disease of Rice: A Review

Mathew S. Baite, Mukesh K. Khokhar and Ram P. Meena

Abstract

Rice (*Oryza sativa* L.) is the most important food crop of the developing world. Among the biotic stresses of false smut is an emerging disease caused by *Ustilaginoidea virens*. The disease reduces both the quality and quantity of rice. The pathogen produces mycotoxins that are harmful to animals and humans. The disease is severe when favorable environmental conditions like high humidity (more than 80%) and temperature ranging from 25 to 30°C, late sowing and high soil fertility as well as using high amount of nitrogen. It has gained the status of a major disease of rice and causing varying yield loss depending on the weather conditions during the crop-growing period and the genotypes. Therefore, the primary concern of the farmers is the disease management methods, which are effective, simple and practical. Since, there is no single effective management strategy for false smut, we have discussed about the potential management options available depending upon the economic status and adoption capacity of the farmers. In the Plant Pathologists point of view, eco-friendly methods of disease management like cultural, biological and use of resistant variety should be advocated for sustainability of agriculture and human being.

Keywords: Management, false smut, rice, disease, *Ustilaginoidea virens*

1. Introduction

Rice is one the most important food crop of India. It is cultivated in all states from North to South and East to West. India is the second largest producer of rice in the world after China. In 2018–2019 India produced 116.47 million tonnes of rice with an average productivity of 2638 kg/hectare (Indiastat.com). However, rice is constantly attacked by biotic stresses namely pathogens, insects and weeds etc. False smut of rice is a destructive inflorescence disease caused by *Ustilaginoidea virens* (Cooke) Takahashi (teleomorph: *Villosiclava virens*). It was a minor disease with sporadic occurrences. However, it has recently become emerging disease in the majority of rice-growing areas of the world due to planting of high-yielding varieties and hybrids and climate change [1, 2]. The disease caused yield losses of rice by 2.8–81% depending on the disease intensity and genotypes [3, 4]. The disease caused grain quality reduction and mycotoxins produced by the pathogen is poisonous to livestock and humans [5]. The pathogen converts individual grains of the rice panicle into greenish spore balls (false smut balls) of a velvety appearance [6], the surface of which are covered by powdery dark-green chlamydospores during maturity (**Figure 1**).

Figure 1.
Rice panicle infected with false smut.

The chlamydospores survive the winter in the soil and act as primary source of infection in the succeeding rice plants. Therefore, the pathogen is primarily soil and air-borne. The pathogen is a slow-growing fungus that forms abundant conidia in cultures which are globose in shape and echinulated under scanning electron microscope [7, 8]. False smut of rice can be managed using appropriate fungicides, cultural practices, bio-agents, plant extracts, resistant cultivar and integrated disease management techniques which are briefly discussed.

2. Management through fungicides

The most common method of plant disease management is by use of chemical pesticides. It is popular with farmers probably due to easy availability and quick action. The control of rice false smut is mostly relied on fungicides. However, they are harmful to environment and increase the cost of cultivation and hence are highly discouraged whenever possible. Therefore, it should be used judiciously as prevention but not as curative measure. The timing and dose of application of fungicides are also important to control the disease. Crop loss is common where fungicide application timing is incorrect or an inadequate concentration of the material is applied [9, 10]. Therefore, need based applications are highly advisable for their usage.

Various fungicides such as Wenquning (a suspension of *Bacillus subtilis* in a solution of validamycin), copper oxychloride, cuproxat, simeconazole, tebuconazole, copper hydroxide, difenoconazole and hexaconazole have been reported for the control over 70% of rice false smut disease [11–16]. Field tests were conducted [17], to determine the effect of fungicide applications to flooded paddy water to control false smut. The results showed that the application of simeconazole granules to the paddy water two to five weeks prior to the heading stage of rice was highly effective against false smut and the fungicide application at three weeks was the most effective. Application of prochloraz + carbendazim followed by chlorothalonil were efficacious in controlling the false smut of rice [18]. There is a report that propiconazole 25EC (0.1%) recorded lowest disease severity than other treatments, followed by trifloxistrobin + tebuconazole 75 WG when sprayed at booting or 50% panicle emergence [19]. Higher yields were obtained when propiconazole 25 EC was sprayed at booting stage and also trifloxystrobin + tebuconazole 75 WG at booting. Spray of propiconazole and hexaconazole were effective in managing the rice false smut [20].

The eventual goal of reducing fungicide use in rice production will be accomplished by using different broad-spectrum, bio-rational fungicides in rotations with traditional fungicides as preventive or need based applications. Further studies are desirable to explore the best fungicide that is specific and effective against *U. virens*, their use as potential, economical phytochemical molecule against false smut of rice.

3. Management through cultural practices

Cultural practices prevent the disease through disease avoidance, escape or protection because they disrupt the favorable interactions of the pathogen, host and environment. Cultural practices like cleaning of bunds and fields reduce the incidence as the disease has been reported on some of the weeds [21]. Date of planting and maturity time of different genotypes have significant effects on the incidence and severity of the false smut [22]. Water management and fertilization affected false smut incidence [23]. The late-maturing varieties exhibited higher rates of infection even though three different sowing dates with an interval of 14 days were set for each variety under examination [24]. Furthermore, early maturing rice varieties escaped from false smut infection, while the late maturing ones did not. Disease avoidance by changing date of sowing/planting is an established fact and very economical and practical for marginal farmers in managing plant disease. Therefore, changing sowing time is a preventive control strategy that can be opted by the marginal farmers when the disease is endemic in a location with a susceptible cultivar.

4. Management through bio-agents

Biological control is the use of living organism to inhibit/kill the other target living organism (**Figure 2**). It is the most eco-friendly and economical method of plant disease management when there is no resistant variety available. The major mechanisms of biological control are follows;

1. Predation/Hyperparasitism

2. Production of Antibiotics

3. Production of Lytic enzymes

4. Production of Unregulated waste products like Ammonia, Hydrogen cyanide etc.

5. Competition for food, space, Siderophore scavenging

6. Induction of host resistance

The management of the rice false smut disease is not well documented, as its striking epidemiological features under field conditions are still uncertain. Therefore, integrated management of the false smut using fungicide applications, cultural practices and deployment of resistant cultivars if available, have been tried before to a certain extent with average results [25].

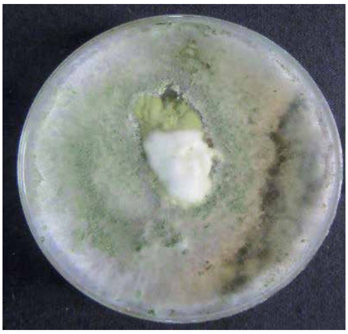

Figure 2.
Mycelial growth inhibition of U. virens *at the Centre by* Trichoderma harzianum *at the periphery.*

Biological control by *Trichoderma viride*, *Trichoderma virens*, *Trichoderma harzianum* and *Trichoderma reesei* were studied under *in vitro* and reported that all the isolates of Trichoderma have showed antagonistic activity against *U. virens* [26] but their utilization is not advisable as they are the preliminary results, which are not tested in fields. There is a report of *Antennariella placitae* (endophyte) as a good candidate for application as safe biological control agent against *U. virens* in vitro and in vivo [27]. The biological control by *Bacillus subtilis* showed least false smut disease severity under field evaluation (First author, unpublished). Biological control is eco-friendly and safe to the environment. They are much cheaper than fungicides. Thus, bio-control of rice false smut disease either individually or in integrated disease management approach might offer a more effective substitute to unsafe chemicals which is uneconomical and cause a substantial damage to the public health, environment as well as groundwater pollution. It is also considered as a very worthy alternative since it mimics the nature's own way of equilibrating the population of living organisms in the ecosystem. Whenever possible, bio-agents should be used because it is a neglected area of false smut research. Future research is desirable to bring out effective bio-agent for false smut disease.

5. Management through plant extracts

The utilization of plant extracts in disease management is a contemporary eco-friendly approach and gaining attention bearing in mind that of its benefits over chemical pesticides. The advantages of such plant products are that they are easily biodegradable, without any residue, non-phytotoxic and are easily absorbed by the plants and cost-effective method. Plant products such as certain leaf extracts and plant oils could also be used to control rice false smut. A group of researchers investigated plant extracts under *in vitro* against rice false smut pathogen which was considerably inhibited by bulb extract of garlic (*Allium sativum*), rhizome extract of turmeric (*Curcuma longa*), leaf extracts of lantana (*Lantana camara*) and bael (*Aegle marmelos*), whereas plant oils lemon grass (*Cymbopogon flexuous*) cinnamon (*Cinnamomum zeylanicum*), and palmarosa (*Cymbopogon martinii*) oils that completely inhibited the *U. virens* growth [19]. Since, fungicides are harmful, plant extracts along with bio-agents offer safe solution to the management of false smut. Future research may focus to find out effective plant extracts to manage false smut disease in rice.

6. Management through resistant variety

Management of plant diseases by use of resistant cultivars is cost-effective, durable and practical strategy. Unfortunately, no progress has been made to develop or improve rice variety/cultivars resistance to false smut disease, which might be due to lack of efficient artificial inoculation method to evaluate disease resistance reliably or absence of resistant gene donor. There are few reports on identification of quantitative trait locus (QTL) in rice against false smut [28–31]. However, their incorporation or utilization to improve rice cultivars against false smut is lacking. Therefore, R-gene should be identified and incorporated into an elite variety without compromising yield and can go a long way as resistant variety.

7. Integrated disease management

Integrated disease management utilizes all available resources, minimum use of chemicals and focus more on cultural practices. All possible methods are combined to manage the disease in a holistic manner because not a single method is effective enough to manage the disease. In the past few years, the disease has become a potential threat to rice cultivation and is difficult to manage by means of both fungicides and crop rotation alone or any other traditional control methods of plant diseases. Thus, an integrated method is important for successful management, especially under challenging conditions of rice production. Incorporation of resistant varieties, good cultural management tactics and use of recommended fungicides and bio-pesticides are indispensable for the management of false smut of rice.

Wenquning, which is a suspension of *Bacillus subtilis* in solution of validamycin, has been widely used in China for the management of false smut of rice [21]. However, there is limitations like the difficulty of on-time application and getting strains from the unfavorable weather around the heading dates had stalled its control efficiency and resulted in failures to control the disease. The success and sustainability of integrated disease management approach, especially with resource-poor farmers, significantly depends on their participation in helping generate locally precise methods and solutions appropriate for their particular farming systems and integrating control mechanisms that are ecologically sound and readily available to them. Future, research is required for integrated disease management in different locations wherever, false smut is severe and threatening. Such methods should be simple to follow, acceptable and easily available with the farmers.

8. Conclusion

False smut is gradually emerging as a potential threat to rice cultivation around the globe. Since, there is no single effective method to combat the disease, all-available and suitable methods should be utilized to manage the disease as a short term strategy. However, for long-term strategy, the breeding and utilization of resistant cultivars are considered as the most effective strategies to manage false smut disease. Yet, little is known about the resistance gene(s) and quantitative trait loci for this important disease as well as molecular mechanisms for resistance against *U. virens*. Consequently, there is an increasing demand for new and effective methods to supplement the existing disease management strategies to achieve superior control of false smut. Therefore, the research for resistant variety is the need of the hour for making the rice production a sustainable movement. Among the management methods available for false smut disease, the method should be chosen based on the disease intensity and economic status of the farmers. If the marginal farmers faced severe threat of false smut, management by cultural practices viz., change of sowing time to avoid the disease is one simple with no-cost involved and wherever available use of effective bio-agents. If the farmers can afford, timely application of fungicides in moderation as a preventive measure but not as curative. The use of resistant cultivar and integrated disease management should also be recommended for such progressive farmers when such varieties are available.

9. Future challenges

For further research, the following points may be taken up with respect to rice false smut disease.

1. Standardization of artificial inoculation technique for false smut disease.
2. The role of toxins in conferring pathogenicity of the pathogen.
3. Role of enzymes like chitinase in management of the disease.
4. The threat pose by false smut with respect to climate change.
5. Biological control of false smut.
6. A rice variety that is both climate resilient and false smut resistant may tackle the twin problems of rice farming in the future.
7. Management of the disease by application of nanotechnology

Conflict of interest

The authors declare no conflict of interest.

Author details

Mathew S. Baite[1]*, Mukesh K. Khokhar[2] and Ram P. Meena[3]

1 ICAR - National Rice Research Institute, Cuttack, India

2 ICAR - National Research Centre for Integrated Pest Management, New Delhi, India

3 ICAR - Directorate of Medicinal and Aromatic Plants Research, Anand, Gujarat, India

*Address all correspondence to: mathew.baite@gmail.com

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Chapter 10

Etiology, Epidemiology and Management of Asian Soybean Rust (ASR) in Brazil and Vulnerability of Chemical Control of Specific without Multisite Fungicides

Fernando Cezar Juliatti and Laércio Zambolim

Abstract

Brazil is the first soybean producer in the world, and the largest exporter. In the 2019/20 harvest, the country produced about 124.85 million tons, representing 30% of world production. Global soy production for 2019/20 reached 337.9 million tons. Asian soybean rust (ASR) is the most pathogen on soybean in Brazil in nowadays. Target spot and Septoria leaf spot plus white mold complete these scenarios. ASR emerged in Brazil in 1979. The use of fungicides in the soybean crop in Brazil intensified after the master of 2002 with the resurgence of soybean rust, where the use of triazoles intensified. The massive sprays to pathogen control reached 3.5 sprays per season. In 2006, the first reports of loss of sensitivity of the fungus to the group appeared, notably for the fungicide flutriafol and tebuconazole used in many situations in a curative way or to eradicate the fungus. From that moment on, the productive system sought to use triazoles and strobilurins. In 2011 came the first reports of loss of sensitivity of the fungus in the group of strobilurins. This fact was due to the use of pyraclostrobin in the vegetative phase of soybeans without protection by multisite. That same year, the introduction of the active ingredients in copper oxychloride, mancozeb and chlorothalonil took place in Brazil. In 2015, the first carboxamides ((benzovindiflupyr) (solatenol and fluxpyroxade) associated in triple mode with triazoles and strobilurins were launched on the Brazilian market. Due to the specific mode of action in the metabolism of the fungus (biosynthesis of ergosterol (triazoles), mitochondrial respiration in the cytochrome oxidase enzyme complex - QOIs (strobilurins) and succin dehydrogenase - SDHIs (carboxamides), the need for their association in the sprayings was seen. To multisite (cuprics, dithiocarbamates and nitriles). For the sustainable management of the disease in Brazil, control strategies are recommended, such as the use of systemic fungicides, with a specific biochemical mechanism of action with the adoption of tank mix with multisite, adoption of cultural practices (sanitary emptiness) and sowing schedule and the use of varieties with quantitative resistance (partial or horizontal resistance). These measures will guarantee the sustainability of the culture and the useful life of systemic fungicides or specific sites.

Keywords: soybean rust, specific fungicides, multisite, management, spraying, host resistance.

1. Introduction

Soybean [*Glycine max* (L.) Merrill] is one of the ten most economically important crops worldwide, as it is one of the main sources of protein concentrates and vegetable oil [1]. Brazil is the first soybean producer in the world, and the largest exporter [2]. In the 2019/20 harvest, the country produced about 124.85 million tons, representing 30% of world production [3]. Global soy production for 2019/20 reached 337.9 million tons [4]. The potential of the soybean crop yield can be affected by several factors, among which stand out the soil fertility, water availability during the harvest, the plant population, the sowing time, the productive potential of the cultivar, the occurrence invasive plants, pest infestation and diseases [5–8]. With the increasing incidence and severity of leaf spots in soybean crops [9, 10] in the last harvests greater attention has been paid to multiple soybean epidemics involving brown spot (*Septoria glycines*), target spot (*Corynespora cassiicola*) and rust itself [9–11]. In this review is appointed the symptoms, etiology and epidemiology of the disease. The calendar system to sowing in Mato Grosso state to seeds production. The use of fungicides in the soybean crop in Brazil intensified after the master of 2002 with the resurgence of soybean rust, where the use of triazoles intensified. The massive sprays to pathogen control reached 3.5 sprays per season. In 2006, the first reports of loss of sensitivity of the fungus to the group appeared, notably for the fungicide flutriafol and tebuconazole used in many situations in a curative way or to eradicate the fungus. From that moment on, the productive system sought to use triazoles and strobilurins. In 2011 came the first reports of loss of sensitivity of the fungus in the group of strobilurins [8]. This fact was due to the use of pyraclostrobin in the vegetative phase of soybeans without protection by multisite. That same year, the introduction of the active ingredients in copper oxychloride, mancozeb and chlorothalonil took place in Brazil. In 2015, the first carboxamides (solatenol and fluxpyroxade) associated in triple mode with triazoles and strobilurins were launched on the Brazilian market. Due to the specific mode of action in the metabolism of the fungus (biosynthesis of ergosterol (triazoles), mitochondrial respiration in the cytochrome oxidase enzyme complex QOIs (strobilurins) and succin dehydrogenase - SDHIs (carboxamides), the needfor their association in the sprayings was seen. to multisite (cuprics, dithiocarbamates and nitriles). For the sustainable management of the disease in Brazil, control strategies are recommended, such as the use of systemic fungicides, with a specific biochemical mechanism of action with the adoption of tank mix with multisite, adoption of cultural practices (sanitary emptiness) and sowing schedule and the use of varieties with quantitative resistance (partial or horizontal resistance). These measures will guarantee the sustainability of the culture and the useful life of systemic fungicides or specific sites [12].

1.1 Damage caused by Asian soybean rust (ASR)

The basic cycle of soybean rust is characterized by the phases of pathogen-host relationships in a few days when it does not show partial or horizontal resistance. Genotypes that are among the most active in Brazil, such as BMX Desafio, Foco, Bonus, and others exhibit this behavior, that is, latency between 7 and 10 days. Genotypes with horizontal and/or conventional resistance such as BRS Conquista, IAC 100 that are no longer cultivated have a latent period of more than 20 days [13–15]. For these genotypes with horizontal or partial resistance, there is greater flexibility in the use of fungicides and or an increase in the range of applications, facilitating programs for the management or monitoring of the pathogen. One of the milestones and systemic action to understand the etiology, epidemiology and control of rust soybean was to hold the 1st Brazilian Workshop on Soybean Rust [16] uniting the entire production chain and companies in an attempt to understand the dynamics of the various interactions in Brazilian biomes and soybean production. Later the first English version was published [17], with the contributions of those involved, in their respective specialties.

1.2 Losses

Among the diseases that occur in soybean crops, Asian soybean rust (FAS), caused by the fungus *Phakopsora pachyrhizi* Sydow, is considered to have the greatest destructive potential, and may cause damage ranging from 10 to 90% in the various geographic regions where it was reported [8, 11, 18–20]. Accounting for the losses related to the decrease in soybean productivity, expenses with chemical control (fungicides and application expenses) and the impact on tax revenue until the 2019/2020 harvest, after its resurgence, rust represented accumulated losses of more than US $ 30 billion [21], a number that exceeds the foreign currency collected by Brazil in soybean exports from 2019 to 2020 [22]. In Brazil, damage attributed to Asian rust of 70% in the 2001/2002 harvest was reported [23–25]. In the same harvest in the region of Chapadão do Sul, MS, damage of up to 100% was recorded [26, 27]. Losses in the 2002–2003 crop reached almost one billion dollars [11, 28]. According to Juliatti et al. [11, 29–31], rust has reappeared in Brazil, with frequent epidemics, due to the use of benzimidazoles fungicides only to control end-of-cycle diseases, increasing the area cultivated in several biomes and varied sowing time allowing the fungus to survive, as well as the presence of green bridges. The attacked plants undergo defoliation and early maturation, in relation to plants not infected by rust, which causes a reduction in the weight and quality of the grains produced [18]. Currently, due to the limited availability of resistant cultivars, adapted to different cultivation regions, the application of fungicides is the main control tool adopted by farmers. As a result, some populations of the pathogen have already shown an increased reduction in sensitivity to certain fungicides [32–34]. Given this scenario, the search for resistant cultivars is fundamental as part of a long-term sustainable control strategy [35]. However, until now, it has not been possible to find varieties with long-lasting rust. There are promising studies for the use of smaller genes for resistance leading to or allowing the use of them and the reduction of fungicide control in the future [15, 36, 37].

2. Chronology of the disease

Asian rust was first described in Japan, in 1902 [38], and in 1914, it had already spread to several countries in Southeast Asia. On the African continent it was first registered in Togo, in 1980 [39], then in Uganda, in 1996 [40], followed in 1998 in Kenya and Rwanda [41], Zimbabwe and Zambia [42]. In 2001, it was found in South Africa and Nigeria [43], Missiones, Argentina in 2003 [44] reaching an epidemic character [45]. In 2007, rust was also reported in Ghana. In the American continent, it was first reported in 1976 in Puerto Rico [46], followed by Hawaii in 1994 [47]. The first report in South America in Brazil was made by Deslandes [48], in the south of the State of Minas Gerais. At that time the mycologist prof. Deslandes detected both American rust (*P. meibomiae*) and Asian soybean rust (*P. pachyrhizi*) [49] (**Figure 1**) in soybean plantations and in semi-perennial

Figure 1.
Detection of soybean rust (A) in Brazil (Phakopsora pachyrhizi and P. meibomiae by Deslandes (right) in 1979). Photo from Fernando C. Juliatti's personal file, kindly provided by J.T. Yorinori("in memorian"). (B) Epidemics of soybean rust in late sowing. Personal archives Fernando C. Juliatti. (C).

legumes [49]. The authors, via molecular comparison with specific primers for the two species, confirmed the studies and the been reported in Bolivia [50] and Colombia [51], progressing in 2004 to Uruguay [52] and 2005, in Ecuador [53], Mexico in 2009 [54]) and the United States [55]. Currently, Asian soybean rust (FAS) is present in all countries, where soybean is cultivated. Its spread was rapid throughout the world, dueto the fungus's urediniospores being disseminated by wind currents [5, 41, 56–60].

The **Figure 1** shows infection of the pathogen in cotyledons, as happened in Primavera do Leste, MT, in 2004 due to frequent infections in irrigated plantations under central pivot and consecutive sowing times. In nowadays is common near the urban cities around the 163 highway to see "guaxas´ plants" (volunteers plants) of soybean with uredines and spores after summer crops in Mato Grosso state (**Figure 2**).

3. Host of the pathogen

The causative agent of FAS is a biotrophic fungus, which survives on green soybeans or other hosts. Hartman et al. [61] report that, unlike other rusts,

Figure 2.
Detection of soybean rust (A) in Brazil (Phakopsora pachyrhizi) in guaxas (volunteers' plants) soybeans plants in highway 163 around the cities in the Mato Grosso state. Personal archives from Fernando C. Juliatti.

P. pachyrhizi can aturally infect a ide range of plant species, including 41 species in 17 genera of the baceaefamily. In ddition, 60 plant species belonging to 26 genera were experimentally infected under controlled conditions [62], reaching up to 90 species [63]. The fungus can also infect and sporulate in species belonging to the subfamily Papilionoideae, family Fabaceae having as main hosts, the species *Glycine max*, *G. oyae*, *Pachyrhizus erosus, Pueraria lobata* and *Vigna unguiculata* More eferences are found in the literature regarding *P. pachyrhizi* hosts, among which the following stand out: *Phaseolus vulgaris* var. *vulgaris*, *Canavalia gladiate* [63, 64], *Phaseolus vulgaris* [65], *Vicia faba, Vigna radiata, V. mungo, Psophocarpus tetragonolobus, Colopogonium muconoides* [64], *Alysicarpus vaginalis, Securigera varia, Melilotus officinalis, Trifolium repens, T. incarnatum,* [62], *Phaseolus lunatus var. lunatus, Sesbania exaltata, Trigonella foenum-graicum* [5, 6], *Phaseolus coccineus* [66], *Pachyrhizus ahipa, Cajanus cajan* [67], *Crotalaria anagyroides*, *C. spectabilis*, *Macropureum* [68]), *Pueraria amontana var. lobata* [69, 70], *Lespedeza cuneata, Kummerowia striata, K. stipulaceae, Pisum sativum*, [71], *Lipinus albus, L. angustifolius, L. luteus, Lotus* spp. [68], among others. In 2015, the pathogen was found in 'jacatupe' (*Pachyrhizus erosus*), near a soybean field in Federal University of Viçosa, Minas Gerais State (MG), Brazil (Zambolim, 2015, unpublished data).

4. Symptoms of the disease

The symptoms caused by FAS, in its initial state, are easily confused with other diseases, such as bacterial pustule (*Xanthomonas axonopodes* pv. *glycines*), bacterial blight (*Pseudomonas savastanoi* pv. *glycinea*) and brown spot (*Septoria glycines*). The fructifications of the causal agents are not very evident, so that with the naked eye, it is difficult to distinguish ferruginous pustules, which give the common name, to this group of diseases [11, 51]. The same author reports that the symptoms caused by soybean rust are called "lesions", and not pustules, like other rusts, because leaf tissue necrosis occurs and each lesion can present several pustules. Symptoms can appear at any stage of development and in different parts of the plant, such as cotyledons, leaves and stems, with leaf symptoms being the most characteristic [11, 72]. The color of the lesions varies from greenish gray to reddish-brown, with one or more globular uredines, mainly in the abaxial part of the leaf [11, 61]. Sporadically uredines may appear at the top of them [72]. The number of lesions and uredines on a leaf (abaxial part) can reach from 26 to 46 per cm2 under controlled conditions. The initial manifestation of the disease is observed as chlorotic leaf areas in a polygonal shape, because of the delimitation imposed by the veins, which may reach a size of 2–5 mm2 [11, 51]. The first lesions, in general, are found in the low leaves close to the soil, when the plants are in the phenological stage, near or after flowering [11, 51]. Progressively, the uredines acquire a light brown to dark brown color, which open in a tiny pore, expelling the urediniospores (**Figures 1** and **2**), hyaline in color that become beige and accumulate around the pores or are removed by the wind [11, 72]. As the sporulation proceeds, the leaf tissue around the first uredines acquires a light brown color, called a susceptible lesion or TAN (tanish) and the other reddish brown, known as a resistant lesion or RB (redish-brown). [6, 11, 72–74]. The final stage of the soybean rust epidemic in a crop is characterized by general yellowing of the foliage, with intense defoliation, reaching the complete fall of the leaves [11, 51].

5. Causal agent of the disease

Taxonomically the fungus is classified as follows: Kingdom: Fungi; Class: Basid iomycetes; Order: Uredinales; Family: Phakopsoraceae; Current name: *Phakopsora pachyrhizi* Sydow and Sydow; Synonyms: Phakopsoraoyae Fujikuro; *Phakopsora calothea* H. Sydow; Malupaoyae (P. Hennings) Ono, Buritica, and Hennen comb. 06 nov. (Anamorph) Uredooyae P. Hennings [75].

6. Conditions that favor the disease

The fungus has a short life cycle, under the following conditions: Fine and frequent rains, long periods of dew and temperatures between 15 and 29° C. FAS epidemics can quickly increase from almost undetectable levels to an extremely high incidence, severity and prevalence. Spore production can last at least three weeks [76–78]. The rapid development of the disease has been correlated with canopy closure at the flowering stage (R1+) [76, 79–81]. For this reason, FAS causes a high defoliation rate of the crop, and continues until the environment is no longer conducive to the development of the disease [11, 28, 82]. Then, FAS progresses until there is complete defoliation of the canopy, or until the environment is no longer conducive to the development of the disease [11, 82]. According Bromfield [5, 6], flowering infection can produce high levels of damage, compromising the formation and filling of pods, the final weight of the grains [11, 83], affecting the oil and protein content [59]. After infection, the fungus produces uredinia and urediniospores between seven and 14 days, according to environmental conditions [76, 80]. The symptoms are grouped into staining lesions from 2 to 5 mm in diameter, with two to five uredines. and abundant sporulation or formation of reddish lesions, with zero to two uredines and sparse sporulation [5, 6].

7. Disease control

The control of FAS must be integrated, as an isolated measure will not result in success, as it is an extremely aggressive pathogen. To reduce the risk of rust damage to the crop, the following management strategies in Brazil are recommended: use of early cycle cultivars, sowing at the beginning of the recommended season, the elimination of voluntary soy plants and the absence of soy cultivation in the off season through the sanitary vacuum (60 to 90 days), monitoring the crop since the beginning of crop development, the use of fungicides in the appearance of symptoms or preventively and the use of resistant cultivars, when available [84]. Therefore, the first step in the control of FAS is based on the adoption of cultural measures and genetic resistance [85, 86] including quantitative resistance and tolerant varieties [82]. Therefore, the solution to control Asian soybean rust is in the integration of methods, with emphasis on cultural, genetic and chemical. Monitoring the disease in soybean crops is of great importance. In studies carried out by the rust consortium coordinated by Embrapa Soybean, it was found that, in at least 20 to 30% of the country's planting areas, the disease did not reach a level of control, due to climatic variations [87–89]. The recommendation of chemical control should always be preventive, since the application after the onset of the disease resulted in reduced productivity [90]. The preventive concept, although vague, should be based on spore collection systems (spore-hunters), sown plots ("sentinels"), at least 30 days before sowing in the region [56, 91] and automatic stations that monitor the climate and favorable conditions (temperature and leaf wetness), the occurrence of the pathogen and disease. In addition, it is essential to use an efficient application technology, as well as the choice of correct spray tips, for each situation [11, 92].

8. Cultural control

One of the indications for cultural control is to increase the area of crop rotation, because where this measure is practiced for a year, with grasses (corn, sorghum and rice), in place of safrinha soybeans, it has facilitated the control of rust [20, 93–97], as it favors the management of voluntary plants. The presence of "tiguera" or voluntary soybeans inside cotton fields, in the states that sow cotton, after soybeans is a sign of the perpetuation of inoculum from one crop to another since the cotton is harvested in June. Voluntary soy that is on the side of highways in Brazil and in urban areas must also be eliminated, for the reduction of inoculum, for the next harvest. Such fungicides are fundamental in the management of soybean rust fungus resistance. In this case, it reduces the directional pressure on resistant or less sensitive populations to specific sites (triazoles, strobilurins and carboxamides) [11, 33, 98–101]. In this way, stabilizing selection is practiced in the field, preventing the emergence of new pathotypes or breeds of the fungus. Even silicate fertilizers via soil or foliar [102], assist in the management of resistance to systemic or penetrating and mobile fungicides [103]. The use of suitable cultivars at each sowing time is essential for the success and sustainability of control programs [104].

The use of early-cycle cultivars decreases the time of exposure of the plant to the pathogen, as does sowing at preferred times, avoiding late sowing [51]. The load or potential of inoculum is greater due to the multiplication of the fungus, in the first crops [20, 60, 96]. The population arrangement of plants can also contribute to mitigate rust. Ramos et al. [105] observed that greater spacing between cultivation lines results in less rust severity, and also allows better distribution of the fungicide, during application, facilitating the management of the disease. If the sowing density is high, in smaller spacing and below 0.5 m, there will be difficulty in penetrating the syrup and, consequently, there may be poor coverage of the leaves in the canopy. In this case, the control of the disease will be deficient, even if an efficient fungicide is adopted [28, 88, 97, 106–115].

In addition to these, the most important is the absence of soybean cultivation in the off-season through the sanitary vacuum (60 to 90 days). Considering the high destructive potential of phytopathogen and disease [17], several states have adopted the "sanitary vacuum", a period of 60 to 90 days without soy plants, in the field, as a strategy to reduce the amount of inoculum, in the off-season, delaying the onset of the disease during the summer harvest. Therefore, it becomes an extremely necessary condition, that cultural measures be practiced, to increase the useful scope of the fungicides of the triazole, strobilurin and carboxamide groups. However, any fungicide control program must be adapted to the host's genotype and also includes the appropriate use of fungicides and monitoring of the pathogen [104, 115]. The adoption of multisite fungicides (cupric, mancozeb and chlorotalonil) [33, 88, 98, 99, 106–114] (**Figure 3**) in Brazil has become if a fundamental tool in the integrated management of the disease, in that case they can be sprayed associated with specific sites or interspersed without limitations of spray tips that suit the condition of the crop and canopy of the crop [92]. At the beginning, a research network was structured with the company UPL (Uniphos Phosphourus Limited), which provided the

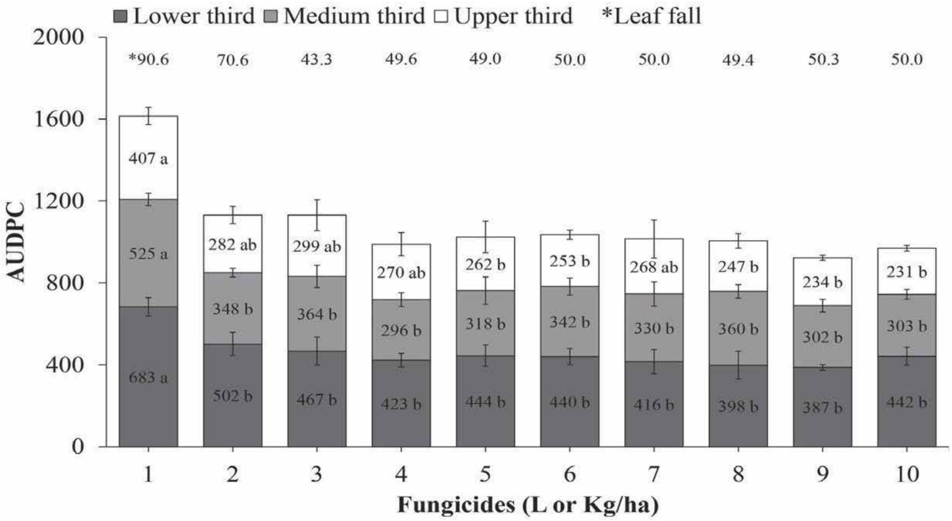

Figure 3.

*Effect of doses of Epoxiconazole with Pyraclostrobin mixtured with multi-site fungicides on the ASR control. Source: Ponce et al. [90]. 1. Control; 2. Epoxiconazole + Pyraclostrobin (33.2 + 10.2 g a.i./ha) associated with Mancozeb (2400 g a.i./ha); 3. Epoxiconazole + Pyraclostrobin (33.2 + 10.2 g a.i./ha) associated with Chlorothalonil (1500 g a.i./ha); 4. Epoxiconazole + Pyraclostrobin (33.2 + 10.2 g a.i./ha) associated with Metiram + Pyraclostrobin (1100 + 100 g a.i./ha); 5. Epoxiconazole + Pyraclostrobin (49.8 + 15.3 g a.i./ha) associated with Mancozeb (2400 g a.i./ha); 6. Epoxiconazole + Pyraclostrobin (33.2 + 10.2 g a.i. associated with ha); 7. Epoxiconazole + Pyraclostrobin (33.2 + 10.2 g a.i./ha) associated with Metiram + Pyraclostrobin (1100 + 100 g. a.i./ha); 8. Epoxiconazole + Pyraclostrobin (66.5 + 20.5 g a.i./ha) associated with Mancozeb (2400 g. a.i./ha); 9. Epoxiconazole + Pyraclostrobin (133.0 + 41.0 g a.i./ha) + Chlorothalonil (1500 g. a.i./ ha); 10. Epoxiconazole + Pyraclostrobin (66.5 + 20.5 g a.i./ha) associated with Metiram + Pyraclostrobin (1100 + 100 g a.i./ha). The bars represent the standard errors of the means. Two experiments were conducted with consistent results; results from one representative experiment are shown. AUDPC – Area under disease progress curve; *leaf fall – (%). Source: Ponce et al. [90].*

researchers with the first tests, which determined the first use of mancozeb, at an experimental level in the region of Uberaba - MG, still in the form of wettable powder, in doses of 1 at 3.0 Kg per ha, in the 2011–2012 and 2012–2013 harvests. In this first experiment, the efficiency of dithiocarbamate in substitution to strobilurins was characterized [116].

The presence of voluntary plants at the beginning of the harvest, favor the maintenance of the inoculum (spores) in the field, and they must be desiccated. In Paraguay and southern Brazil (Paraná and Santa Catarina), in addition to soy, the kudzu legume (*Pueraria lobata*) is an important source of inoculum, as it is a perennial plant, widely established and highly susceptible to rust. Attention is also drawn to the soybean sown in Bolivia in the winter (high levels of water in the soil) and summer in the Santa Cruz de La Sierra region, which perpetuate the inoculum that can be sent to Brazil via air currents, in several months of the year and thus reaching crops in Mato Grosso, Brazil (Juliatti, unpublished data). Another management measure that can be adopted is the sowing schedule, in relation to the crop cycle. Early varieties spend less time in the field, are harvested earlier and, thus, can “escape” the disease or have lower final severities. As in most regions, there is no soy in the winter, in the first sowing, the fungus is not yet present in the field; the tendency is for the inoculum to increase with the advance of the harvest. Thus, earlier sowing also has an escape mechanism regarding the concentration of the inoculum of the fungus in the canopy of plants. Other measures that can result in improved management and control efficiency are:

a. use earlier cultivars, sown at the beginning of the recommended season, for each region, and thus avoid prolonging the sowing period, to escape the greater concentration of the inoculum,

b. monitoring of crops, especially in crop sites subject to high soil moisture, c. observes the temperature conditions (15–28°C) and the wetting period above 6 hours, which are favorable to infection. However, the ideal way to control rust is through genetic resistance. However, until now even though there are resistant cultivars available commercially, using the RPPs genes, for example the “Inox Technology” [117] and others RPPs genes [85, 118–120], this resistance is easily overcome in the field, also requiring protection with fungicides and often the genetic materials already launched have less potential. Productive than the susceptible ones, of the same cycle and maturation group. When the disease is already occurring in the field, chemical control with fungicide is, until now, the main measure. The strategy that has been used most often, is the monitoring of the disease, aiming at the initial inoculum (Xo) that reaches the culture, to support the chemical control. The decision on the time of application, should be based on the factors necessary For the appearance of rust (presence of the fungus in the region, age of the plants And favorable climatic condition), the application logistics (availability of equipment and size of the property), the presence of other diseases and the cost of control. The delay in application, after the initial symptoms are observed, can lead to a reduction in productivity, if climatic conditions favor the progress of the disease. The number and the need for reapplications will be determined by the stage in which the disease is identified in the crop, and by the residual period of the products.

9. Genetic resistance

The most efficient method of controlling plant disease is the cultivation of resistant varieties. The use of genetic resistance to soybean rust, is one of the most effective strategies in the long term, to control the disease [121]. However, already in the 1970s, Van der Plank [122] pointed out the difficulty of finding materials with vertical resistance to rust. In addition, the few materials classified as resistant, had vertical or monogenic resistance [121], lacking horizontal or polygenic resistance, due to the genetic variability of the causal agents. *Phakopsora pachyrhizi* is a pathogen that has high genetic variability. For a long time in Asia, countries have used five sources of genetic resistance in soybean improvement programs, aiming to control rust: Rpp1 [123]; Rpp2 [124]; Rpp3 [6, 125]; Rpp4 [85, 126] and Rpp5 [120]. Genetic and molecular analyzes suggest several alleles or linked genes that govern soybean rust resistance [120]. Zambenedetti et al. [127] studying the genotypes PI 230970 and PI 459025, found that they had a low percentage of germinated urediniospores and appressoria formation. In these genotypes, the formation of appressorium began six hours after inoculation, whereas in the other cultivars occurred four hours after inoculation. Such genotypes may have resistance genes Rpp2 and Rpp4, respectively [85, 123, 126]. Another study by Pham et al. [128] in the evaluation of the known sources of resistance (Rpp1 to Rpp4), to three isolates of *Phakopsora pachyrhizi*, found that the cultivars PI 200492 (Rpp1) and PI462312 (Rpp3), produced differential response. While PI230970 (Rpp2) and PI459025B (Rpp4) produced susceptible lesions (TAN). Koga et al. [129] evaluating the components of resistance to FAS in 48 cultivars, selected some groups of genotypes, which can be considered promising, as sources of genes of resistance to the disease. Recently, a study was carried out on the reaction of several soybean genotypes to three populations of *Phakopsora pachyrhizi*, one from Japan and two from Brazil, finding only two resistance genes, being Rpp4, present in the PI 459025 variety, and whether such cultivars are maintained, with adequate levels for quantitative resistance. As mentioned earlier, these genotypes are dependent on fungicides, such as 03 susceptible ones. They require the same care, with gains in application or relaxation 04 intervals and lesser concerns in prolonged rainy periods, where spraying is not possible.

Now, there is not a worldwide variety that has absolute resistance to the disease, that is, a variety with complete resistance. What is understood as an almost impossible task in breeding programs. In the absence of this type of resistance, researchers from abroad and Brazil are looking for cultivars with partial resistance or that have some level of quantitative resistance [13–15, 35, 37, 130]. Strains with partial resistance to rust can be selected from segregating populations, developing under conditions of greater rust severity [131]. The selection by productivity can also be used, in different breeding programs in non-segregating strains, under high severity of the pathogen. Such cultivars with partial resistance and/or tolerance, may require less application of fungicides and, thus, reduce the cost of disease control. According to Silva et al. [121, 132], partial resistance allows the establishment of the commercial use of fungicides allowing stability in the production system. Furthermore, it is possible to use alternative control methods such as foliar silicates based on calcium or magnesium, in fungicide programs [102]. Cultivars with partial, quantitative, or horizontal resistance, will allow adequate rust control, but only with atomization of the plants. Therefore, if there are no cultivars with complete resistance, to be used commercially, chemical control becomes the alternative, more effective in the control of Asian soybean rust combined with cultural practices [58].

Rpp5 in the Shiranui variety which conferred resistance to three populations of the fungus [133]. The Rpps genes for resistance to the fungus *P. pachyrhizi* (Rpp) have been found and described in countless soybean accessions and at least 10 Rpps, genes have been found, or alleles have been mapped in seven gene loci [134]. Obtaining a soybean cultivar resistant to Asian rust has been a challenge for research.

The existence of a large number of pathotypes, makes control difficult through vertical resistance. Dominant genes for resistance, called Rpp1 to Rpp4, identified in plant introductions (PI's) reported in the literature [6, 126] have doubtful stability, due to the great variability of the pathogen. Eighteen pathotypes were identified, in samples collected from soybean plants, and wild hosts in Japan [135]. Studies carried out in Taiwan, showed the existence of at least one patotype, containing three virulence genes [136]. In Brazil, studies carried out by Embrapa Soybean, Brazil, have identified 11 cultivars with resistance to rust [95]; however, this resistance was quickly superseded, with isolates of the fungus from the state of Mato Grosso. Of the four sources of resistance already described in the literature, only those with the Rpp2 and Rpp4 genes remained resistant to rust in Brazil, until the year 2004 [118]. Today, these genes no longer provide vertical resistance to the phytopathogen. Martins and Juliatti [35] determined that partial resistance in IAC 100 can be governed by more than a dozen smaller genes depending on the cross or parent lineage involved. Other RPPs genes have been described in the world and added to germplasm banks for future use and manipulation in breeding programs. Only time will tell about their stability.

Another type of resistance to be explored is the horizontal one, which involves a reduction in the rate of development of the disease, being more effective against agreater number of races of the pathogen. However, the quantification of this type of resistance is more difficult, thus limiting its use [137]. After 20 years of working with smaller and allele genes from the IAC 100 cultivar [14, 15, 35, 130, 131], the authors report success in the generation of soybean strains adapted to various cultivation regions in Brazil, in different maturation groups. Due to the instability of vertical strength and the difficulties associated with the identification and quantification of horizontal strength, other methods have been used, aiming to avoid reductions in productivity caused by rust., highlighting the tolerance of cultivars. A review was presented on the control of soybean rust and studies on the management of the disease and the use of Rpps genes [138]. The authors demonstrated the leadership of the USA, followed by Brazil, Germany, Japan and Argentina in the study of the pathosystems.

Tolerance can be defined as the capacity of the plant to support the development of the pathogen, without showing a significant reduction, in productivity or product quality [139]. Losses in productivity are generally used to assess the level of tolerance and therefore, the lower the loss, the greater the level of tolerance. Losses can be quantified by the difference in productivity between severely infected plots and plots without disease [140]. Epidemiologically, tolerance and resistance are different concepts [122]. Normally, the genetic material that is tolerant is under the same intensity or severity of the disease as the susceptible, so the differences are quantified in numbers or productivity values in the tolerant genotype in relation to the susceptible.

Melo et al. [141] studied the tolerance in Brazilian soy germplasm and separated this type of classification from the reaction of the genotypes was for partial resistance [142]. The genotypes BRS7560 and BRS 239 were classified as tolerant because they did not show a reduction in productivity with and without chemical control. In Brazil, for the 2009–2010 harvest, soybean cultivars TMG 801-INOX® and TMG 803-INOX® with some incomplete resistance, Asian rust, were made available to farmers in some Brazilian regions [117, 119]. However, it is not known until now.

10. Sowing times, production of quality seeds in Mato Grosso and chemical rust control

There is a great debate in Brazil without scientific evidence that in the sowing schedule from December to February, the frequency of mutants increases, such as

F129L [143] (mutation for loss of sensitivity to triazoles or inhibitors of demethylation) and I86F (mutation for loss sensitivity to carboxamides). The genetic adaptation occurred in the Quinone oxidase enzyme gene at position 129 of the sequence, where the amino acid phenylalanine was replaced by leucine, in the first case. In the second case in the Succinate Dehydrogenase - C enzyme, the amino acid isoleucine (I) was replaced by phenylalanine (F), at position 86 of the protein sequence (sdhC-186F mutation) [144]. In the study of monitoring of raccoon soybeans carried out by FRAC-BR, the presence of resistant Asian rust inoculum with high frequency of the 186F mutation was detected in the years 2017, 2018 and 2019, in practically all soybeans' regions of Brazil. The data reinforce the importance of the sanitary vacuum for the reduction of resistant populations and warn of the importance of another phytosanitary measure, which has become essential for soybean production in Brazil: the sowing schedule. In relation to the sowing schedule, this is particularly important, as long as the producer is not forbidden to obtain his own seed. December sowing, as a limit for seed production, leads to low physiological and health quality of this, in addition to harvesting in Mato Grosso, under rain and with lower yields. In addition to the greater severity of soybean rust. When sowing of February to make seeds in Mato Grosso, the producer will have better health quality, higher yields compared to December sowing. There will also be a mini sanitary vacuum from December to February (60 days). As less leaf wetness occurs, fewer fungicides were applied, compared to December, which is the sowing deadline, for making seeds in Mato Grosso [145]. Therefore, it is questioned the scientific and Mato Grosso authorities, in addition to MAPA, to prevent such practice without scientific validation. The results by Reis et al. [145], point out the opposite of technical and political decisions, in relation to seed production in the state of Mato Grosso. It is well known that sowing in February would not enter the sanitary void and would allow the farmer to make his seeds of quality and at a lower cost compared to the month of December, which would remain within the calendar and without advancing in the sanitary void, as happens in the states of Tocantins (Lagoa da Confusão) and Goiás (Luis Alves and São Miguel do Araguaia), where large seeders harvest their seeds in September–October and advance in the Brazilian sanitary vacuum.

11. Chemical control

The main groups of fungicides registered for the control of Asian soybean rust (ASR) are: demethylation inhibitors (DMI's - tebuconazole, cyproconazole, protioconazole (triazolintione), epoxiconazole and others); quinone oxidase inhibitors (QoI's - azoxystrobin, trifloxystrobin, picoxystrobin and pyraclostrobin), succinate dehydrogenase inhibitors (SDHI's - fluxpyroxade, bixafen and benzovindiflupyr), cupric (oxychloride), nitriles (e 3), until the year 2020. Currently, more than 120 molecules are registered with the Ministry of Agriculture, Livestock and Supply (MAPA), for the control of Asian soybean rust. Most records are composed of fungicides, of the triazole groups formulated with strobilurins. The fungicides of the DMI's, QoI's and SDHI's groups act only at a specific location, out of thousands of biochemical reactions in the fungal cell [143]. Therefore, such groups of fungicides are vulnerable to fungal strains for reduction or loss of sensitivity. They are of high risk for the development of resistance [143] and, therefore, their use in isolation, for the control of any fungal disease, notably ASR is not recommended.

In Brazil, since the discovery of ASR in the south of the country, losses in grain production have only been reduced thanks to chemical control, carried out with triazole and strobilurins fungicides [11, 33, 142]. Despite the high risk of emergence of less sensitive or resistant mutants, in the population of the fungus *P. pachyrhizi*, in the field, with the use of fungicides with specific mode of action, chemical control of ASR, at present is the only solution available, for reduce the damage caused by the disease, due to the absence of cultivars with an adequate level, basal resistance and low efficiency of prophylactic strategies. However, in atomization programs, multisite and protective fungicides must be employed, formulated or not with systemic and strobilurins.

12. Risk factors for the use of fungicides with specific mode of action

Due to the fact that systemic fungicides, acting specifically in a single action site, are subject to risk factors for the development of resistance in the population of fungi. The risk factors are: 1. Use of fungicides specific, systemic or mobile and penetrating sites, as the only form of control, 2. Use of specific or systemic fungicides in extensive cultivation areas, 3. Use in more than two sprayings of mobile and penetrating fungicides, called specific sites, 4. Change in the recommended dose. The dose to be used in the atomization must always be the one that is in the product leaflet, 5. Repetitive application of the active ingredient, with the same mode of action, 6. Application of systemic fungicide after the onset of the epidemic as a dressing, 7. Characteristics of the pathogen, such as number of generations per crop cycle, sporulation capacity and ease of dissemination, 8. Extensive window for sowing soybeans for grain production. The sowing period runs from September to December. In some regions the sowing window may even double, 9. In late sowing, the interval of application of fungicides should be shorter due to the greater pressure of inoculum in the fields of cultivation. Growers must also use the specific site fungicide in more than one application, associated with multisites [115]. Give preference to the use of alternating or associated multisites in the initial applications and not at the end of the spraying schedule. Considering the latent period of the fungus from seven to nine days, in a period of 45 to 55 days (appearance of the first symptoms of the disease in the field until the senescence of the leaves), we would have eight to ten cycles of the pathogen.

13. Use of triazoles to control Asian soybean rust

The first chemicals used to control ASR belonged to the triazole fungicides or demethylation inhibitors (DMI), especially cyproconazole, epoxiconazole, flutriafol and tebuconazole. Diphenoconazole, myclobutanil and tetraconazole, fungicides with specific mode of action, were also used. There is also triazolintione (protioconazole [103]. The fungicide is a combination of cyproconazole and sulfur at the molecular level). Until 2020, the most commercialized triazole in Brazil is cyproconazole and soon this leadership should be changed to protioconazole (It was used in isolation in Brazil for the first time in the 2006–2007 harvest [103]), under experimental conditions compared to assets present in the Brazilian market and at the time it proved to be the most effective in controlling rust in isolation. Alves and Juliatti [98] published the beneficial effects of mancozeb in isolation and in association with other fungicides used in soy. The increase in chlorophyll A and B, carbon fixation in the plant and the green effect and increase in the mass of the grains stand out, allowing in addition to increasing productivity, the management of fungal resistance [34, 103], as *Phakopsora pachyrhizi.*. Certainly, the green effect on the plant is due to zinc (3% in the formulation) and manganese (12%) which are added to the effect of the fungicide. The mancozeb fungicide is an active carrier into the plant, in addition to its reducing effect on the phytotoxicity of some more aggressive triazoles. After five seasons of growth (from 2002/03), using DMI alone, Silva et al. [121] reported failure to control ASR, in the state of Goiás, in 2006/07, for cyproconazole, flutriafol and tebuconazole. Until then, flutriafol had been highly effective and used by researchers as a standard, becoming the market leader. As of 2005/06, there was a reduction in the effectiveness of flutriafol, in the State of Mato Grosso [119]. After the decline of flutriafol, tebuconazole became widely used with high efficiency and was adopted as a reference fungicide to control ASR In the 2005/06 season, the average ASR control by DMI's was 90.3%. After just eight seasons, corresponding to 2012/13, the control with DMI's was 52.0, therefore there was a 42% reduction in control effectiveness [111, 112]. In other states of the federation, such as Minas Gerais, in the 2005 and 2006 harvest, the same behavior was found with the reduction in the efficiency of triazoles [11, 16, 29–31, 33, 103, 146], which in many situations reached 50% or less of effectiveness.

14. Reduction of the sensitivity of *Phakopsora pachyrhizi* to triazole Fungicides

Observations from the 2007/2008 harvest showed that the samples collected in the main soy producing regions of Brazil - in March - predominated populations of 03 *Phakopsora pachyrhizi*, less sensitive to DMI's, first generation, mainly tebuconazole, in some states of the Midwest. In the 2008/2009 harvest, the samples collected in the same month and the locations of the 2007/2008 harvest, showed that the predominance of populations less sensitive to first generation DMI's, extended to other locations in the country, in addition to states in the regions. Midwest, Southwest (São Paulo and Minas Gerais) also the southern states (Paraná and Rio Grande do Sul). Between the 2009/2010 and 2013/2014 harvests, it was observed that populations less sensitive to the first generation DMI's were detected in all Brazilian states, which produce soybeans [147–150]. Therefore, over the years, there has been a gradual reduction in the effectiveness of DMI (tebuconazole) in controlling ASR in soybean production fields in the country [147–150]. The effectiveness of ASR control with tebuconazole was 90 and 91% in 2003/05 soybean crops, 77% in 2005/06, 58% in 2006/08, 39% in 2008/09 and only 24% in 2009/10 [110].

Fungicides	Control efficiency of Asian soybean rust (%)						
	Year						
	2009	2010	2011	2012	2013	2014	2015
Cyp. + Azo.*	72	80	70	67	63	47	40
Epo. + Pyr.	70	79	76	70	62	28	—
Cyp. + Pico.	71	80	72	70	69	60	59
Teb. + Pico	72	80	80	77	75	70	67

**Respectively: Cyp. + azo. (cyproconazole + azoxystrobin); Epo. + pyr. (Epoxiconazole + Pyraclostrobina); Cyp. + peak. (Cyproconazole + picoxystrobin); Teb. + peak. (Tebuconazole + picoxystrobin). Source: Godoy et al. [87–89, 151, 152].*

Table 1.
Reduction in the sensitivity of Phakopsora pachyrhizi (control%) to groups of demethylation inhibitor (DMI's) and DMI's + Strobilurin (QoI) from 2003/2004 to 2014/2015.

The difficulty in controlling ASR with isolated DMI's fungicides was becoming increasingly evident, proving the high adaptability of *Phakopsora pachyrhizi* [110] (**Table 1**).

The reduction in the sensitivity of *Phakopsora pachyrhizi* (Pp) to the fungicides tebuconazole and cyproconazole, with only 42 and 38% of control, respectively, was also confirmed by Godoy et al [109, 110].

15. Introduction of the group of carboxamides and triple formulations for the control of soybean rust

In 2012–2013, new fungicides belonging to the Carboxamide group were introduced, which have a specific mode of action, inhibiting fungal respiration, of complex II - succinate dehydrogenase (SDHI), to control ASR [153]. In Brazil, the three fungicides of the carboxamide group available on the market are bixafen, fluxopyiraxade and benzovindiflupyr. Fungicides benzovindiflupyr, bixafen, fluxapyroxad, furametpyr, isopyrazam, penflufen, penthiopyrad and silkxane, resent a medium to high risk for resistance. Numerous cases of resistance to other pathogens have already been documented for the carboxamide group in other countries [147–150, 153]. It is concluded that the introduction of this fungicide group, for the control of ASR, probably will not solve the problem, since they present a specific mode of action, subject to resistance in the population of *Phakopsora pachyrhizi.* Due to these facts, the fungicides of this group, were not recommended for use alone, in the control of rust. Hence the associations or triple mixtures, for use in soybean crops and for the target *Phakopsora pachyrhizi*, arose. In the years 2013/14, there was the registration of triple mixtures, involving fungicides from the groups DMI's + QoI's + SDHI's. The fungicides of the SDHI group, launched on the market, to compose the triple mixtures with triazoles and strobilurins were: benzovindiflupir and fluxpyroxade, bixafen [33, 36, 147–150].

16. Emergence of proticonazole from the DMI's group

In the period comprising 2013–2015, a new fungicide from the DMI's group, protioconazole, appeared. From the beginning of monitoring until its launch on the market, protioconazole has shown the lowest effective concentration values 50 (EC50) in the rust monitoring program. The introduction of this fungicide on the market was the result of hundreds of experiments, conducted in demonstration's areas, from different soy producing regions in Brazil. The protioconazole was then evaluated in a mixture with the QoI fungicide, trifloxystrobin. The comparison was made with fungicides launched on the market, such as the combinations of strobilurins (QoI) and carboxamides (SDHI). Because it is a fungicide, composed of an innovative active ingredient with differentiated binding at the fungus action site, protioconazole constituted the new generation, in the chemical group of DMI's, being chemically classified as triazolintione (Frac classification on mode of action 2014 - www.frac.info). The first studies in Brazil with protioconazole to control soybean rust were carried out by Furtado et al. [103]. The combination protioconazole + trifloxystrobin acts in two ways: 1. in the control of Asian soybean rust, and 2. in the disease complex (such as target spot, powdery mildew, molasses, anthracnose, and end-of-cycle diseases). Therefore, its use is recommended preventively, in the first application or in the first two, when the plan of use of foliar fungicides, is of more than two applications. In this way, it is possible to explore the spectrum of action of this fungicide well, starting in a robust way the prevention and control of soybean rust and, consequently, an improvement in the performance of the subsequent fungicide.

17. Introduction of the dithiocarbamate group to control Asian soybean rust

In the years 2014 to 2015, the idea of introducing multi-site fungicides into the ASR control programs began to be considered, such as mancozeb, chlorothalonil and others. The introduction of multisite fungicides in ASR control programs could be an especially important tool for the management of resistance to *Phakopsora pachyrhizi*, with the potential to preserve the useful life of specific fungicides DMI's, Qo'sI and SDHI ', s in soybean culture [144, 153]. Multisite fungicides (mancozeb, chlorothalonil, metiram and others) have the great advantage, because in addition to being of low price, they act in multiple sites of action in the fungal cell, interfering with numerous metabolic processes of the fungus, and consequently, resistance to fungicide group would be rare or non-existent [97]. Recent work involving mancozeb, in the control of ASR was developed in Uberlândia - MG and in Rio Verde - Goiás, demonstrated that the product has the potential to control the disease, even in isolated applications [101, 116] (**Figure 4**). Multisite fungicides, such as mancozeb, therefore have the chance to be strong allies in the defense against Asian soybean rust.

Studies carried out at the Federal University of Viçosa on the control of ASR, with fungicides from the triazole group (DMI) + strobilurins (QoI) associated with multisite fungicides (MSF) mancozeb, chlorothalonil or met, in the agricultural years 2013 to 2015, performed by Ponce et al. [90], showed that the association of DMI and QoI with MSF (Alves and [99]), in different environmental conditions,

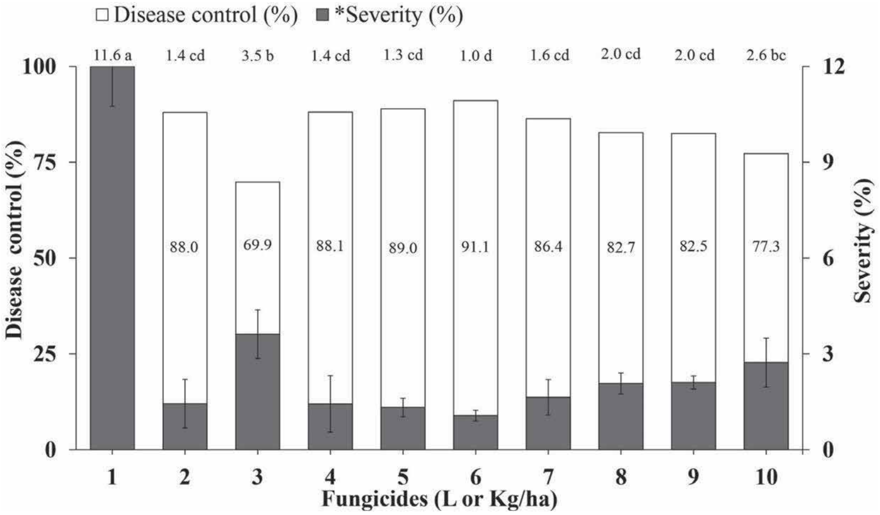

Figure 4.

*Residual effects of DMI and QoI, alone or in mixture and multi-site fungicides on ASR in the greenhouse. Source: Ponce et al. [90]. 1. Control; 2. Epoxiconazole + Pyraclostrobin (33.0 + 10.2 g a.i./ha); 3. Cyproconazole + Trifloxystrobin (16.8.0 + 7.2 g a.i./ha); 4. Protioconazole + Trifloxystrobin (28.0 + 16.0 g a.i./ha); 5. Cyproconazole + Azoxystrobin (18.0 + 7.2.0 g a.i./ha) + Nimbus (0.5% v/v); 6. Pyraclostrobin (75.0 g a.i./ha); 7. Mancozeb (240 g a.i./ha); 8. Chlorothalonil (150 g a.i./ha); 9. Metiram + Piraclostrobin (400 g a.i./ha), 10. Tebuconazol + Trifloxistrobina (100.0 + 50.0 g a.i./ha). The bars represent the standard errors of the means. Two experiments were conducted with consistent results; results from one representative experiment are shown. AUDPC – Area under disease progress curve; *leaf fall – (%). Source: Ponce et al. [90].*

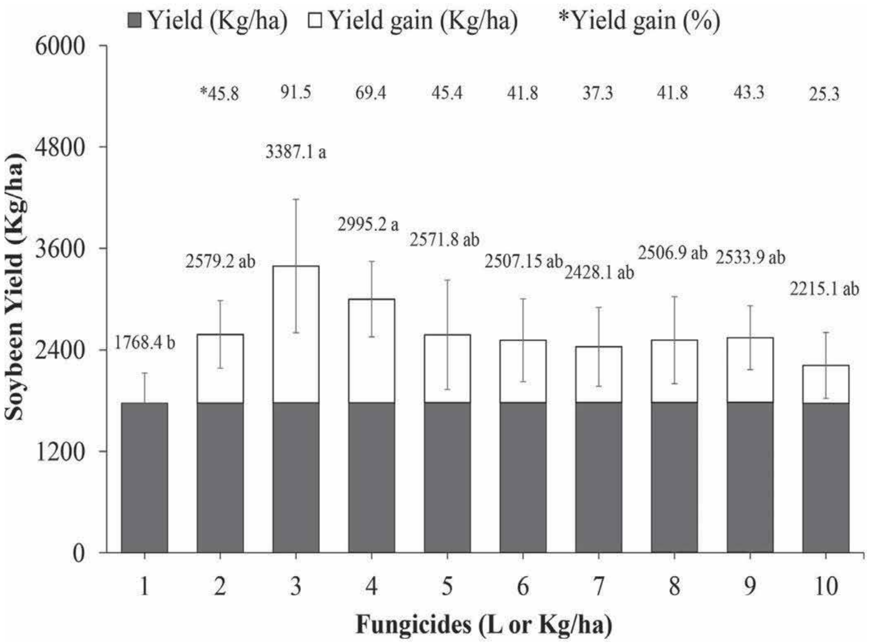

Figure 5.
*Effect of doses Epoxiconazole with Pyraclostrobin mixtured with multi-site fungicides, on soybean grain yield. Source: Ponce et al. [90]. 1. Control; 2. Epoxiconazole + Pyraclostrobin (33.2 + 10.2 g a.i./ha) associated with Mancozeb (1400 g a.i./ha); 3. Epoxiconazole + Pyraclostrobin (33.2 + 10.2 g a.i./ha) associated with Chlorothalonil (1500 g a.i./ha); 4. Epoxiconazole + Pyraclostrobin (33.2 + 10.2 g a.i./ha) associated with Metiram + Pyraclostrobin (1100 + 100 g a.i./ha); 5. Epoxiconazole + Pyraclostrobin (49.8 + 15.3 g a.i./ha) associated with Mancozeb (1400 g a.i./ha, 3.0 kg c.p./ha); 6. Epoxiconazole + Pyraclostrobin (opera SC; 33.2 + 10.2 g a.i./ha, 0.5 L c.p./ha) associated with Chlorothalonil (1500 g a.i./ha); 7. Epoxiconazole + Pyraclostrobin (33.2 + 10.2 g a.i./ha) associated with Metiram + Pyraclostrobin (1100 + 100 g. a.i./ha); 8. Epoxiconazole + Pyraclostrobin (66.5 + 20.5 g a.i./ha) associated with Mancozeb (1400 g. a.i./ha); 9. Epoxiconazole + Pyraclostrobin (133.0 + 41.0 g a.i./ha) associated with Chlorothalonil (1500 g. a.i./ha); 10. Epoxiconazole + Pyraclostrobin (66.5 + 20.5 g a.i./ha) associated with Metiram + Pyraclostrobin (1100 + 100 g a.i./ha). CV = 18.3%. The bars represent the standard errors of the means. Two experiments were conducted with consistent results; results from one representative experiment are shown. *yield gain – Was obtained in relation to the control treatment. Source: Ponce et al. [90].*

improved the efficacy in the control of the disease and the productivity of the soybean (**Figure 5**). In the greenhouse, triazole fungicides mixed with strobilurin associated with MSF effectively controlled FAS, applied before inoculation (protective effect). On the other hand, triazoles or strobilurins were not effective in controlling ASR in some cultivation areas in Brazil [116]). In this situation, the use of multisites such as mancozeb was providential [33, 116]. There are two possible explanations for this hiring: 1st. failures in the application of fungicides in the field. The application technology is based on three premises: time of application, environmental conditions, and the target to be reached. These are the points that are generally overlooked by producers when applying fungicides, 2nd. the fungus may have acquired resistance to triazole or strobilurin in the field, where soybeans were grown extensively, in the savana's region, when such fungicides were applied alone. The anastomosis of germ tubes, and the migration of nuclei from the hyphae of germ tubes of the soybean rust pathogen, *Phakopsora pachyrhizi*, may explain, how the fungus recombines its genetic material, and develops resistance to fungicides with specific mode of action [154]. It is possible that this mechanism could occur in nature, due to the fact that millions and millions of urediniospores are produced in soybean leaves, in the field and are then dispersed by the wind.

Based on the results obtained, three field experiments were carried out (doses of triazoles with strobilurins associated with MSF (mancozeb, chlorothalonil and metiram) [90]. The hypothesis is that the fungicides of the DMI's and QoI's groups may mixed with MSF's to improve ASR control and increase soybean productivity.

The results showed that the average ASR control with the application of triazolewith strobilurin associated with protective fungicides (mancozeb, chlorothalonil and metiram) was 70.2%. The efficiency of rust control was not higher, because the 04 products were applied after the beginning of the disease epidemic in the field. The 05 field tests were sprayed, when the disease severity had already reached 2.0 to 5.0%, 06 on the leaves of the lower part of the plants. This result shows that any of the three 07 protective fungicides can be used in the mixture with epoxiconazole with piraclostrobin or cyproconazole with azoxystrobin [90]. In general, the DMI's + QoI's fungicides associated with MSF had an efficiency greater than 68.0% of control and produced more than 70.0% of the control (control). These results show that it is possible to control ASR even after the disease severity has reached 2.0 to 5.0%, at the time of plant spraying. In this work, the protective fungicides mancozeb and chlorothalonil associated with epoxiconazole + pyraclostrobin (0.5 kg bw/ha) or cyproconazole + azoxystrobin (0.30 kg bw/ha) increased the yield of soybeans by 89.5% and 109, 0%, respectively. Based on the information above, it is suggested that the application of triazole and strobirulin associated with FMS, starting at the stages of soybean culture (V9 or R1, R2), may promote better control of the disease, especially in the leaves at the bottom of the plant, which is the main source of inoculum, for the upper part and for the whole field. Therefore, the combination of fungicides from the DMI + QoI or SDHI group, associated with MSF, can be recommended as a new strategy for the control of ASR in the short and long term. In addition, due to the residual effect of multisite fungicides [10, 33, 98] on soybean leaves, (mancozeb, chlorothalonil and metiram) can promote greater longevity of the DMI, QoI and SDHI molecules and decrease the number of applications.

The addition of mancozeb to reinforce the fight against fungal resistance is not a new strategy. Mancozeb has been included in mixtures, to contribute to the management of resistance, and to expand the spectrum of fungicides with specific mode of action, for numerous plant diseases. To stabilize ASR control, the same strategy could be used for soybeans, to chemically manage ASR. Examples of fungicides that are already used in mixture with mancozeb include benalaxyl, cymoxanil, dimetomorph, famoxadone, fenamidone, folpet, fosetil-aluminum, iprovalicarb, mandipropamide, metalaxyl and zoxamide. Likewise, this could be followed in the control of ASR, both in Brazil and elsewhere. To reinforce the role of mancozeb, in anti-resistance strategies, in the control of fungal diseases, in more than six decades of continuous use, they have been recorded in more than 70 cultures and in 400different diseases [144, 153]. The introduction of MSF in the ASR control program can be an important tool for managing resistance. Such fungicides have the potential to preserve the useful life of specific fungicides, such as (DMI, QoI and SDHI), in soybean crops.

It was observed that the fungicides of the DMI's group (tebuconazole, epoxiconazole) and the QoI's (azoxystrobin) alone, lost about 40 to 50% of efficiency, in the control of ASR, during this period. The percentage of control of mixtures of DMI's with QoI's ranged from 75% (highest level of control) to 55% (lowest level of control). For the fungicides tebuconazole, cyproconazole and azoxystrobin applied alone, the highest level of control in 2010/2011 was 56% and the lowest 19%. The introduction of fungicides of the SDHI group (bixafen, benzovindiflupir and fluxapiroxad) associated with DMI (protioconazole) and Qo's (picoxystrobin, trifloxystrobin) in triple mixes and in double mixtures (trifloxystrobin + fluxapiroxad + benzoxystrin + maxoxystrobin of control ranging from 69 to 82% (**Table 2**). The most efficient combinations in the control of ASR were those that 08 had the fungicides of the SDHI group in double mixture, with fungicides of the QoI 09 group (pyraclostrobin and azoxystrobin). Therefore, these results suggest that the addition of fungicides from the SDHI group were more efficient both in the control and in the productivity of soybeans (**Table 3**). The highest yields corresponded to the groups' fungicides, which provided the best controls for ASR. Therefore, there was a correlation between ASR control and productivity. The highest yields also corresponded to the mixtures, which had the participation of the fungicides of the SDHI group (bixafen, benzovindiflupyr and fluxapiroxad). In disease control programs, they are often applied as 'dressings' (**Table 2**). **Table 2** shows us that rust control must be done preventively.

Location	Fungicides Sprays without symptoms (0) and with symptoms (1)	Yield (Redution - %)
Tomarara – PR	0	39
Londrina – PR	1	72
Paulinia – SP	1	24
Planaltina – DF	1	74
Ipameri – GO	1	37
Alvorada – TO	0	14
Dourados - MS	1	22
Riachão – MA	0	25
Chapadão do Sul – MS	1	68
Senador Canedo – GO	1	69

Source: Godoy et al. [113].
Difference between the production of the check and the best treatments were: Application without symptoms) - 52% and with symptoms - 34%.

Table 2.
Reduction of soybean productivity, in different regions with application of fungicides, before the first symptoms and after the Asian soybean rust (ASR) entry in the crop in many states of Brazil.

Duble and triple mixes	(%) of Control	Yield (Kg/ha)
2015/2016		
Piraclostrobin + benzovindiflupir	78,0	(3479,0)
Azoxystrobin + benzovindiflupir*	82,0	(3428,0)
Piraclostrobin + epoxiconazole + fluxapiroxade	69,0	(3246,0)
Trifloxystobin + protioconazole + fluxopiraxade	71,0	(3303,0)
Picoxystrobin + tebuconazole + mancozeb	64,0	(3126,0)
Azoxystrobin + tebuconazole + mancozeb	59,0	(3065,0)

Source: Godoy et al. [113].
*In 2016–2017 the efficiency reduction was 40–50% after fungus mutation to carboximides (gene I86F).

Table 3.
Percent of control (%) and Yield for double mixtures and casings used to control Asian soybean rust, in 2015/2016.

Table 2 summarizes the results of three agricultural years of studies, with fungicides DMI's, QoL's, SDHI's and dithiocarbamate in various regions of the country carried out in 2010/2011 until 2015/2016 [36, 113, 114, 155].

18. Conclusions

To reduce the risk of damage to the crop, the management strategies recommended in Brazil for this disease are:

1. Prioritize the rotation of fungicides with different biochemical mechanisms of action and adapting the programs to the time of sowing. It is mandatory to include multisite and/or protective or residual fungicides in tank mixes.

2. Sequential and curative applications should be avoided to decrease the pressure of selection of resistance to the fungus. Rust control must always be preventive, as it is an aggressive pathogen.

3. Use early cycle cultivars and sowing at the beginning of the recommended season when possible.

4. Eliminate voluntary soybeans plants and raccoons.

5. The off-season must be free from soybean cultivation (pay attention to the sanitary vacuum that varies from 60 to 90 days according to the region).

6. Monitor the crop, since the beginning of the development of the crop. Control will only be effective if the disease is diagnosed early.

7. Atomize the crop to control Asian soybean rust, at least once, before planting lines are closed.

8. Avoid late sowing in relation to the recommended season.

9. The adoption of a single model for the management of the disease is not justified, and it is important that this be done in a rational manner depending on the situation in each location.

10. The use of fungicides must be planned, according to the risk factors, which are monitored during the harvest.

11. The timing of application and reapplication, at the right time, is of fundamental importance in controlling the disease.

12. The use of fungicides with a prolonged residual effect such as multisite/protectors is fundamental in preserving the useful life of systemic fungicides in the field.

13. Use cultivars with partial resistance already available in Brazil, when these allow levels of productivity and adaptation to the different macro-regions of Brazil. Even in these genotypes, the use of the fungicide is fundamental, given the variability of the pathogen.

Author details

Fernando Cezar Juliatti[1]* and Laércio Zambolim[2]

1 Laboratory of Mycology and Plant Protection, Institute of Agricultural Sciences, Federal University of Uberlândia, Brazil

2 Department of Plant Pathology, Federal University of Viçosa, Brazil

*Address all correspondence to: juliatti@ufu.br

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Chapter 11

Barley Grain Development during Drought Stress: Current Status and Perspectives

Mortaza Khodaeiaminjan and Véronique Bergougnoux

Abstract

Barley (*Hordeum vulgare* L.) belongs to small grain cereals that cover more than 78% of the daily calorie consumption of humans. With a prediction of 9.7 billion humans in 2050 (FAO stats) and climatic changes, the question of increasing small grain cereal's production has become an agricultural challenge. Drought exerts a strong environmental pressure, causing large yield losses worldwide. Therefore, understanding the mechanisms responsible for grain development from the fertilization to the mature dry grain is essential to understand how drought can affect this developmental program. In this book chapter, we present the physiological, molecular and hormonal regulation of barley grain development. In a second part, we describe the consequences of drought at different stage of barley development, with a special focus on the reproductive phase. Finally, in the last part, we present the different methods used to decipher new genetic information related to drought-tolerance. All this knowledge contributes to understanding the tolerance mechanisms of barley and to developing breeding strategies aiming to bring about new varieties with sustained yield in harsh conditions.

Keywords: barley, drought, grain development, QTLs, GWAS

1. Introduction

Small grain cereals (rice, maize wheat, barley, rye and oat) are the most important food supply, representing more than 78% of the calories consumed each day by humans (FAO Stat). Cultivated barley (*Hordeum vulgare* L.) is the fourth most important cereal worldwide, serving as a model species for the temperate cereals. Indeed, barley can grow in highly contrasting habitats and tolerate stress conditions such as drought, high and low temperature, and salinity [1, 2]. The use of grains as a source of food begun already during the Middle Stone Age, long before cereal domestication [3]. The early domestication resulted in drastically altered seed size and grain number; later the modern plant breeding in combination with agricultural technics concurred to the nowadays high yields [4]. However, substantial increases in yield have to be reach to ensure food security for the ever-growing worldwide population that is estimated to reach more than 9.7 billions inhabitants in 2050 (FAO statistics). Moreover, in the current context of climatic changes, the sustainability of cereal grain yield has already become a challenge for food security. In the current era, such goals can be reached solely by the use of the molecular breeding that requires a deep understanding of the molecular mechanisms controling seed and plant development [4].

In agriculture, yield is defined usually by the classical concept of number of inflorescences per cultivated area. Nowadays, grain yield takes also into consideration the grain number per inflorescence and the grain weight, often measured as thousand grain weight (TGW) [5]. Factors affecting the overall plant development (water and nutrients uptake from soil, development of photosynthetic tissues for carbon fixation and storage, carbon and nutrient relocation during grain filling) can have important consequences on grain yield [6]. Whereas the number of florets determines grain number per inflorescence, grain weight is determined by the grain size, and the amount of starch and protein accumulated during grain filling [7]. Grain weight reflects the size of the grain, itself determined by length, width and volume or filling, among other parameters. All these parameters describe the grain architecture. The genetics behond grain architecture is complex, involving maternal and paternal developmental signals, hormonal regulation and integrating the environmental information such as photoperiod, biotic and abiotic stresses [8]. The genetic and molecular bases of this agronomic trait have attracted attention in the last decades. In this regards, several studies based on quantitative trait loci (QTL) mapping or Genome-wide Association Study (GWAS), combined with mutant identification, identified new genes involved in barley grain development and yield-related genes [9–14].

As already mentionned, grain yield is a complex genetic trait, greatly affected by the environment and cultivation conditions. Water deficit or drought is undoubtedly the most important environmental factor affecting the global productivity of crops [15, 16]. However the extent of the damages, the recovery capacity and the impact on the final grain size depend on the developmental stage during which the plant faces the stress [16]. In the last decades, improving crop growth and yield under changing environmental conditions, especially drought, became a major goal of plant breeding programs [17, 18]. Drought tolerance is a complex genetic trait, involving multiple genes [19, 20]. Many studies have investigated the genetic bases of drought tolerance in barley [18–21]. QTL studies are one of the most used approaches to identify genomic regions controlling agronomic performance under water-limiting conditions [22, 23]. Recent advances in barley genome sequencing provide great potential for genetic studies, such as QTL studies and recent Genome Wide Association Studies (GWAS) [24–28]. Very recently, a 50 k iSelect SNP Array, based on exome capture, has been developed from a wide range of European barley germplasm containing 394 cultivated accessions. This large data set is of great interest for further genetic studies in barley [29]. The ability of a plant to adapt to a specific environment relies mainly on the genetic variability that is a long process of adaptation to the environmental pressure. To face fast changing conditions, plants possess epigenetic regulation of gene expression, kind of switch on/off mechanism. Epigenetic relies on structural and chemical modification of the genome without affecting the genetic information. It promotes fast, and most importantly reversible changes in phenotype in response to environment modification [30]. A recent study on the hare barley (*Hordeum murinum subsp. leporinum*) strongly suggested that the response to climate change involves epigenetic regulation of gene expression to maintain homeostasis and ensure functional stability [31].

It has to be considered that the domestication and breeding strategies, based on inter-crossing elite or high-performance varieties, led to a loss of genetic diversity [32]. This genetic bottleneck could be overcome by the use of wild relative species that constitute a great resource of diversity, useful for new breeding strategies [33].

Understanding the physiology of grain development, as well as the effect of drought in this process are crucial for developing efficient breeding programs aiming to improve or at least sustain barley productivity in water deficit conditions.

In this book chapter, we will focus only on the development of barley grain. For more information related to inflorescence development in barley, one can refer to recent articles [34, 35]. In a first part, we will describe grain development in barley taking into account the hormonal and molecular regulation. In a second part, we will identify how water deficit or drought can affect grain development. Finally, in the last part, we describe methods used to unravel and study drought tolerant-associated genes.

2. Grain development in barley

The reproductive phase of development starts with the transition of the vegetative meristem into a reproductive meristem (inflorescence primordia), and ends with the physiological maturity of the grain characterized by dessication of the grain and entrance into dormancy [16]. The entire reproductive phase can be divided into several substages: floral initiation, differentiation of inflorescence and florets, male and female gametogenesis, pollination, fertilization and seed development [16]. From anthesis to maturity, grain development progresses through several phases that are commonly divided into three phases. The phase I, called pre-storage phase, is a phase of active cell division and differentiation that includes double fertilization, syncitium formation and cellularization. At this phase, the potential size is determined by the number of cells formed in the endosperm, as well as the main cell types, such as transfer cells, aleurone, starchy endosperm, embryo surrounding cells. The phase II, called storage or maturation phase, is the period of grain filling; one can observe a fast increase in grain dry weight. Finally, the phase III, or dessication phase, is characterized by water losses [4, 16, 36].

In barley, the grain is refers as to a caryopsis, type of fruit in which seed and fruit coats are fused. Surrounded by husks, the caryopsis consists of a diploid embryo and a large triploid endospern, surrounded by tissues of maternal origin (pericarp and testa) (**Figure 1**). The endosperm, tissue of nutritional value, is composed of several types of cells: aleurone (AL), starchy endosperm and endosperm transfer cells (ETC). Besides starch, the cell of the endosperm accumulate hordeins, the major source of proteins in barley grain [37]. The aleurone layer is source of lipids and vitamins; it also contains soluble proteins, including enzymes required for the remobilization of carbohydrates during the germination [6]. The endosperm develops with the synchronous division of nuclei without completion of cytokinesis. This phase of development is called the syncytial or coenocytic stage [38, 39]. The embryo is made of two main parts: the embryo axes and the scutellum, a nursing tissue. During grain development, scutellum drives the transport of nutrients to the developing embryo while later, during germination, it will contribute to the redistribution of sugars from the endosperm to the germinating embryo [6, 37, 40].

Few days after pollination (DAP), cellularization and differentiation occur, enclosing nuclei in cell walls and leading to the cell fate specification of the endosperm (**Figure 1**). The overall size of the grain partially depends on the number of nuclei formed during the syncytial phase; this number can exceed 2000 in Triticum and Hordeum [36, 41].

The main steps of barley grain development are summarized here. However, detailed information can be found in [6, 12, 36]. During the first 6 days after pollination (DAP), in barley, the endosperm cellularizes. Programmed cell death (PCD) occurs in the nucellus, except in the region in viscinity with the vascular bundle, leading to the differentiation of the nucellar projection (NP). In the same time, the region of the syncytium close to the NP initiate cellularization and differentiate into the endosperm transfer cells (ETC). During the transition phase (6 to 8 DAP),

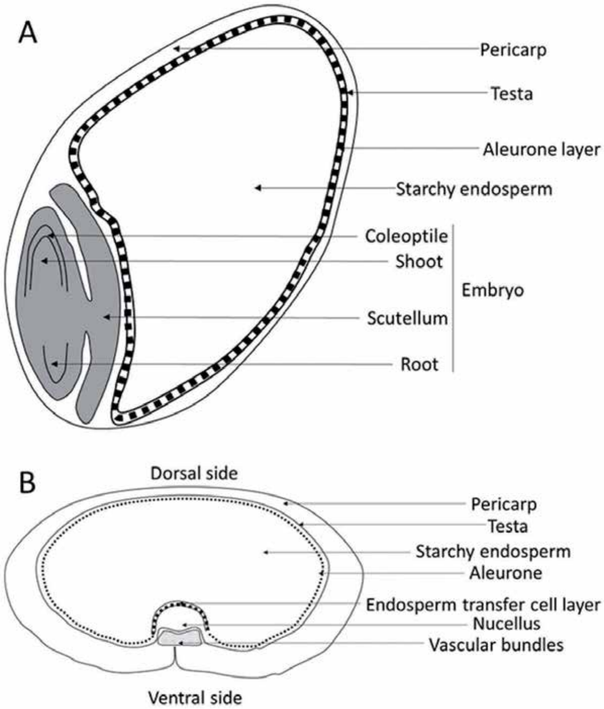

Figure 1.
Longitudinal (A) and transversal (B) schematic representation of sections of barley grain showing the different tissues (adapted from [6]).

transcriptional and physiological reprogramming occurs, involving the expression of genes encoding proteins with function in energy production and storage product synthesis [39, 42]. This phase is marked by endoreduplication, a modified mitotic cycle during which nuclei undergo one or more additional rounds of DNA replication; endoreduplication is common in plant and is often associated with higher cell volume [36, 43]. The final composition of the mature grain is then determined during the storage phase that lasts from 9 to 23 DAP. Both NP and ETC control the fluxes of assimilates into the endosperm [38].

The extremely complex mechanisms defining the grain structures composing the seed are tighltly controlled by hormones and involved permanent exchange of signals from and to the maternal tissues, but also between embryo and endosperm. Whereas the role of abscisic acid (ABA) and gibberellins (GAs) is well documented in their role in controling dormancy and germination [44–46], information related to the hormonal control of grain development are more scarce. Most of the advanced insights come from studies conducted on rice, that is considered as a plant model for cereals. The overall point of view is that cytokinin (CK) are most probably synthesized in endosperm where they act as a negative regulator of grain width but a positive regulator of grain length. Auxin, brassinosteroid and GAs (synthesized in the embryo) all promote grain length. The accumulation of CK, short after fertilization, corresponds with the formation of syncitium [47]. A recent study, based on transcriptomic studies, paved the first steps towards understanding the role of hormones during grain development in barley [48]. The NP, a mitotically active tissue, is characterized by events of differentiaon/elongation/cell death that form a top-down gradient, persisting throughout grain development. GAs might contribute to establishing and maintaining this gradient [48]. PCD is an essential process throughout grain development, participating in the formation of the NP at the early phase of development, of the starchy endosperm, of the vascular tissue, and of the scutellum. PCD of the pericarp cells is also important during grain's enlargement [49]. These processes are regulated by ethylene, jasmonate, ABA, auxin and GAs [49]. During grain filling, ABA, auxin and CK regulate the source photoassimilates during remobilization. Notably they can alter the synchronization between source activity and sink strength [50].

In a recent study, Sharma et al. [51] carried out a GWA study using nested association mapping populations combining the genetic information of 25 ancestor genotypes of *H. vulgare* subsp. *spontaneum* into the cultivated barley elite cultivar Barke. Authors identified a hotspot located on chromosome 7 showing a highly significant association with almost all traits. The ancestral allele increases several grain parameters, especially grain length. The region contains two genes: THOUSAND GRAIN WEIGHT 6 (TGW6), an IAA-glucose hydrolase, and MAP KINASE 6 (MAPK6), a mitogen-activated protein kinase. Interstingly, both genes have been demonstrated to influence grain size, weight and biomass in rice [52]. In the rice cultivar Nipponbare, *TGW6* expression peaked two DAP before decreasing rapidly in older seeds. In the Indian landrace rice Kasalath, *TGW6* contains 7 SNPs, including a − 1 bp deletion causing a frameshift that prevents the production of the mature, active protein. The Nipponbare near-isogenic lines containing the Kasalath haplotype accumulated markedly less IAA than wild type at 3 DAP, and had larger mature grains [52]. The authors concluded that the functional TGW6 affects the duration of the coenocytic stage by controlling IAA supply, limiting cell number and the subsequent grain size. It is noteworthy that the *tgw6* loss-of-function resulted in increased carbohydrate storage capacity before heading [53].

3. How drought affect the grain development and grain yield

Drought stress can drastically affect plant growth and development at any time of the crop life cycle. However, the extent of damages, the recovery capacity, as well as the impact on the yield depend on the stage of development at which the crop undergoes the stress [17]. Early drought stress at the seed germination stage reduces seed germination ratio. Drying soil surface after seedling emergence can cause seedling's failure [54, 55]. During the early vegetative phase, shoot elongation, leaf area, and tillering can be limited by drought stress [56]. Drought affects the most yield when it occurs at the onset of meiosis, i.e. during gametogenesis, and at the early grain initiation [16].

The most sensitive stage of barley growth to drought stress is the spike emergence and the initial stage of grain development [16, 50]. At the beginning of the reproductive stage, drought stress can affect the differentiation of floral meristem, and subsequently the spikelet's number. Exposure to the drought stress during the gametogenesis leads to pollen sterility; during flower induction and inflorescence development, it leads to a delay or complete inhibition in/of flowering. Later, drought results in the reduction in the grain size and weight by limiting the number of endosperm cells, consequently reducing the potential size of the grain. Finally, at later phase of development, drought affects the rate and duration of starch accumulation in the endosperm [16, 17].

Seed filling is the terminal stage of cereal grain development. Several biochemical processes associated with carbohydrate, protein and lipid synthesis in seeds and import of constituents are involved [6]. During the storage phase, endosperm cell division and accumulation of seed reserves are largely influenced by the moisture status of the cells. Water deficit elevates endogenous ABA concentration, reduces starch accumulation and results in ovary abortion leading to poor grain yield [57].

Flag leaf and ear are the main photosynthetically active organs that provide assimilates during grain filling at the end of the plant's life cycle [58]. Drought stress during this period negatively affects the net photosynthetic rate of the flag leaf. However, despite the high vapor pressure deficit condition, there is no significant effect on the grain-filling [59]. Perhaps, the remobilization of vegetative reserves maintains the grain growth rate under drought stress [60]. Whereas drought stress during the grain-filling stage enhances assimilate remobilization, it fastens senescence, reducing the grain-filling duration [61].

If one needs to summarize, drought stress is characterized by a low soil moisture that negatively affect nutrient uptake and assimilation at the root level. The consequence is a reduced photosynthetic ability, an altered sugar translocation, a pre-mature leaf senescence, an altered source/sink equilibrium. Finally, this is translated into alteration of the reproductive developmental stage and a shorter period of grain filling. All together, this participates to reduce the number of grains whose size and quality are highly deteriorated [50].

4. QTL, GWAS and other studies to identify new genetic resources of tolerance to drought

Breeding programs are the most effective method to improve the yield stability under drought stress condition [62]. The genetic and molecular bases of grain yield, quality and sustainability under drough have been studied in mapping quantitative trait loci (QTL) or Genome-wide Association (GWA) studies, combined with mutant identification. The number of studies focusing on the discovery of genes controlling yield in cereals and understanding their functions has increased in the last years [10]. However, it has to be considered that the domestication and breeding strategies, based on inter-crossing elite or high-performance varieties, led to a loss of genetic diversity [32]. This bottleneck can be overcome by the use of wild relative species and landraces that constitute a great resource of diversity, useful for new breeding strategies [32, 33, 63]. In this regards, *Hordeum spontaneum*, the wild barley ancestor, shows larger adaptation abilities to the unfavorable environmental conditions, including drought, compared to the cultivated barley, and an unexploited genetic variability [62]. Therefore, screening drought-tolerant germplasms from wild barley to integrate elite traits to the cultivated barley is one of the breeding approaches to improve drought tolerance in barley [19].

As already mentioned, drought tolerance in plants is a complex quantitative trait which is controlled by several genes with small effect or by QTLs [56]. Functional genomics and QTL mapping are the most useful approaches to identify the key genes and networks mediating the yield response under drought stress [64]. A large coverage of the plant genome by markers is essential to identify most relevant QTL associated with a trait of interest. Among others, single nucleotide polymorphism (SNP) is the most widely used type of markers in genomic studies. Recent advanced technologies based on high throughput next-generation sequencing (NGS) allow cheap and quick deep sequencing of genome of model and non-model crops, largely increasing the available genetic information. NGS encompasses different sequencing technologies and genotyping methods including restriction site-associated sequencing (RADseq) [65], diversity array technology sequencing (DArTseq) [66], and exome capture [67]. The recent barley genome sequencing [25] makes possible to identify the accurate positions and locations of the markers on the chromosome, as therefore to perform an effective QTL search in barley germplasm. Genome-wide association studies (GWAS) are a powerful tool to dissect the genetics of complex traits such as drought stress [23, 27, 68]. Genes identified in these studies can be used directly in molecular breeding in countries where the GMO regulation allows it, or indirectly in marker-assisted selection (MAS). In MAS, the selection is performed as soon as during early developmental stage of plants, reducing the time and cost of breeding researches [69–71].

Several factors have to be taken into consideration while considering reliable QTLs and markers in GWAS. First, allele frequency differences due to population stratification (systematic ancestry differences) is one of those factors. Population stratification can cause spurious associations in QTL mapping studies [70]. Therefore, the population structure (i.e. geographical origins and breeding history) needs to be analyzed prior to QTL/marker mapping, using statistical methods such as the principal component approach (PCA) [70]. Second, one might consider the environmental effects on the QTL expression. Specific environmental conditions such as abiotic stresses can increase the expression of specific QTLs named adaptive QTL. The presence and quantity of adaptive QTLs vary between different environments and experiments. The interaction between QTLs and environment (Q × E) can therefore modify the effect of a specific QTL according to the environmental conditions that can be the intensity of drought stress or the combination with different stresses such as heat or salinity [72]. An alternative to QTL studies, based on inheritability of markers across offspring, is to use natural populations and map traits by an association analysis, named linkage disequilibrium (LD) mapping. LD or gametic disequilibrium is the "nonrandom association of alleles at different loci". In simpler words, it reflects the correlation between polymorphisms. LD is caused by the mutation and recombination in a large, randomly mated population with independent loci segregations. In small populations with less individuals, the rare allelic combinations might be lost because of genetic drift [73].

To date, some QTLs involved in drought stress response have been identified in barley. Jabbari et al. [68] reported eight markers over the 3H, 5H and 6H chromosomes, significantly associated with grain number per spike using association mapping based on LD under the irrigated and water deficit conditions in barley. Honsdorf et al. [74] found an unknown wild barley QTL allele on chromosome 4H that improved thousand-grain weight under terminal drought stress. Similarly, a QTL on chromosome 4H related to increased biomass under both drought and control conditions was identified by GWAS, in a study involving offspring of a cross between wild barley accessions and an elite barley cultivar [27]. These results show that wild barley *Hordeum spontaneum* is a useful source of drought tolerance alleles in barley breeding programs. The use of recombinant inbred lines (RILs) resulting from a cross between Syrian and European cultivars identified that the earliness allele from the Syrian parent confered higher yield performance under drought conditions [75]. Drought response-specific QTLs were identified within the confidence intervals of candidate genes encoding antioxidants, carboxylic acid biosynthesis enzymes, heat shock proteins, small auxin up-regulated RNAs, nitric oxide synthase, ATP sulfurylases, and flowering time regulation proteins [75]. Adjustment of flowering time and in particular early flowering represents an escape strategy of plants to complete the sensitive reproductive stage before unfavorable environmental conditions. In barley, most of the seed dry weight is composed of carbohydrates which are produced and transferred to the seeds from the photosynthetic organs of the spike such as lemma, palea and awn [76]. Spike is more resilient to drought stress compare to the flag leaf and awn is the major photosynthetic organ under terminal drought stress and plays a crucial role in grain filling [77]. Several QTLs for grain plumpness and yield in doubled haploid populations of barley with significant Q × E interaction have been identified [78].

Another widely used method to identify drought-associated genes is to analyze gene expression profiles at the transcriptional level of the drought-resistant and sensitive line exposed to drought stress [79–81]. Barley transcriptomic data reported differentially expressed genes in drought-tolerant and sensitive genotypes, in relation to terminal drought stress. Several genes with known or predicted function were found to be constitutively expressed in the drought-tolerant barley genotypes, representing a potential mechanism of adaptation to the stress. To date, several drought tolerance-associated genes have been reported in plant species [82, 83]. However, their overexpression in transgenic plants did not significantly improve drought tolerance [84] indicating that drought tolerance is a complex mechanism that might involve different regulation at the genetic level.

The regulation of gene expression is an important process, in part controlled by microRNAs (miRNAs). MiRNAs are single-stranded noncoding RNAs composed of 20–24 nucleotides that play an important role as gene regulators in a wide range of organisms by cleavage of target messenger RNAs (mRNA), translational repression and DNA methylation [85]. Drought-responsive miRNAs have been reported in many plants to participate in the regulation of drought-responsive genes [86]. Moreover, the expression of miRNAs itself is altered in response to drought stress. Four drought stress-induced miRNAs (hvu-miR156a, hvu-miR166, hvu-miR171 and hvu-miR408) were reported in barley leaves differentially expressed under drought conditions [87]. Lv et al. [88] reported three miRNAs (miR-n026a, miR-n029 and miR-n035) up-regulated under drought and salinity stresses in barley leaves. Hackenberg et al. [89] identified a miRNA, hvu-miR5049b up-regulated, under the drought conditions. Additionally, authors indicated that hvu-miR168-5p was up-regulated under drought stress only in leaves while its expression level remained unchanged in barley roots suggesting that some of the drought-regulated miRNAs can be expressed differently in barley tissues. Ferdous et al. [90] determined that Hv-miR827 enhances drought tolerance in barley. Several miRNAs were identified with different abundance in two different drought-sensitive and tolerant barley cultivars as drought-responsive miRNAs [91]. Recently, 2 conserved and 10 novel miRNAs were identified as drought-tolerant miRNAs in two different drought-tolerant and sensitive wild barley genotypes [92]. These miRNAs can regulate many different genes involved in numerous biological and metabolic processes in plants such as growth, development, hormone signaling, consequently affecting the stress response in plants.

Besides miRNAs, epigenetic factors such as DNA methylation and histone modifications in response to environmental conditions lead to changes in chromatin structure. Open and closed chromatin states cause gene activation and gene silencing, respectively, and regulate a wide range of developmental processes in plants in response to changing environment [93]. Chromatin dynamic and DNA-methylation have been reported as tolerance mechanisms to drought stress in crops [93, 94].

Beyond that what has been discussed above, the role of transcription factors (TFs) in the regulatory networks underlying plant responses to abiotic stresses is crucial [95]. Recently, Collin et al. [96] showed that the barley mutant carrying *ABA INSENSITIVE 5* (*ABI5*) genes (HvABI5) is drought tolerant compared to its parents. ABI5 is a basic leucine zipper (bZIP) transcription factor which acts in the ABA network. ABA is the crucial regulator of plant responses to abiotic stresses. ABA-dependent signaling alters the activity of stress-responsive genes and thus regulate physiological processes, such as photosynthesis, stomatal closure and osmoprotectant biosynthesis in response to drought stress [97, 98]. *MYB* genes encode another class of TFs known for their involvement in the regulation of drought stress responses [99]. Harb et al. [79] reported that NAC transcription factors are specifically induced in drought-tolerant barley compared to sensitive genotype. The improvement roles of *NAC* genes in response to the drought stress have been reported previously [100].

Alternative splicing (AS) was also found to differ between genotypes as a key mechanism controlling the expression of the drought-responsive gene in barley [101]. In the gene expression process, during the transcription of DNA to RNA, first precursor mRNA (pre-mRNAs) are produced, containing the introns which interrupt the protein-coding regions. Splicing is an essential step to remove the introns through the pre-mRNAs [102]. In AS, a single pre-mRNA can produce more than one mRNA through the use of alternative splice sites. Alternative mRNAs encoding different isoforms of proteins increases the diversity of an organism's transcriptome and proteome [103]. AS can regulate the gene expression at the transcript levels by producing unstable mRNA isoforms, which can be degraded by nonsense-mediated decay (NMD) [104].

5. Concluding remarks

Plant responses to drought stress, including different tolerance mechanisms and genetic controls, are complex. Further studies are required to determine the molecular basis of yield-related traits in barley before their integration into breeding programs focused on tolerance to drought stress and sustainable yield under adverse conditions.

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Author details

Mortaza Khodaeiaminjan and Véronique Bergougnoux*
Centre of Region Haná for Biotechnological and Agricultural Research,
Czech Advanced Technology and Research Institute, Palacký University Olomouc,
Czech Republic

*Address all correspondence to: veronique.bergougnoux@upol.cz

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Chapter 12

Salinity Stress in Maize: Effects of Stress and Recent Developments of Tolerance for Improvement

*Ayman EL Sabagh, Fatih Çiğ, Seyithan Seydoşoğlu,
Martin Leonardo Battaglia, Talha Javed,
Muhammad Aamir Iqbal, Muhammad Mubeen,
Musaddiq Ali, Mazhar Ali, Gülşah Bengisu, Ömer Konuşkan,
Celaleddin Barutcular, Murat Erman, Semih Açikbaş,
Akbar Hossain, Mohammad Sohidul Islam, Allah Wasaya,
Disna Ratnasekera, Muhammad Arif, Zahoor Ahmad
and Mahrous Awad*

Abstract

Soil salinity has emerged as a global threat to sustainability of farming systems by deteriorating the quality and productivity of crops particularly in the coastal regions of the world. Although, as a C4 plant, maize (*Zea mays* L.) has ability to tolerate a medium level of salinity; but initial growth stages of maize are sensitive to salinity stress. Therefore, it is crucial to expand our understanding pertaining to maize response to salt stress and tolerance mechanisms for devising approaches to enhance maize adaptability in saline environments. Moreover, maize crop undergoes several physiological changes and adapts some mechanism to overcome the salinity stress. Different mitigation strategies like application of chemicals, plant growth-promoting hormones, and use of genetic and molecular techniques are used to manage salinity and may ensure crop productivity under changing climate. This chapter aimed to assess the recent advancement pertaining to salinity stress influence on the physio-biochemical processes in maize and to draw the relationship between yield components and salinity stress. In addition, current study also highlights research gaps by focusing the seed enhancement techniques, phytohormones exogenous application and genetic improvement of maize under soil salinity.

Keywords: Salt stress, adverse effects, maize, productivity, seed enhancement

1. Introduction

Among various abiotic stresses, salt stress has posed one of the most severe threat to modern commercial oriented and profit-driven crop production at a global scale [1–4]. Besides soil salinity, utilization of saline water for irrigation purposes, particularly in the

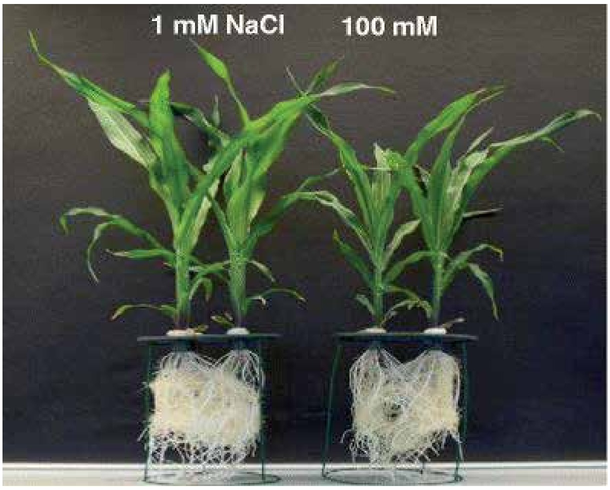

Figure 1.
Effect of salt stress on the initial growth of maize (adapted from Farooq et al. [12].

low-lying coastal regions of many countries, has also been identified as a major yield-limiting factor for boosting agriculture production [5, 6]. The detrimental impacts of salt stress manifest through a reduction in the relative water potential of plants which causes decline in plants growth [7], coupled to a negative effect in soil and water quality both in the short and long term [8, 9]. Salt stress is associated with the moisture stress that decreases plant growth and ultimately reduces plant yield even at soil moisture contents that are not limiting for crop productivity (**Figure 1**) [10, 11].

Similar to other C4 plants, maize is able to grow in both saline and non-saline conditions due to its stress adaptive potential and relatively tolerance against salinity [12–14]. Although salinity adversely affects maize growth and yield attributes throughout most of the plant cycle, the final impact on plant productivity depends upon the length and severity of the stress and the growth phase when the stress occurs [15, 16]. In general, and similar to the case for other row crops, the initial growth stage of maize is highly sensitive to salt stress. In a hydroponically grown study, Farooq et al. [12] observed the growth of roots and shoots of salt-treated (1.0 and 100 mM NaCl, applied one week after transplanting) maize variety cv. 'Pioneer 3906'. Authors reported a significant reduction in the plant height and dry matter biomass of plants treated with the highest salt concentration just 21 days after the beginning of the salt soaking study [12]. However, lower salt concentrations can severely impact normal crop growth and several studies have demonstrated that very low salt concentrations can reduce the growth cycle of maize plant due to oxidative stress before the occurrence of sodium toxicity in the plant [17–19]. The objectives of this chapter are to discuss a) the current and most recent knowledge regarding the influence of salinity stress on physio-biochemical processes and yield components in maize, and b) the seed enhancement technologies, phytohormones exogenous application and genetic improvement of maize against soil salinity stress.

2. Adverse effects of salinity on growth and development of maize

2.1 Effect on germination

Seedling establishment is an important phase in the plant life cycle. Salt stress adversely affects seed germination [20], due to the decrease in the osmotic potential created in the soil solution that prevents the entry of water into the seed [21]. During seedling establishment, intake of sodium and chloride ions causes toxicity in the plant cells, thus reducing seed germination rates and the growth of seedlings that have already germinated [22]. Besides its negative impact in the germination rates, salinity stress also delays the overall germination process, thus reducing the survival chances of those seeds that were able to germinate [23, 24]. Because of its potential to drastically reduce crop productivity, it is of paramount importance to recognize these early deleterious impacts of soil and water salinity in plant growth and development [25].

Salinity reduces seedling establishment by increasing the oxidative stress through the absorption of Na^+ and Cl^- ions in the seeds that cause toxicity in the embryogenesis and protein synthesis. Maximum oxidative stress caused by Na^+ and Cl^- ions toxicity during germination lowers or stunts the germination of plants [26]. In case of maize production, just Na^+ toxicity was found more detrimental in reducing the germination under salt-stressed environments.

Under arid and semi-arid conditions salt stress is commonly considered as the more threatening factor reducing the seed emergence rates and the overall crop stands [9, 27, 28]. Therefore, salinity constitutes one of the most significant abiotic factors limiting crop productivity, while changing climate scenario has even further worsened the situation [29]. The ability of seeds to germinate at high salt concentrations in the soil is of crucial importance for the survival of many plant species. However, the effects of salinity are modified by its interactions with other environmental factors such as temperature and light [30]. In saline habitats, satisfactory seed germination typically takes place after high precipitation events, when soil salinity is reduced [31]. Seed priming stimulates numerous metabolic processes involved in the early phases of germination, and it was observed that seedlings from primed seeds can grow more vigorously and perform better under adverse environmental conditions compared to non-primed seeds [32].

2.2 Effect on maize growth

El Sayed, [33] observed dramatic decreases in maize plant root elongation, plant height, leaf area, photosynthesis, mitotic division and root and shoot biomass in a sandy soil under salt stress conditions. Salinity promotes suberization of the hypodermis and endodermis, and the Casparian strip develops closer to the root tip compared to roots growing in non-saline soils [34]. Although roots are the first organ exposed to salt stress, shoots are more sensitive to salt stress [35]. Salinity reduces shoot growth by suppressing leaf initiation and expansion, as well as internode growth, and by accelerating leaf abscission [36]. Salt stress rapidly reduces leaf growth rate due to a reduction in the number of elongating cells and the rate of cell elongation [37, 38]. As a salt-sensitive crop, shoot growth in maize is strongly inhibited in the first phase of salt stress [38]. Schubert et al. [39] observed stunted maize growth with dark green leaves without any toxicity symptoms during the first phase of salt stress, owing to impaired extension growth as osmotic adjustment and turgor maintenance were not limiting. Likewise, growth of salt-resistant hybrids has shown that it was not turgor but cell wall extensibility which restricted cell extension growth during the first phase of salt stress [39].

Salt stress may also displace Ca^{+2} ions from plasma membrane-binding sites, thus causing membrane leakiness as a primary cellular response to salt stress [40]. When the integrity of the plasma membrane is affected by high salt concentrations in soil, a cell wall acidification process occurs due to the reduction in the cell wall ability to pump protons out across the intact plasma membrane [41]. Conversely, pH in the apoplastic space tends to increase in salt-sensitive maize genotypes subjected to salt stress and this reduces the extension growth of the cell due to less acidification of the apoplast [41, 42]. Comparing salt tolerant and susceptible genotypes of maize, Pitann et al. [43] found that salt-tolerant genotypes better regulated hydrogen ions concentration and decreased the pH in the apoplastic space, while also loosen the cell wall turgidity according to the acid growth theory [44]. According to this theory, the increased in the cell wall expansion triggers a protein synthesis process that ultimately results in cell growth. The enzymes that are responsible for the loosening process in the cell wall and the regulation of cell elongation are present in the apoplastic space of cells located in the leaves [42]. The extent to which these enzymes will loosen the cell wall for further extension depends upon the acid concentration in the apoplastic space and the existence of a cell wall pH under 5 [45, 46]. Research shows that, when grown under salt stress conditions, the amount and activity of β-expansion proteins decreased in salt susceptible genotypes of maize, while it was only slightly affected in salt-tolerant genotypes [47, 48]. In general, β-expansions proteins have been more heavily studied than α-expansion proteins in salt-stress related research [49]. These β-expansion proteins are responsible for important cell functions and have a specific set of matrix polysaccharides and structural proteins in maize [49].

Early in the growth cycle, high salt concentrations reduced the growth of tissues in corn which may be partially accountable for a reduction in the overall photosynthetic capacity of the plant [50]. Moreover, salt stress has shown to produce structural variations in the cell wall that alter its correct functioning [51]. For instance, salt stress stimulates the production of ROS (Reactive Oxygen Species) such as peroxidase and hydrogen peroxide in the cell apoplastic space, and this increases the biosynthesis of diferulates which inhibits maize cell wall growth [52–54]. Moreover, increased in the ROS results in peroxidation of lipid and DNA damage [55–57]. In other studies, a temporary increase in the concentration of apoplastic peroxidase terminated cell wall elongation [58, 59], and increased the oxidation of phenolics compounds in maize [60]. A persistent salt stress condition across the plant growth cycle can result in a significant decrease in the length of the shoots and the extent and duration of the flowering process in the plant, which ultimately affects the reproduction and the productivity of crops. In this context, salt stress resulted in the deterioration and further abscission of old leaves of plants while the growth of young leaves was not affected by salt stress at grain cob initiation stage [1].

2.3 Effect on development and yield

The number and weight of kernels are the two most important yield components to calculate grain yield in maize [61–64]. In a recent study, and compared to non-saline conditions, a salt concentration of 100 mM NaCl applied at the reproductive phase of maize reduced the kernel yield and the kernel weight by 25% and 8%, respectively (**Figure 2**) [65]. Katerji et al. [66] studied the effect of three irrigation water treatments [i.e., fresh, unsalted water; 15 and 30 mEQ l^{-1} (NaCl and $CaCl_2$)] in maize yield and yield components in a clay and a loamy soil. Compared to non-saline treatment, authors found that 15 mEQ l^{-1} reduced maize grain yield by 11.3% in the clay soil through a reduction of 7.6% in the kernel set without changes in the kernel weight. Conversely, the 15 mEQ l^{-1} salt treatment did not affect grain yield in the loamy soil. Application of 30 mEQ l^{-1} salt treatment reduced the grain yield by 24.5% in the clay, and by 21.4% in the loamy soil as a result of decreases in both the kernel set and kernel weight in the two soils.

Photosynthesis reduction and sink limitation induced by salinity are among the main reasons for poor kernel setting and reduced grain number [67]. Under salt stress conditions, a sink limitation disrupts kernel setting more than the resulting reduction in the photo-assimilation production in maize. Research showed that the

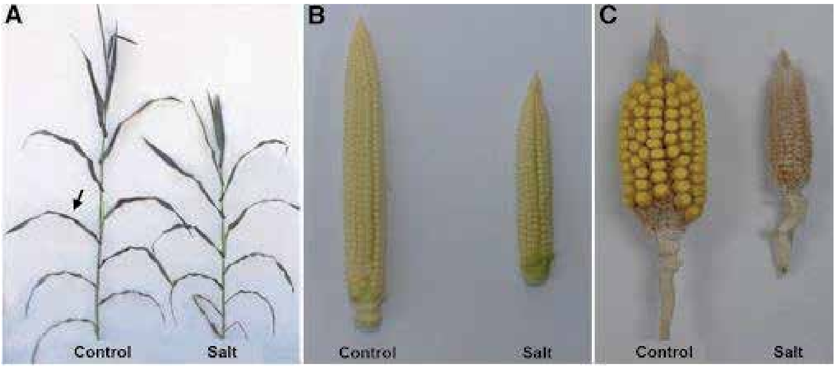

Figure 2.
Salt stress effects on maize plant growth and yield (from Kaya et al. [65]). A: Effect of salt stress on growth; B: cob length; and C: grain filling of maize.

salt stress-induced reduction in the sink activity in maize causes a reduction in the acid invertase activity, which further reduces the final grain number in maize [68]. At the eco-physiological level, however, a decrease in the translocation of assimilates from leaves to the emerging grains is the main driver for poor kernel set and reduced grain weight, and thus final grain yield, in maize plant stands subjected to salt stress conditions [69].

In salt-stressed maize plant, growth is affected by lack of nitrogen due to the antagonistic action of nitrate ions with chloride ions [34, 70]; hence, maize yield significantly improved with the addition of nitrogen under salt stress. Application of nitrogen in the amount of 120 kg ha^{-1} neutralized the harmful effects of salinity; in particular, it improved nitrogen absorption, growth and productivity under of salt stress conditions [71].

2.4 Effect on grain quality

Different environmental conditions can greatly affect the grain quality in maize [72]. Among these, the negative impact of salt stress in grain quality has not been extensively studied. Working with five saline irrigation levels [1, 2, 3, 4, and 5 g L^{-1} of total dissolved solids (TDS)] in a 2-yr study in China, Li et al. [73] found no difference in the oil, crude fiber and ash contents of maize grain. Conversely, grain moisture and starch content decreased with increased salinity, with maximum values ocurring with 1, 2 and 3 g L^{-1} of TDS in both cases, while protein content increased with increased salinity, reaching maximum values >12% with 4 and 5 g L^{-1} of TDS. While the impacts of different salinity treatments were antagonistic for starch and protein content, two of the key quality components in maize grain, salt levels in the irrigation water should balance the content of each component. Low grain moisture content can be beneficial for storing purposes, as these conditions are detrimental for proliferation of fungal pathogens, which can cause mycotoxin contamination and reduction in the maize grain quality (**Table 1**) [74].

Cucci et al. [75] found no difference in the kernel composition due to irrigation water quality in the first year of a study conducted in Italy. Contrarily, in the third year, brackish water irrigation increased the grain protein content by 6.9% and decreased the moisture content by 9.3% compared to grain irrigated with freshwater, which is similar to the findings from Li et al. (2019) [73]. Finally, there was no effect of irrigation scheduling and the interaction among salinity and irrigation scheduling on grain quality either in the first or the third year under study.

Years	Water Quality	Protein %	Starch %	Fats %	Grain Moisture %
1st	Brackish water	9.1a	72.1a	4.2a	15.2a
	Fresh water	8.9a	71.8a	4.1a	15.5a
3rd	Brackish water	9.2a	71.6a	4.1a	14.6b
	Fresh water	8.6b	71.7a	4.3a	16.1a

Different letters indicate significant difference according to Duncan test (p = 0.05).

Table 1.
Grain quality of maize as affected by the different quality of irrigation water in the first and third year of crop rotation [75].

3. Recent approaches for improvement of maize tolerance under salinity

3.1 Application of hormones and osmoprotectants

Exogenous applications of growth hormones and osmolytes have been found to be effective to cope against the negative impacts of soil and water salinity. The role of plant growth regulators and osmoprotectants under salt stress is important in modulating physiological responses leading to adaptation to such unfavorable environments. Accumulation of osmolytes under low water potential conditions, such as those occurring soils with elevated salt concentrations, helps to maintain the plant water status in a process known as osmoregulation [76]. More than 20 years ago, osmoprotectants were chemically grouped as amino acids (proline), ammonium compounds (glycine betaine), polyols and sugars (mannitol, dononitol, trehalose, fructans) [77]. In a recent study, osmoprotectants were classified into two major groups, namely organic (eg. glycine betaine, proline, sugars, and proteins) and inorganic (eg. Ca, K, PO_4, NO_3, SO_4) osmoprotectant solutes preserving water without impairing the regular metabolism of the plant [78]. Among them, proline, glycine betaine, and mannitol are commonly found in cytosol and chloroplast in plants. Under stressed environments, exogenous application of osmoprotectants act to maintain the regular plant cellular functions [79–81], by playing key roles in regulating the enzyme activity, ROS homeostasis, maintaining the membrane integrity, and balancing the ionic transport across the cell membrane [82].

The exogenous application of gibberellic acid (GA) and cytokinin (CK) at the maize vegetative stage was effective to remediate the damage in the cellular membranes of maize plants subjected to water deficit stress [83], by decreasing the electrolyte leakage and lipid peroxidation [84].

Similarly, exogenously applied GA, CK and auxin improved the tolerance to water deficit resistance in maize plants growing in saline soils by mitigating the membrane oxidative damage and improving the overall plant water status [85]. Moreover, application of GA, Indole-acetic acid and proline combined with organic amendment enhanced heavy metal tolerance and increased protection against oxidative stress in maize compared to non-applied control, thus providing a promising approach as an osmoprotectant that could be used in saline soils [86].

Salicylic acid (SA) plays dual roles as both a plant growth regulator and an antioxidant, improving crop performance under abiotic and biotic stresses [87, 88]. Salicylic acid-induced antioxidant system was reported in maize in water deficit environments [89]. Foliar application of SA in maize has a potential to increase the relative water content and membrane stability index in maize grown under water deficit environments [90]. Moreover, in salt stressed maize plants, exogenous application of SA improved plant growth, antioxidant enzyme contents and stabilized the overall photosynthetic process [91]. In this regard, foliar application of SA in maize seedlings reversed the negative impacts of soil salinity in the plant gas exchange, rubisco activity and photosynthetic efficiency [92, 93], while also increasing the production of soluble sugars, proline and nutrient uptake particularly K^+ [94]. When SA was applied to roots, increases in the photosynthetic rates, gas exchange levels, and internal CO_2 exchange and grain yield of maize were observed in saline soils [95, 96]. Pre-treatment of maize seeds by exogenous application of SA (2 mM) exhibited improved seedling emergence and stand establishment maize [97].

The exogenously applied methyl jasmonate (MeJA) can ameliorate the plant tolerance to abiotic stresses such as drought and salinity by enhancing the defense-oriented metabolism of plants [98, 99]. Pre-treatment of maize seeds with MeJA can suppress the harmful effects of water stress by maintaining the total protein, proline, carbohydrate contents and antioxidant activities under saline conditions [100]. Additionally, seed and foliar pre-treatments with exogenous MeJa showed positive effects on drought-induced oxidative stress responses of maize seedlings by modulating the levels of osmolytes, endogenous abscisic acid (ABA), and the activities of antioxidant enzymes [101].

3.2 Seed priming

The occurrence of an even and fast germination process has long been considered as a critical stage for final yield determination in most crops [102]. The seedling stage of maize plant is more sensitive to salinity [103] than mature stages [104]. Seed priming entails pre-sowing seed treatment with different priming agents including water, growth regulators [105], which facilitates the germination process by increasing the energy metabolism of the plant, promoting a more efficient mobilization of food reserves, enhancing expansion of the seed embryo [106], inducing formation of stress-responsive systems such as heat shock proteins, catalase and other antioxidant scavenging enzymes and upregulating the genes encoding peroxiredoxin [2, 107]. Increased germination rate and vigorous seedling establishment have been documented for primed seeds especially hydro-priming, and priming with growth regulators [108, 109]. The use of seed priming in the form of inorganic chemicals, plant extracts or microorganisms is one of the most efficient technologies to improve the germination rates and the synchronization of seedling emergence in plants [110]. Seed priming technique tend to boost water status of the seed which leads to activation of the pre-germination metabolism of the seed. In the second stage, the seed is dried to prevent radicle emergence before seed sowing [111].

Seed priming techniques utilize different osmotic solutions as seed priming agents including inorganic salts, sugars, growth regulators and polyethylene glycol [111]. Broadly, there are two seed priming techniques, known as uncontrolled hydration or hydro-priming [112], and controlled hydration, which includes methods such as osmotic priming, solid matrix priming, and hormonal priming [113]. Among others, polyethylene glycol (PEG), chlorides, sulphates, nitrates, glycerol, sorbitol have also been commonly used as osmotic priming agents having germination enhancing effect for different cereals including maize [23].

Nutrient priming with various inorganic compounds has been effectively applied to enhance germination and growth of maize under saline environment. For example, KNO_3 has shown better establishment of seedlings at low temperatures in maize [114]. Micronutrients have been reported as nano-seed priming agents for boosting germination percentage and seedling development and vigor [115]. Also, priming maize seeds with NaCl before sowing induced physiological and biochemical changes thereby enhancing salinity tolerance and better performances under varying degree of saline environments [116]. Priming of maize seeds with $CaCl_2$ increased the germination rate, and both the fresh and dry biomasses of plumules and radicles in maize compared to untreated control and hydro primed seeds under salinity stress [117]. Further, authors measured significantly higher concentrations of Na^+, K^+ and Ca^{2+} in growing seedling tissues when seeds were primed with inorganic salts such as NaC1, KCI, or $CaC1_2$ [117]. Maize seeds priming with 1% $ZnSO_4$ exhibited improved plant growth, increased final grain yield and enriched Zn^{2+} contents in seed on soils with limited Zn^{2+} availability, and a more efficient translocation of Zn^{2+} to growing shoots during germination and early seedling development [118], in saline environments. Moreover, use of Zn as a seed primer increased the accumulation of Zn^{2+} in the aleurone layer of maize seeds, and resulted in a higher plant biomass production and mineral nutrient uptake in plants subjected to salt stress [119].

Maize seeds primed by SA (2 mM) exhibited improved seedling emergence and establishment maize under salt stress [97]. Kinetin and indole acetic acid application on foliage negate the harmful effects of salt stress, while it does not affect maize plant salinity resistance. In addition, the salt content increases the sodium concentration in corn leaves at the disbursement of potassium and calcium, while kinetin and indole acetic acid foliar applications correct these effects and raise the potassium and calcium content in the leaves. Thus, 2 mM concentration of kinetin and indole acetic acid foliar application counteracted the adverse effects of salt on maize growth and yield by increasing membrane permeability and absorption of essential nutrients [40]. Yang et al. [120] reported that exogenous application of glycine betaine on maize plant under salt stress enhanced growth, net photosynthesis, leaf water content, and quantum yield of photosynthesis.

3.3 Genetic improvement of maize tolerance to salinity stress

In the recent past, molecular marker-assisted selection and other biotechnological techniques are being used in the context of the physiological basis of stress tolerance along with conventional breeding strategies to increase tolerance to abiotic stresses (heat, drought, and salinity) in maize. However, poor success in establishing maize cultivars tolerant to stress is mainly due to poor screening and selection techniques, poor selection criteria, and poor understanding mechanism of stress tolerance. However, some reports, in other species, are available which demonstrated the successful use of molecular marker for the development of tolerant cultivars against abiotic stresses [121]. As an illustration, the maintenance of potassium homeostasis in salt-tolerant plants was regulated by *SKC1*, which was mapped on chromosome 1 [122]. This molecular marker can be used for selecting salt-tolerant cultivars. Development of transgenic plants with improved resistance against heat, drought and salt stresses is also a possible approach as high throughput sequencing techniques help in exploring the expression of genes specific for abiotic stress tolerance [123].

The scope of breeding for the salinity, heat and drought is limited due to less selection efficiency, inadequate screening techniques, and the minimum understanding of the interaction between environment and stress. Now the molecular marker technology is helpful to develop the new maize cultivars with improved traits. However, the reasonable way at this stage is the improvement of transgenic maize with enhanced resistance against heat, drought and salt stresses. The high-throughput integrated approaches that are provided by the genomic technologies are helpful to examine the expression of the genes for all abiotic stresses including drought [2]. Microarray profiling under drought stress effects has been studied in different plant species i.e., *Arabidopsis* [124]. These studies recognized the multiple expressed transcripts of the genes which are involved in the photosynthesis, biosynthesis of osmoprotectants, ABA biosynthesis and signaling, water uptake, detoxification of reactive oxygen, and a myriad of transcription factors of various members of the zinc finger, protein stability and protection, bZIP and WRKY families (**Table 2**) [2].

Gene Family	Gene	Tolerance Mechanism	Reference
WRKY	*ZmWRKY33*	Overexpression of *ZmWRKY33* in Arabidopsis activated stress-induced genes, for example, *RD29A*, under normal growth condition and improved salt stress tolerance under stress condition.	[125]
	WRKY25 and *WRKY33*	Upstream intergenic regions from each gene that were sufficient to confer stress-inducible expression on a reporter gene; W-box in their upstream regions also might be responsible to confer salt tolerance	[126]
MYB	*ZmMYB3R*	Overexpression of *ZmMYB3R* confer salt tolerance in transgenic plants	[127]
	ZmMYB30	Ectopic expression of *ZmMYB30* in transgenic Arabidopsis plants promoted salt-stress tolerance and also increased the expression of a number of abiotic stress-related genes, allowing the plants to overcome adverse conditions	[128]
AP2/ERF	*ZmEREB20*	Overexpression of *ZmEREB20* confer salt tolerance in transgenic plants	[129]
bZIP	*ZmbZIP72*	Overexpression of *ZmbZIP72* enhanced the expression of ABA-inducible genes such as *RD29B, RAB18*, and *HIS1–3*, which resulted in enhanced salinity tolerance	[130]
	ZmbZIP60	Overexpression of *ZmbZIP60* confer salt tolerance in transgenic plants	[131]
	ZmbZIP4	*ZmbZIP4* could positively regulate a number of stress response genes, such as *ZmLEA2, ZmRD20, ZmRD21, ZmRab18, ZmNHX3, ZmGEA6*, and *ZmERD*, and some abscisic acid synthesis-related genes, including *NCED*, *ABA1*, *AAO3*, and *LOS5* to enhance salinity tolerance	[132]

Table 2.
Transcription factors mediated salinity tolerance in maize.

4. Conclusion

The changing climate scenario has worsened the salinity problem while global warming has caused significant increase in salt affected lands and thus has jeopardized the food security of millions of people across the globe. As a C4 plant, maize can moderately tolerate salinity; however, the initial growth stage of maize is highly sensitive to salinity stress. The adverse effect of salinity can be mitigated through understanding the adaptability of maize in saline environments. Several seed enhancement and genetic approaches can be adapted to overcome the adverse effects of salinity stress. Among them, biological enhancement through seed priming, application of antioxidants and growth hormones, genetic and molecular techniques for development of tolerant cultivars, and several agronomic management practices such as optimizing sowing time and seed rate etc. can be useful to cope with the adverse effect of salinity. Ultimately, these approaches have the potential to multiply maize production and nutritional quality in saline environments under current and future scenario of climate change.

Conflict of interest

The authors declare no conflict of interest.

Author details

Ayman EL Sabagh[1,2]*, Fatih Çiğ[2], Seyithan Seydoşoğlu[2],
Martin Leonardo Battaglia[3], Talha Javed[4], Muhammad Aamir Iqbal[5],
Muhammad Mubeen[6], Musaddiq Ali[6], Mazhar Ali[6], Gülşah Bengisu[7],
Ömer Konuşkan[8], Celaleddin Barutcular[9], Murat Erman[2], Semih Açikbaş[2],
Akbar Hossain[10], Mohammad Sohidul Islam[11], Allah Wasaya[12], Disna Ratnasekera[13],
Muhammad Arif[14], Zahoor Ahmad[15] and Mahrous Awad[16]

1 Department of Agronomy, Faculty of Agriculture, University of Kafrelsheikh, Egypt

2 Department of Field Crops, Faculty of Agriculture, Siirt University, Turkey

3 Department of Animal Sciences, Cornell University, Ithaca, NY, USA

4 College of Agriculture, Fujian Agriculture and Forestry University, Fuzhou, China

5 Department of Agronomy, Faculty of Agriculture, University of Poonch Rawalakot (AJK), Pakistan

6 Department of Environmental Sciences, COMSATS University Islamabad, Vehari, Pakistan

7 Department of Field Crops, Faculty of Agriculture, Harran University, Şanlıurfa-Mardin Karayolu Üzeri 18.Km, Harran, Sanliurfa, Turkey

8 Department of Field Crops, Faculty of Agriculture, Hatay Mustafa Kemal University, Hatay, Turkey

9 Department of Field Crops, Faculty of Agriculture, University of Çukurova, Turkey

10 Bangladesh Wheat and Maize Research Institute, Dinajpur, Bangladesh

11 Department of Agronomy, Hajee Mohammad Danesh Science and Technology University, Bangladesh

12 College of Agriculture, Bahauddin Zakariya University, Bahadur Sub-Campus Layyah, Pakistan

13 Department of Agricultural Biology, Faculty of Agriculture, University of Ruhuna, Sri Lanka

14 Department of Agronomy, The University of Haripur, Haripur, Pakistan

15 University of Central Punjab, Bahawalpur Campus, Pakistan

16 Department of Soils and Water, Faculty of Agriculture, Al-Azhar University, Assiut, Egypt

*Address all correspondence to: ayman.elsabagh@agr.kfs.edu.eg

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Over the past 50 years, cereals such as maize, rice, wheat, sorghum, and barley have emerged as rapidly evolving crops because of new technologies and advances in agronomy, breeding, biotechnology, genetics, and so on. Population growth and climate change have led to new challenges, among which are feeding the growing global population and mitigating adverse effects on the environment. One way to deal with these issues is through sustainable cereal production. This book discusses ways to achieve sustainable production of cereals via agronomy, breeding, transcriptomics, proteomics, and metabolomics. Chapters review research, examine challenges, and present prospects in the field. This volume is an excellent resource for students, researchers, and scientists interested in and working in the area of sustainable crop production.

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