



Breeding Strategies for Developing Disease-Resistant Wheat: Present, Past, and Future

8

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Abstract

Since its origin in Southeast Turkey, wheat (*Triticum aestivum* L. AABBDD; Family Poaceae) has been a prime dietary cultivated cereal that is consumed worldwide by nearly 20% of the world population. However, there are a wide plethora of biological variables that seriously threaten production around the world. Among the biological stresses, phytopathogens are considered the most serious threat to yield. This can be further elaborated by the fact that since the nineteenth century, more than 30 diseases have been reported to have had a drastic impact as epidemics, including karnal bunt, smut, mildew, blight, rust, etc. So far, in response, various landraces and several wild-related genera (such as *Thinopyrum*, *Triticum*, *Hordeum*, *Aegilopsis*, *Elymus*, and *Leymus*) represent the different gene pools that have been utilized in developing disease-resistant varieties. With the emergence of advanced molecular markers, whole genome sequences, and new genomic approaches, there are multiple ways and tools for researchers to enhance durability and wide-range disease resistance in a short period. The present documentation of trait introgression offers an effective option to narrow down the cost of unsustainable fungicides. Therefore, the current

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137

chapter is an attempt to incorporate various successful reports regarding the development of more resistant wheat cultivars using new breeding strategies.

Keywords

Wheat · Diseases · Productivity · Fusarium · Spot blotch · *Lr9* gene

Abbreviations

AgRenSeq	Associated genetics R gene enrichment sequencing
Cas9	CRISPR-associated protein 9
CRISPR	Clustered regularly interspaced palindromic repeats
dsRNA	Double-stranded RNA
EMS	Ethyl methanesulfonate
FHB	Fusarium head blight
GE	Genome editing
GWAS	Genome-wide association sequences
LRR	Leucine-rich repeat proteins
MAPK	Mitogen-activated protein kinase
miRNA	MicroRNA
MNs	Meganucleases
MutChromSeq	Mutant chromosome sequencing
NBS	Nucleotide-binding site
NLR	Nucleotide-binding and leucine-rich repeat
PGT	<i>Puccinia graminis</i> f. sp. <i>tritici</i>
PST	<i>Puccinia striiformis</i> f. sp. <i>tritici</i>
PT	<i>Puccinia triticina</i>
QTL	Quantitative trait locus
R gene	Resistance gene
siRNA	Small interfering RNAs
SSNs	Sequence-specific nucleases
TACCA	Targeted chromosome-based cloning via long-range assembly
TAL	Transcription-activator-like
TALENs	Transcription activator-like effector nucleases
ZFNs	Zinc-finger nucleases

8.1 Introduction

With the doubling of the human population, the past decade has witnessed significant growth in cereal production, resulting in a remarkable reduction in global food hunger (FAO STAT 2018; Liu et al. 2018; Grote et al. 2021; Jiang et al. 2020; Liu et al. 2021; Li et al. 2020a, b, c; Singh et al. 2021a). Despite no exaggeration, the

level of global poverty is currently lower than any recorded in modern times. Nonetheless, the goal of “zero hunger” is not achieved and requires significantly increased efforts (Mujeeb-Kazi et al. 2019; Shakeel et al. 2021; Singh et al. 2021b). However, more than one in seven individuals did not fulfill the prerequisite of a complete diet, and a higher number experienced different forms of malnutrition. However, demand for food surges exponentially, causing the continuous rise in population. As a result, qualitative and quantitative food production must be done in a remarkable two-fold manner that is both socially and environmentally sustainable (Hickey et al. 2019). The average grain production has increased from 1.35 tons/hectare (1961) to 3.35 tons/hectare (2007) and is expected to reach 4.8 tons/hectare by 2040. Recently, the agriculture area has been shrinking, with overarching issues like a serious threat of climate change, posing issues of how adaptation and mitigation mechanisms may impact food supply (Singh et al. 2022; Choudhary et al. 2022; FAO STAT 2018; Liu et al. 2018; Hickey et al. 2019; Kumar et al. 2021a; Paul et al. 2021).

Certain wheat diseases prominently contribute to losses by pathogens including viruses, bacteria, and fungi responsible for blight, scab, rust, smut, blotches, and blast diseases (Kumar et al. 2022a). Better management of fungal diseases is the need of the hour, which results in a 15–20% yield loss of wheat per year. Rust fungi are obligate biotrophic organisms that belong to the family Basidiomycete, which means they are dependent on the living cells of plants for growth and reproduction. Stem, stripe, and leaf rust are mainly three types of wheat rust diseases. Although the causative agent of black rust disease (wheat stem rust), *Puccinia graminis* sp. *tritici*, is widely distributed throughout the world, it is uncommon in comparison to other rust diseases. Although rust diseases are controlled in yield in most parts of the world, there are still global losses estimated at about 6.2 million metric tons per year (Pardey et al. 2013; Figueroa et al. 2018; Kumar et al. 2021b). There is a reduction in grain size along with the lodging of plants due to rust diseases (Miedaner and Juroszek 2021). Thus, the emergence of recent fascinating approaches, including clustered regularly interspaced palindromic repeats (CRISPR), CRISPR-associated protein 9 (Cas9), genome-wide association sequences (GWAS), transcription activator-like effector nucleases (TALENs), transcription-activator-like (TAL), Meganucleases (MNs), and zinc-finger nucleases (ZFNs), etc., helps to overcome the biotic and abiotic challenges in wheat (Mehta et al. 2020; Dilawari et al. 2021; Chattopadhyay et al. 2022; Schenke and Cai 2020; Razzaq et al. 2021). The understanding of plant–pathogen interaction and the advancement of new approaches or molecular techniques including speed breeding, genome editing, CRISPR/Cas9 (Cluster Regularly interspaced Palindromic Sequences/CRISPR-associated protein 9), RNA interference (RNAi) Silencing, etc. are being harnessed for gene editing or alteration of traits (Chattopadhyay et al. 2022; Schenke and Cai 2020; Paul et al. 2021; Zhang et al. 2017a, b; Kis et al. 2019; Verma et al. 2021). Presently, conventional breeding approaches help to manage disease-free, highly productive, nutritious, and safe crops. It also includes interspecific hybridization, pure line selection, backcross, and pedigree methods (Kaiser et al. 2020).

In the present document, we highlight the significant role of emerging breeding techniques in the introgression of the novel resistance gene. We see advanced breeding strategies as an affordable and efficient way forward to overcome the consequences of climate change through the development of new resilient varieties. There are many strategies like integrated or multidisciplinary includes in agronomy pathology, seed production, pathology, postharvest methods, and extension (Raffan et al. 2021; Li et al. 2018, 2020a, b).

8.2 Disease's Epidemics and Their Impact on Productivity

Wheat is the most essential staple crop that impregnates the human diet with protein and calories (Rasool et al. 2021; Kumar et al. 2021b). The genetic diversity in the wheat gene pool has been statistically increased, offering the most promising possibilities to combat pathogen emergence meant to reduce the threat of diseases to global wheat production (Kumar et al. 2022b). The preliminary step has been integrated with traditional as well as advanced breeding tools to repair signaling loops that effectively combat a variety of pathogens.

Rust pathogens have a long history dating back to the domestication of crops. They have a good image in the hindrance of global wheat production. The global losses due to wheat rust pathogens are estimated in the range of 4.3–5 billion US dollars annually (Pardey et al. 2013; Tehseen et al. 2021). These are the obligatory biotrophic pathogens that have completed their life cycle for nutritional resources (Różewicz et al. 2021). Globally, there are three well-known rust diseases of wheat caused by genus *Puccinia* (belongs to family Basidiomycetes), stem rust caused by *Puccinia graminis* sp. *tritici* (PGT), stripe rust caused by *Puccinia striiformis* sp. *tritici* (PST), and leaf rust caused by *Puccinia triticina* (PT) (Różewicz et al. 2021). Wheat stem or black rust usually prevails in moist and warm conditions and materializes as red brick urediniospores on the stem, sheath, leaf, awns, and glumes of susceptible cultivars (Kolmer 2005; Gupta et al. 2017). However, Leonard and Szabo (2005) reported that the yield losses are due to the lodging of plants and grain size reduction in the infected cultivars. Stem rust epidemics have historically affected all major wheat-producing regions, and disease control was one of the major milestones in the development of stem rust-resistant high-yielding wheat cultivars during the green revolution (Figuerola et al. 2016).

According to forecasting models, the average loss is 6.2 million metric tons annually during serious epidemics in the absence of durable, resistant varieties (Pardey et al. 2013). The emergence of a new PGT population poses a threat on a global scale, such as the Ug99 race in Uganda (1998), which expanded within Africa, towards the Middle East, and was reported as Ug99 variants, showing the immense threat to the wheat crop (Pretorius et al. 2000; Singh et al. 2015). It has been estimated that about 90% of wheat varieties are prone to the Ug99 attack (Singh et al. 2011). The 'Digalu' race became an epidemic in 2014 in Ethiopia and was also observed in Germany (Olivera Firpo et al. 2015, 2017). Similarly, a "broadly" disease race was reported as the Sicily wheat outbreak in 2016 (Bhattacharya

2017). Subsequently, it was reported in Bangladesh in Asia and Zambia in Africa. Researchers have warned that there may be a possible expansion of disease to other continents as well (Tembo et al. 2020).

Wheat stripe or yellow rust is prevailing in the cool and wet conditions of temperate regions (Chen et al. 2014; Jamil et al. 2020). PGT is efficiently declining the wheat yield by affecting nearly 100% of the susceptible cultivars. It has been targeting 88% of the wheat varieties globally and losing 1 billion US dollars per year (Wellings 2011; Beddow et al. 2015). Moreover, Murray and Brennan (2009) reported 127 million AU dollar losses from stripe rust in Australia. In the last 50 years, PST has affected nearly 60 countries (Beddow et al. 2015). Since 2000, PST virulence races have been spread to the non-affected regions of the world by adapting to the higher temperatures of climates (Ali et al. 2014). The clonal distribution of PST in Australia, North America, and Europe showed a significant level of genetic diversity in the populations of pathogens (Chen et al. 2014). The variants were also found in Central Asia and Western China, as well as the Himalayas and their surrounding areas (Ali et al. 2014). Other race groups that originated in the Himalayan regions (Hovmøller et al. 2015) also appeared and spread in 2011, 2012/2013, and 2015 throughout Europe. Recent studies regarding *P. striiformis* concluded that most of the recombinant population structure and the highest levels of genetic diversity come from the Himalayan and its nearby regions, which shows that this may be the area of its center of origin and diversity (Sheikh et al. 2021).

Leaf rust is a well-known, common, and more widely distributed condition with a prevalence in moist and mild temperature conditions (Bolton et al. 2008). The yield losses are associated with the reduction in grains per head and the kernel weight. About 350 million US dollars in losses have been estimated from the period of 2000 to 2004 in America (Huerta-Espino et al. 2011). There were total losses estimated to be 12 million AU in Australia (Murray and Brennan 2009). The upper hand of the leaf rust is due to high diversity in the pathogen population and emerged strains showing wider adaptability too in a wide climatic range (Huerta-Espino et al. 2011; McCallum et al. 2016).

Blotch diseases including *Septoria nodorum*, blotch tan spot, and *Septoria tritici* blotch are caused by the *Pyrenophora tritici-repentis*, *Parastagonospora nodorum*, and *Zymoseptoria tritici*, respectively. *Septoria tritici* blotch is the leaf disease of wheat flourishing in the temperate regions. It is causing a primary threat to the wheat yield at the cost of 280–1200 EU € annually in Europe (Fones and Gurr 2015). This disease is causing 20 million AU\$ losses in Australia, annually (Murray and Brennan 2009). Tan spot disease is found in most wheat-growing regions such as North America, Australia, and Europe. The yield losses are due to reducing the grains per head and kernel weight (Shabeer and Bockus 1988). The yield losses are 200 million AU\$ in Australia due to this disease annually (Murray and Brennan 2009).

Interestingly, *Septoria nodorum* blotch was fully replacing the *Septoria tritici* blotch in the UK in the 1980s. The disease has been reported to be prevalent in France and Scandinavian countries. The disease has a high prevalence in Australia,

causing 100 million AU\$ annually (Murray and Brennan 2009). There are three resistant alleles of tan spot disease investigated from germplasm present on chromosomes *3AS*, *3AL*, *3BS*, and *6AL* along with genes *tsn1* and *tsc2* (Simón et al. 2021; Kokhmetova et al. 2021).

Fusarium head blight, or scab disease, or ear blight, or wheat scab, is caused by *Fusarium graminearum* (belongs to Ascomycetes). The pathogen is causing premature senescence of wheat heads and, in combination with other *Fusarium* species, is inducing severe epidemics (Brown and Proctor 2013). The disease onset rate is every fourth to fifth year in the USA, EU, UK, Brazil, Africa, and China. Hence, the disease is of prime concern and most hazardous. The yield losses in the USA were 3 billion US dollars between 1990 and 2008 due to fusarium head blight (Schumann and D'Arcy 2009). During the anthesis stage, the disease is infecting the wheat crop under the prevailing rain conditions. Grain quality, grain yield, and aggregation of type B toxin deoxynivalenol (sesquiterpenoid trichothecene mycotoxin) reduce the overall harvest of crop production and market value. The toxin poses a health risk to humans, animals, and natural ecosystems. The legal limit has been set for the permitted level of mycotoxins. For instance, permitted levels are 1250–2000 ppb in the EU and 200–1000 ppb for the finished product in the USA (<http://scabusa.org>). In North America, the Fg strain has been reported to produce two novel types, NX-2 and NX-3 (trichothecene mycotoxins) (Varga et al. 2015).

Bipolaris sorokiniana causes spot blotch to have foliar and root damage. The disease has a major impact and is reported in the eastern Gigantic plains, specifically in India, Nepal, and Bangladesh (Duveiller and Sharma 2009). Significant losses have been observed in South America under warm and humid climatic conditions (Duveiller and Sharma 2012). *Magnaporthe oryzae* is another Triticum pathotype causing wheat blast and recognized by head disease. The symptoms have appeared as elliptical lesions to entire bleaching as well as empty spikes (Igarashi et al. 1986). Warm (25 °C) and humid (10-h wetting period) conditions are the prerequisites for the development of wheat blasts (Cardoso et al. 2008). It was first observed in the Paraná state of Brazil in 1985, followed by dissemination to Paraguay, Bolivia, and Argentina (Igarashi et al. 1986). Previously, these pathogens were restricted to regions of South America. However, they were discovered in 2016 in Bangladesh and followed by India (Islam et al. 2016; Bhattacharya 2017).

8.3 Genepools Contribution in Disease Management

Race-specific resistance or qualitative or seedling resistance is conferring the 150 genes for rust resistance reported in local wheat varieties or their wild cousins. Almost 50 genes are nominated for stem rust resistance genes against the reactions of PGT. *Sr31* is widely known for race-specific resistance against the PGT (Singh et al. 2004). However, *Sr31* also led to the emergence of Ug99; besides this, resistance due to *Sr38*, *Sr36*, *Sr24*, *Sr21*, and *SrTmp* has also been conquered by Dgalu and Ug99 races (Jin et al. 2008; Pretorius et al. 2010; Olivera Firpo et al. 2015).

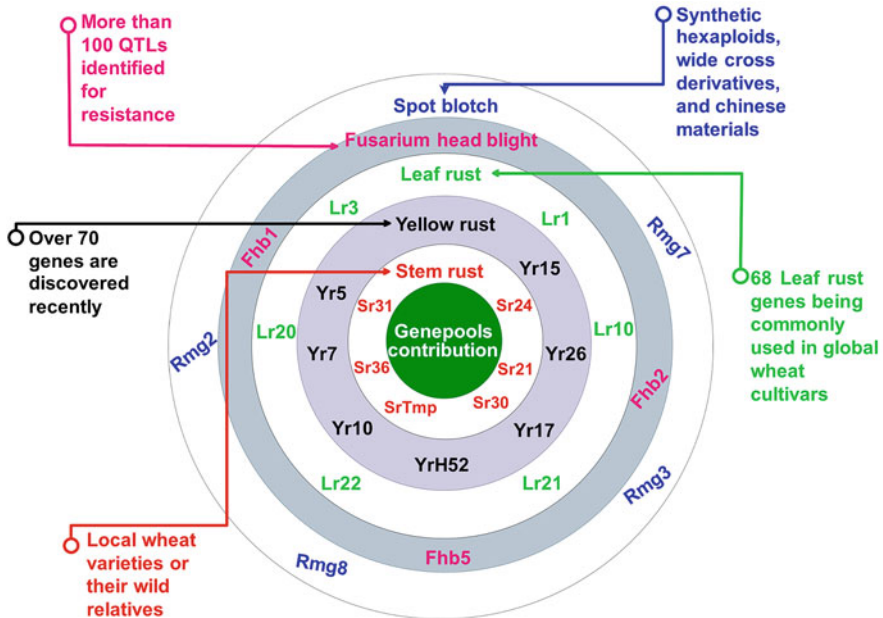


Fig. 8.1 Illustration showing overview on major fungal diseases in wheat and associated genes/QTLs for imparting resistance

Sr50, *Sr45*, *Sr35*, *Sr33*, *Sr25*, *Sr23*, and *Sr2* are the most important genes against the recently emerged races (Singh et al. 2015). Over 70 genes are nominated against the yellow rust disease rust diseases (Jamil et al. 2020). Dakouri et al. (2013) studied about 68 genes including the most common *Lr20*, *Lr10*, *Lr3*, and *Lr1* widely used against the leaf rust in global wheat cultivars. Similarly, *Lr22*, *Lr21*, *Lr10*, *Lr1*, *Sr50*, *Sr45*, *Sr35*, *Sr33*, *Sr22*, and *Yr10* are the 10 race-specific genes of wheat encoding the nucleotide-binding site (NBS) leucine-rich repeat (LRR) proteins (Mago et al. 2015; Thind et al. 2017) (Fig. 8.1). Therefore, the resistance is conferred by the indirect or direct recognition of avirulence (Avr) factors.

More than 24 major genes have been addressed against the resistance of *Septoria tritici* blotch (Brown et al. 2015). One hundred and sixty seven genomic regions are anchoring the quantitative trait loci (QTL) providing genetic resistance against the *Zymoseptoria tritici*. The phenotyping study has been displaying the role of QTLs against the sporulation, latency, and necrosis of different disease progression stages.

Against the *Fusarium* head blight, a few moderately resistant sources such as Fontana from Brazil and Sumai-3 from China have been recognized. Several major and minor QTLs have conferred the resistance to *Fusarium* head blight linked with yield penalty or fitness cost (Gilbert and Haber 2013). More precisely, two of the commercially important types of resistances, viz., Type I and type II, are considered such as resistance to initial infection and resistance to spreading of *Fusarium* head blight inside the host (Cuthbert et al. 2006).

The resistance to spot blotch and *Helminthosporium* leaf blight is quantitatively conquered in wheat (Singh et al. 2016). Wheat germplasm from China, Zambia, and Brazil has resistance to both diseases including synthetic hexaploids, wide cross derivatives, and Chinese materials. Association mapping and QTL are displaying the involvement of several genes for resistance (Singh et al. 2016). Several genes such as *Rmg8*, *Rmg7*, *Rmg3*, and *Rmg2* might show promising results, but required field confirmations for effective controls (Ahn et al. 2015).

Adult plant resistance or non-race-specific has conferred the resistance against the rusts in wheat (Periyannan et al. 2017). Several genes such as *Lr68*, *Lr67*, *Lr46*, *Lr34*, *Sr2*, and *Yr36* are potential members in resistance (Ellis et al. 2014). Among them, *Yr36*, *Lr67*, and *Lr34* encode for cytoplasmic protein kinase, hexose transporter, and ATP-binding cassette transporter, respectively, which are directly involved in facilitating resistance (Fu et al. 2009; Dodds and Lagudah 2016).

8.4 New Breeding Tools to Attain Higher Disease Resistance

8.4.1 Pathogen-Resistant Germplasm

The adoption of monoculture and high-yield crops has been reducing the diversity positioning and crop genetic diversity in modern crops at a high risk of disease epidemics. The wild, landraces, or progenitor species are excellent sources of *R* genes for effective pathogen control against the dominant pathogen races. Several *R* genes have been introgressed successfully from the wild progenitor or landraces/local varieties. For instance, *Fhb7* (Fusarium head blight) has been introgressed from the wild relatives of wheat to confer resistance against the *Fhb* (Wang et al. 2020). Hence, the wild relatives and landraces are favorable mines for mining the new *R* genes for the improvement of modern wheat cultivars (Dwivedi et al. 2016). The identification of *R* genes requires efficient field trials for resistance evaluation for utilization in breeding programs. Natural nursery-based selection should be set up for pandemic pathogens in the diverse screening of highly resistant germplasm. Under high selection pressure in natural nurseries, plants are under a mixed and continuous type of infection in all growth stages.

Therefore, exclusive plasma member-anchored pattern recognition receptors (for pathogen triggered immunity) and nucleotide-binding leucine-rich repeat proteins (for effectors triggered immunity) will be identified to confer the broad-spectrum resistance. A study was conducted in the Huang Huai-Hai region of china where 146 wheat entries were inoculated with races of PST, FHB, and BGT. *Yr15*, *Yr18*, *Pm21*, and *Fhb1* are recommended for breeding programs in combination with other effective genes for broad-spectrum and durable resistance, whereas *Yr10*, *Yr9*, *Yr26*, and *Yr17* were ineffective against the PST races (Ma et al. 2021).

8.4.2 Identifying New R Genes Using High-Throughput Genomic Approaches

Recent advances in genomic sequencing and bioinformatics have accelerated approaches to improving R gene cloning. Sequencing-based mapping is regarded as a potential tool in the mapping and cloning of R genes in plants (Wulff and Moscou 2014; Mascher et al. 2014). With the aid of a GWAS, the genetic architecture of many economically important crops, including wheat, has been studied with the aid of a GWAS (Huang et al. 2010; Li et al. 2019; Lin et al. 2020). Kumar et al. (2020) have been conducting the GWAS on spring wheat panels for leaf rust, stem rust, and stripe rust. A total of 16, 18, and 27 QTLs have been discovered for resistance against stripe rust, leaf rust, and stem rust, respectively. In seedling and adult plant responses, a number of these regions were annotated with ABC transporter protein, E3ubiquitin-protein ligase, and NB-LRR. According to Jupe et al. (2013), resistance gene enrichment gene sequencing is another powerful tool to identify newly NLR-like genes from landraces or wild species.

Steuernagel et al. (2016) demonstrated that MutRenSeq (combined approaches of EMS and RenSeq mutagenesis) is used to identify NLR genes and used in isolating *Sr22* and *Sr45* (stem rust-resistance genes) in wheat. Thind et al. (2017) also investigated how the TACCA method was used to isolate *Lr22a* (R gene) from wheat polyploidy genomes. MutChromSeq (a combined technique of high-throughput sequencing, chromosome flow sorting, and EMS mutagenesis) was used to identify the *Pm2* gene (Sanchez-Martin et al. 2016). Similarly, AgRenSeq (combining association genetics with RenSeq) was used to exploit the pan-genome variations for the cloning of R genes from the diverse panels of germplasm in wheat, such as *SrTA1662*, *Sr46*, *Sr45*, and *Sr33* (Arora et al. 2019). Allele mining is a simple and effective approach for the identification of elite alleles of R genes from wild germplasm and landraces (Ashkani et al. 2015). In a study in which wild germplasms of wheat were studied for resistance against the powdery mildew, *Pm3* alleles were observed in wild *T. dicoccoides* accessions (Kaur 2008).

8.4.3 Expanding NLR Recognition Specificity Through BSR Genes Engineering

The period of resistance the R resistance gene induces is shortened by the adapted virulence of the pathogen (McDonald and Linde 2002). This bottleneck can be overcome with the aid of genetic engineering of NLR variants where engineered NLR can respond to numerous pathogen effectors. According to Segretin et al. (2014), different conserved domains and integrated domains of NLRs can be altered to attain the new capability to progress in disease resistance against different pathogens and strains. A few nucleotide differences among the coding regions of genes, prime genome editing technology, and CRISPR-mediated homology direct repair can be practiced to produce new R alleles with a broad resistance spectrum (Lin et al. 2020). For example, using CRISPR/Cas9, *EDR1*, which acts as a negative

regulator in defensive responses against powdery mildew, was knocked out to generate powdery mildew-resistant wheat plants (Zhang et al. 2017a, b). Similarly, random elimination in the start codon containing a sequence of the TaHRC gene in the Bobwhite (wheat variety cultivar) confirmed resistance against the Fusarium head blight (Su et al. 2019). Modifications in the decoys or integrated domains of NLRs can be helpful in the expansion of effector recognition specificity (Maqbool et al. 2015; Kim et al. 2016). Therefore, various R variants can be produced for the selection of required wide-range resistance in the crop by using CRISPR/Cas9 technology (Fig. 8.2).

8.4.4 GWAS: A Step Ahead Toward Wheat Breeding

GWAS is currently known as the most common approach for decoding the genotype-phenotype association in crop plants (Liu and Yan 2019). GWAS is the more statistical strategy for mapping QTL to coordinate the desired phenotype with the genotypes on the significance of historic linkage disequilibrium. GWAS can increase the likelihood of identifying loci linked to crop domestication, crop improvement, and grain yield (Li et al. 2019; Lujan Basile et al. 2019; Hao et al. 2020). Re-sequencing and GWAS studies on 145 elite wheat cultivars in China help in the discovery of genomic regions integrated with crop improvement as well as domestication, providing genetic resources for wheat improvement programs (Hao et al. 2020). The study was conducted on 175 winter wheat genotypes from NordGen and GWAS analysis was done. The phenotypic data indicated a significant variation between genotypes in disease resistance response to *Septoria tritici* blotch as well as powdery mildew. The genomic-assisted germplasm selection with superior alleles for disease resistance in wheat could be then integrated into active breeding programs (Alemu et al. 2021).

8.4.5 Speed Breeding

Generally, breeders take 8–10 years to develop novel wheat cultivars. Therefore, novel elite crop development of wheat is a difficult task in terms of time consumption and laboriousness. Speed breeding is one of the possible solutions to overcome this prolonged time barrier. It involves specific growing conditions, including optimal temperature and light intensity, photoperiod requirement, premature seed harvesting, and shortening of generation time by up to 8–10 weeks. Speed breeding was successfully deployed to obtain six generations in one year for bread wheat. The attempt was made by Alahmad et al. (2018) to *Triticum durum* Desf. with the key traits' involvement, such as phenotyping for resistance to leaf rust, tolerance to crown rot, seminal root angle, seminal root number, and plant height.

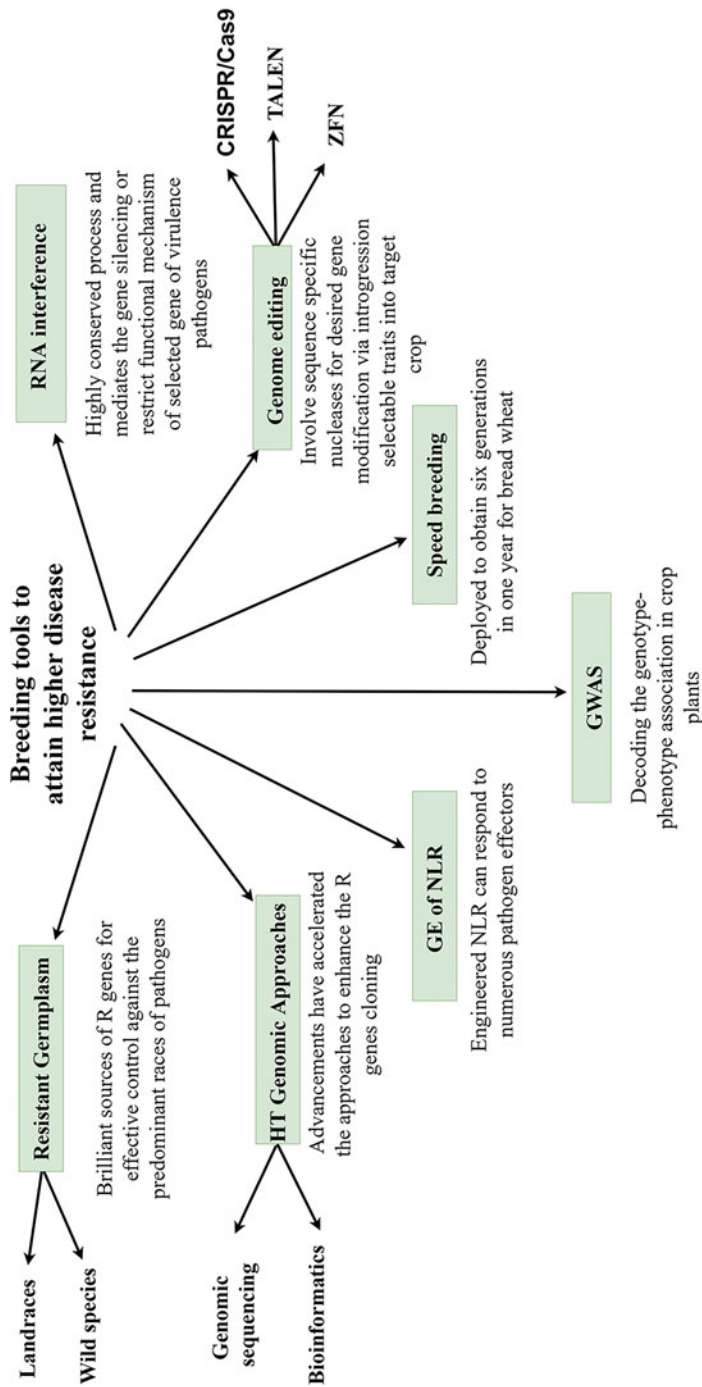


Fig. 8.2 Landmarks for significant achievement in the deployment of trait improvement approaches

8.4.6 Genome Editing (GE)

GE involves sequence-specific nucleases (SSNs) for desired gene modification via introgression of selectable traits into a target crop in a transgenic-free selected genome. SSNs induce specific alteration at the chromosomal level, leading to insertion, substitution, or deletion of undesired sequence from a particular position (Mehta et al. 2020; Dilawari et al. 2021; Chattopadhyay et al. 2022). Several SSNs types are used, such as the CRISPR/Cas, TALENs, and ZFNs system are particularly used for genomic modification. Such target genomic alteration has become a distinct genetic tool for the introduction of disease resistance genes against different pathogenic diseases (Jamil et al. 2020; Shakeel et al. 2020). Indeed, crop susceptible genes are eliminated, edited, or restructured in such a manner to change them into tolerant genes.

For instance, in *T. aestivum*, CRISPR/Cas9 has exhibited complete resistance against powdery mildew by developing mutants like *TaEDR1* by continuous editing of *TaEDR1* along with other homolog sequences. However, CRISPR/Cas9 was significant for developing transgenic cultivars against fungal pathogens via deletion (Jamil et al. 2020). In another study, successful editing of various genes has been done using CRISPR/Cas9 such as *TansLTP9*, *TaNFXL1*, and *TaABCC6*, with protoplast fusion in wheat for stimulation of resistant mechanism toward *Fusarium* head blight (FHB). Additionally, there are various reports on rust-resistant using CRISPR/Cas9. Several reports have been published on stripe rust resistance gene introgression into cultivated wheat (For detailed extension see Tables 8.1 and 8.2).

8.4.7 RNA Interface (RNAi) Silencing

RNAi silencing is a highly conserved process that mediates gene silencing or restricts the functional mechanism of a selected gene of virulence pathogens. The gene silencing RNAi involves double-stranded RNA (dsRNA), a homologous gene of interest. The silencing process offers dsRNA cleavage into small RNA (21–26 nucleotide long), which are microRNA (miRNA) and small interfering RNAs (siRNA). These miRNA or sRNA possibly stimulate the various cascade, viz., regulating RNA stability, processing of signals, and response to a different pathogen in crop plants.

In *stripe mosaic virus*, the *Pst* from PR genes has been silenced that acts as a vector for dsRNA homologous expression to *Pst* target gene (Qi et al. 2019; Jamil et al. 2020). The transcription factor-like mitogen-activated protein kinase (MAPK) stimulating gene (*FUZ7*), which is the crucial pathogenic factor of *Pst* mediating fungal hyphal morphology and infection and triggering pathogenesis in the host plant, was eliminated using RNAi. However, in the transgenic wheat line, RNAi prepares *Afuz7* targeting of *Pst* which was significantly expressed and strongly confirmed the durable resistance against pathogenic strains. On contrary, another *CPK1* was eliminated in transgenic wheat lines with the help of RNAi. Moreover, *Pst* knockdown uses different transgenic wheat lines that are *PstGSRE1* and *PsHXT1* genes (hexose transporter) (Qi et al. 2018; Satheesh et al. 2019; Ahmad et al. 2020; Chang et al. 2020).

Table 8.1 Overview on the discovery of major disease-resistant genes and techniques used for their introgression

Gene	Techniques used	Resistant against	Reference
<i>mtlD</i>	Plasmid-mediated gene transfer	Mosaic virus (<i>Aceria tosichella</i>)	Abebe et al. (2003)
<i>pac1</i>	<i>Agrobacterium</i> -mediated gene transfer	Barley yellow dwarf virus (Cereal aphids)	Yan et al. (2006)
<i>β-1,3-glucanase</i>	<i>Agrobacterium</i> -mediated gene transfer	Powdery mildew (<i>Blumeria graminis</i>)	Zhao et al. (2006)
<i>TiERF1</i>	Biolistics method	Sharp eyespot (<i>Rhizoctonia cerealis</i>)	Liang et al. (2008)
<i>TaPIMP1</i>	<i>Agrobacterium</i> -mediated gene transfer	Root rot (<i>Bipolaris sorokiniana</i>)	Zhang et al. (2012)
<i>TiMYB2R-1</i>	Biolistics method	Take-all disease (<i>Gaeumannomyces graminis</i>)	Liu et al. (2013)
<i>TaCLP1</i>	Biolistics method	Stripe rust (<i>Puccinia striiformis</i>)	Zhang et al. (2013)
<i>SN1</i>	Biolistics method	Take all disease (<i>Gaeumannomyces graminis</i>)	Rong et al. (2013)
<i>Bt</i>	<i>Agrobacterium</i> -mediated gene transfer	Armyworm (<i>Spodoptera frugiperda</i>)	Huang et al. (2014)
<i>TaERF3</i>	Virus-induced gene silencing	Stripe mosaic virus (Hordeivirus)	Rong et al. (2014)
<i>Nib8</i>	Biolistics method	Yellow mosaic virus (<i>Polymyxa graminis</i>)	He et al. (2015)
<i>Ta-Mlo RC24</i>	<i>Agrobacterium</i> -mediated method	Powdery mildew (<i>Blumeria graminis</i>)	Acevedo-Garcia et al. (2017)
<i>viviparous 1</i>	<i>Agrobacterium</i> -mediated gene transfer	Rust (<i>Puccinia triticina</i>)	Kocheshkova et al. (2017)
<i>KN2</i>	Biolistics method	Powdery mildew (<i>Blumeria graminis</i>)	Zhang et al. (2017a, b)
<i>Mrl40</i>	<i>Agrobacterium</i> -mediated method	Powdery mildew (<i>Blumeria graminis</i>)	Tang et al. (2018)
<i>BADH</i>	Particle bombardment method	Smut (<i>Ustilago tritici</i>)	Khan et al. (2019)
<i>GhDREB</i>	Plasmid-mediated gene transfer	Rust (<i>Puccinia triticina</i>)	Andersen et al. (2020)
<i>TaNAC21</i>	<i>Agrobacterium</i> -mediated method	Stripe rust (<i>Puccinia striiformis</i>)	Feng et al. (2014)
<i>TaNAC069</i>	<i>Agrobacterium</i> -mediated gene method	Leaf rust fungus (<i>Puccinia triticina</i>)	Zhang et al. (2021)

Table 8.2 Introgression of major disease-resistant genes from wild relative species into a wheat plant

Wild progenitor species	Target Gene	Introgression technique	Resistance	Reference
<i>Aegilops ventricosa</i>	<i>Cre2</i>	Recombination	Cyst nematode	Jahier et al. (2001)
<i>Taxodium distichum</i>	<i>Sr2</i>	Spontaneous	Leaf rust	Prins et al. (2001)
<i>Aegilops umbellulata</i>	<i>Lr9</i>	Spontaneous	Leaf rust	Gupta et al. (2005)
<i>Aegilops triuncialis</i>	<i>Lr58</i>	Recombination	Leaf rust	Kuraparthi et al. (2007)
<i>Aegilops umbellulata</i>	<i>Lr9</i>	Irradiation	Leaf rust	Chhuneja et al. (2007)
<i>Aegilops ventricosa</i>	<i>Rkn2</i>	Recombination	Root-knot nematode	Williamson et al. (2013)
<i>Aegilops speltoides</i>	<i>Sr32</i>	Recombination	Stem rust	Mago et al. (2013)
<i>Africallagma elongatum</i>	<i>Lr19</i>	Irradiation	Stem rust	Worku et al. (2016)
<i>Triticum timopheevii</i>	<i>Sr23</i>	Homoeologous recombination	Powdery mildew	Liu et al. (2017)
<i>Africallagma elongatum</i>	<i>Lr24</i>	Spontaneous	Stem rust	Kumar et al. (2017)
<i>Africallagma elongatum</i>	<i>Sr26</i>	Irradiation	Stem rust	Rai et al. (2017)
<i>Secale cereale</i>	<i>Pm8</i>	Spontaneous	Stem rust	Crespo-Herrera et al. (2017)
<i>Aegilops ventricosa</i>	<i>Yr17</i>	Recombination	Stripe rust	Coriton et al. (2019)
<i>Aegilops ventricosa</i>	<i>Pch1</i>	Recombination	Eyespot	Pasquariello et al. (2020)
<i>Aegilops longissima</i>	<i>Pm66</i>	Spontaneous	Powdery mildew	Li et al. (2020a, b, c, d)
<i>Aegilops tauschii</i>	<i>Dn3</i>	Recombination	Russian wheat aphid	Kisten et al. (2020)

8.4.8 CRISPR/Cas9 and Disease Resistance: A Way Forward to More Reliability

CRISPR/Cas9 genome editing is an established mechanism in bacteria that helps protect them from harmful plasmids and bacteriophages. The spacer (a DNA fragment of foreign pathogen and host) acts as a genetic memory for future infection. During similar pathogenic attacks in the future, the CRISPR array gets transcribed and processed, leading to the synthesis of CRISPR RNA fragments (Single Guide RNA) via the activity of endonuclease (CAS9). The advancement of plant genome editing, including CRISPR/Cas9 systems, suggests that this application is more

feasible and reliable. It significantly helps to increase multiple beneficial traits as well as disease resistance in wheat (Langner et al. 2018; Zaynab et al. 2020). However, genes encoding proteins that associate between plants and pathogens have been targeted through CRISPR/Cas9 to explain the underlying genetic pathways of plant–pathogen recognition and to produce investigation systems for disease resistance (Li et al. 2018). Disease caused by viruses, bacteria, and fungi could dramatically decrease the quality and quantity of wheat.

CRISPR/Cas9 has been significantly eliminating disease susceptible genes to produce new resistance wheat cultivars. More likely, loss of function in *MLO* (Mildew resistance locus) leads to gains of resistance against powdery mildew. Such reports confirm a broad-spectrum range of *MLO* as a favorable site for CRISPR/Cas9 to reduce susceptibility against powdery mildew (Gil-Humanes and Voytas 2014). According to Wang et al. (2014), CRISPR/Cas9-guided wheat mutant, a *TaMLO-A1* (mildew resistance locus) of the homoalleles exhibited enhanced resistance to infection against *Blumeria graminis*. CRISPR/Cas9 application system to useful fungal pathogens including *Trichoderma* sp. to increase plant defense system as a biocontrol agent against oomycetes and fungal is also a promising agent. Certain *MLO* homo-alleles including *TaMLO-B1*, *TaMLO-A1*, and *TaMLO-D1* were edited using CRISPR/Cas9 and showed that *TaMLO-A1*-mutagenized wheat plants have confirmed resistance against *Blumeria graminis* (Tyagi et al. 2021). Such techniques like CRISPR/Cas9-dependent plant–pathogen genome editing will draw much attention as well-adapted to increased pathogenic resistance and transgenic-free plants and will be required for global food demand (Paul et al. 2021).

In another study, the fusarium head blight, induced by *Fusarium* spp., was managed in CRISPR/CAS9-silenced mutants. Studies demonstrated that RNA interference on trehalose 6-mutant ($\Delta tri 6$) of *Fusarium* spp. confirmed lowered disease indices that lie from 40 to 80% in durum wheat (Muñoz et al. 2019). However, two mutants ($\Delta tri 1$ and $\Delta tri 6$) of *Fusarium* spp. were incapable of pathogenic response to the inflorescence and also elicited plant defense response. Moreover, $\Delta map 1$ mutants of *Fusarium* spp. demonstrated two times reduction in the production of mycotoxins, but was unable to colonize pathogens in other plant parts except for grains. Such competition for nutrients and space between non-virulent and virulent strains could decrease the disease severity, and the field liberation of non-virulent CRISPR/Cas9-mutant strains of *Fusarium* spp. might help to overcome the emerging issues (Zaidi et al. 2020; Zaynab et al. 2020; Zhang et al. 2017a, b; Wang et al. 2020; Verma et al. 2021; Liu et al. 2021).

According to Wang et al. (2014), using CRISPR/Cas9 to mutate wheat cultivars exhibits improved resistance toward powdery mildew resistance, caused by *Blumeria graminis*. Additionally, CRISPR/Cas9 mediated site-specific mutagenesis in springer and wheat varieties (Hahn et al. 2021). Similarly, mutagenization of 3 genes such as *AURI* (a visual marker), *Tri5* (toxin production and infection), and *MGV1* (required for infection and reproduction) was done by CRISPR/Cas9. More likely, silencing of *Tri5* and *MGV1* could suppress the fungal ability to suppress infection in crops, whereas *AURI* silencing acts as an effective visual marker during

mutagenesis (Sack 2020). Recently, in wheat a serious fungal pathogen like powdery mildews caused by *Podosphaera xanthii* was enhanced via editing *Mildew Locus O (MLO)* gene through CRISPR/Cas9 technique. Knockdown of susceptibility loci becomes highly complicated in wheat like targeting *MLO* homologous genes and *Enhanced disease resistance 1 (EDR1)* using CRISPR/Cas9 editing (Wang et al. 2020; Verma et al. 2021; Raffan et al. 2021; Li et al. 2018, 2020a, b).

However, various target locus in the *wheat dwarf virus (WDA)* genome was screened using CRISPR/Cas 9 direct sequences enclosing the PAMs motif. Several target positions were designated that demonstrated no specific effect and were efficient in attacking different viral DNA sequences. The single-guided RNA WDA1 (sgRNA WDA1) displays the complementary overlapping in certain coding sites; sgWDA2 targets the Rep/Rep (Shahriar et al. 2021). Moreover, crop engineering using CRISPR/Cas9 like techniques has helped to develop disease-resistant varieties that are more resilient to climate change (Zaidi et al. 2020). Application of CRISPR/Cas9 ultimately helps to improve disease resistance in wheat and other crops and is well-documented (Schenke and Cai 2020; Paul et al. 2021; Zhang et al. 2017a, b; Kis et al. 2019; Verma et al. 2021; Gil-Humanes and Voytas 2014; Tyagi et al. 2021; Duy et al. 2021).

8.5 Concluding Remarks

The conventional breeding approaches for disease-free wheat in modern agriculture are transgenic, mutation breeding, and cross-breeding. These are laborious, time-consuming, and unfocused crop improvement programs that are unable to meet food demand. To cope with these challenges and to increase crop selection ability, transgenic and marker-assisted breeding has been developed, harnessing target traits via introgression into elite wheat varieties. Such advancements in plant breeding are an excellent tool that maintains rapid mutation and can recognize the significant genetic approaches for disease resistance. No doubt, crop breeding strategies are propelled by next-generation breeding methods. New breeding resistant varieties should remain the key focus. Some alternate approaches, viz., shifting plantation date, integrating fungicide, and eradicating volunteer plants, should also be considered. Precise modification of existing allelic diversity via advanced genomic editing is an efficient alternative for accelerating wheat improvement and sustainably increasing wheat production. Although it is convenient to attain precise allele/gene targeting or replacement in different cereal plant species, impressive work has been published in past years in wheat molecular breeding, which eradicates the constraints of the pathogen during crop improvement programs. In precise genome editing, replacement, deletion, site-directed artificial evolution, knockdown module, and insertion of allele/gene will be significantly facilitated by functional genomics. The advancement of the different genome modifications provides ease to gene pyramiding of novel resistance genes in the desired cultivar in a user-derived way immediately, efficiently, and cost-effectively without any linkage drag from undesired genes. More recently, CRISPR/Cas9 like techniques help in the transformation

of agriculture via the deletion or addition of alleles. No doubt, such techniques are cost-effective but eco-friendly, thus becoming a reliable trend. However, approaches like GWAS, RNAi silencing, genome edition, speed breeding, etc. will offer a huge amount of genetic information and enhance disease resistance via genomic editing. Genome editing approaches have various advantages over conventional breeding techniques, given their high efficiency, simplicity, amenability to multiplexing, and high specificity. Breeders strongly believe that combining molecular approaches with numerous breeding strategies will underpin an attempt to create super wheat cultivars for sustainable agriculture and ensure food security in an eco-friendly way.

References

- Abebe T, Guenzi AC, Martin B, Cushman JC (2003) Tolerance of mannitol-accumulating transgenic wheat to water stress and salinity. *Plant Physiol* 131:1748–1755
- Acevedo-Garcia J, Spencer D, Thieron H, Reinstädler A, Hammond-Kosack K, Phillips AL, Panstruga R (2017) mlo-based powdery mildew resistance in hexaploid bread wheat generated by a non-transgenic TILLING approach. *Plant Biotechnol J* 15:367–378
- Ahmad S, Wei X, Sheng Z, Hu P, Tang S (2020) CRISPR/Cas9 for development of disease resistance in plants: recent progress, limitations and future prospects. *Brief Func Genomics* 19:26–39
- Ahn SY, Kim SA, Yun HK (2015) Inhibition of *Botrytis cinerea* and accumulation of stilbene compounds by lightemitting diodes of grapevine leaves and differential expression of defense-related genes. *Eur J Plant Pathol* 143(4):753–765
- Alahmad S, Dinglasan E, Leung KM, Riaz A, Derbal N, Voss-Fels KP, Able JA, Bassi FM, Christopher J, Hickey LT (2018) Speed breeding for multiple quantitative traits in durum wheat. *Plant Meth* 14:1–15
- Alemu A, Brazauskas G, Gaikpa DS, Henriksson T, Islamov B, Ørgensen LN, Koppel M, Koppel R, Liatukas Ž, Svensson JT, Chawade A (2021) Genome-wide association analysis and genomic prediction for adult-plant resistance to *Septoria Tritici* blotch and powdery mildew in winter wheat. *Front Genet* 12:661742
- Ali S, Gladieux P, Leconte M, Gautier A, Justesen AF, Hovmøller MS, Enjalbert J, de Vallavieille-Pope C (2014) Origin, migration routes and worldwide population genetic structure of the wheat yellow rust pathogen *Puccinia striiformis* f. sp. *tritici*. *PLoS Pathog* 10:e1003903
- Andersen EJ, Nepal MP, Purintun JM, Nelson D, Mermigka G, Sarris PF (2020) Wheat disease resistance genes and their diversification through integrated domain fusions. *Front Genet* 11:898
- Arora S, Steuernagel B, Gaurav K, Chandramohan S, Long Y, Matny O, Johnson R, Enk J, Periyannan S, Singh N (2019) Resistance gene cloning from a wild crop relative by sequence capture and association genetics. *Nat Biotechnol* 37:139–143
- Ashkani S, Yusop MR, Shabanimofrad M, Azady A, Ghasemzadeh A, Azizi P, Latif MA (2015) Allele mining strategies: principles and utilisation for blast resistance genes in rice (*Oryza sativa* L.). *Curr Issues Mol Biol* 17:57–73
- Beddow JM, Pardey PG, Chai Y, Hurley TM, Kriticos DJ, Braun HJ, Park RF, Cuddy WS, Yonow T (2015) Research investment implications of shifts in the global geography of wheat stripe rust. *Nat Plants* 15:132
- Bhattacharya S (2017) Deadly new wheat disease threatens Europe's crops. *Nature* 542:145–146
- Bolton MD, Kolmer JA, Garvin DF (2008) Wheat leaf rust caused by *Puccinia triticina*. *Mol Plant Pathol* 9:563–575
- Brown DW, Proctor RH (2013) *Fusarium: genomics, molecular and cellular biology*. Caister Academic Press, Norfolk

- Brown JKM, Chartrain L, Lasserre-Zuber P, Saintenac C (2015) Genetics of resistance to *Zymoseptoria tritici* and applications to wheat breeding. *Fungal Genet Biol* 79:33–41
- Cardoso CADA, Reis EM, Moreira EN (2008) Development of a warning system for wheat blast caused by *Pyricularia grisea*. *Summa Phytopathol* 34:216–221
- Chang Q, Lin X, Yao M, Liu P, Guo J, Huang L (2020) Hexose transporter PsHXT1-mediated sugar uptake is required for pathogenicity of wheat stripe rust. *Plant Biotechnol J* 18(12): 2367–2369
- Chattopadhyay A, Purohit J, Mehta S, Parmar H, Karippadakam S, Rashid A, Balamurugan A, Bansal S, Prakash G, Achary VMM, Reddy MK (2022) Precision genome editing toolbox: applications and approaches for improving rice's genetic resistance to pathogens. *Agronomy* 12:565
- Chen W, Wellings C, Chen X, Kang Z, Liu T (2014) Wheat stripe (yellow) rust caused by *Puccinia striiformis* f. sp. tritici. *Mol Plant Pathol* 15:433–446
- Chhuneja P, Kaur S, Goel R, Aghae M, Dhaliwal H (2007) Introgression of leaf rust and stripe rust resistance genes from *Aegilops Umbellulata* to hexaploid wheat through induced homoeologous pairing. *Phytopathology* 105:872–884
- Choudhary JR, Tripathi A, Kaldate R, Rana M, Mehta S, Ahlawat J, Bansal M, Zaid A, Wani SH (2022) Breeding Efforts for Crop Productivity in Abiotic Stress Environment. In: *Augmenting Crop Productivity in Stress Environment*. Springer, Singapore, pp 63–103
- Coriton O, Jahier J, Leconte M, Virginie H, Gwenn T, Dedryver F, deVallavieille PC (2019) Double dose efficiency of the yellow rust resistance gene Yr17 in bread wheat lines. *Plant Breed* 139:263–271
- Crespo-Herrera LA, Garkava-Gustavsson L, Åhman I (2017) A systematic review of rye (*Secale cereale* L.) as a source of resistance to pathogens and pests in wheat (*Triticum aestivum* L.). *Hereditas* 154:14
- Cuthbert PA, Somers DJ, Thomas J, Cloutier S, Brule-Babel A (2006) Fine mapping Fhb1, a major gene controlling fusarium head blight resistance in bread wheat (*Triticum aestivum* L.). *Theor Appl Genet* 112:1465–1472
- Dakouri A, McCallum BD, Radovanovic N, Cloutier S (2013) Molecular and phenotypic characterization of seedling and adult plant leaf rust resistance in a world wheat collection. *Mol Breed* 32:663–677
- Dilawari R, Kaur N, Priyadarshi N, Kumar B, Abdelmotelb KF, Lal SK, Singh B, Tripathi A, Aggarwal SK, Jat BS, Mehta S (2021) Genome Editing: A Tool from the Vault of Science for Engineering Climate-Resilient Cereals. In: *Harsh environment and plant resilience: molecular and functional aspects*. Springer, Cham, pp 45–72
- Dodds PN, Lagudah ES (2016) Starving the enemy. *Science* 354:1377–1378
- Duveiller E, Sharma RC (2009) Genetic improvement and crop management strategies to minimize yield losses in warm non-traditional wheat growing areas due to spot blotch pathogen *Cochliobolus sativus*. *J Phytopathol* 157:521–534
- Duveiller E, Sharma RC (2012) Wheat resistance to spot blotch or foliar blight. In: Sharma I (ed) *Disease resistance in wheat*. CABI, Wallingford, pp 120–135
- Duy PN, Lan DT, Pham Thu H, Thi Thu HP, Nguyen Thanh H, Pham NP et al (2021) Improved bacterial leaf blight disease resistance in the major elite Vietnamese rice cultivar TBR225 via editing of the *OsSWEET14* promoter. *PLoS One* 16:9
- Dwivedi SL, Ceccarelli S, Blair MW, Upadhyaya HD, Are AK, Ortiz R (2016) Landrace germplasm for improving yield and abiotic stress adaptation. *Trends Plant Sci* 21:31–42
- Ellis JG, Lagudah ES, Spielmeyer W, Dodds PN (2014) The past, present and future of breeding rust resistant wheat. *Front Plant Sci* 5:641
- FAO STAT (2018) FAO online database. Available at: <http://www.fao.org/faostat/en/#data>. Last Access: May 2019
- Feng H, Duan X, Zhang Q, Li X, Wang B, Huang L, Wang X, Kang Z (2014) The target gene of taemiR164, a novel NAC transcription factor from the NAM subfamily, negatively regulates resistance of wheat to stripe rust. *Mol Plant Pathol* 15:284–296

- Figuerola M, Upadhyaya NM, Sperschneider J, Park RF, Szabo LJ, Steffenson B, Ellis JG, Dodds PN (2016) Changing the game: using integrative genomics to probe virulence mechanisms of the stem rust pathogen *Puccinia graminis* f. sp. *tritici*. *Front Plant Sci* 7:205
- Figuerola M, Hammond-Kosack KE, Solomon PS (2018) A review of wheat diseases—a field perspective. *Mol Plant Pathol* 19:1523–1536
- Fones H, Gurr S (2015) The impact of *Septoria tritici* Blotch disease on wheat: an EU perspective. *Fungal Genet Biol* 79:3–7
- Fu D, Uauy C, Distelfeld A, Blechl A, Epstein L, Chen X, Sela H, Fahima T, Dubcovsky J (2009) A kinase-START gene confers temperature dependent resistance to wheat stripe rust. *Science* 323:1357–1360
- Gilbert J, Haber S (2013) Overview of some recent research developments in fusarium head blight of wheat. *Can J Plant Pathol* 35:149–174
- Gil-Humanes J, Voytas DF (2014) Wheat rescued from fungal disease. *Nat Biotechnol* 32:886–887
- Grote U, Fasse A, Nguyen TT, Erenstein O (2021) Food security and the dynamics of wheat and maize value chains in Africa and Asia. *Front Sustain Food Syst* 4:617009
- Gupta SK, Ashwini C, Sunita K, Kumble VP, Qazi MRH (2005) Development and validation of molecular markers linked to an *Aegilops umbellulata*-derived leaf-rust-resistance gene, *Lr9*, for marker-assisted selection in bread wheat. *Genome* 48:823–830
- Gupta N, Batra N, Bhardwaj SC (2017) Wheat rust research—Status, efforts and way ahead. *J Wheat Res* 9:72–86
- Hahn F, Loures SL, Sparks CA, Kanyuka K, Nekrasov V (2021) Efficient CRISPR/ cas-mediated targeted mutagenesis in spring and winter wheat varieties. *Plan Theory* 10:1481
- Hao C, Jiao C, Hou J, Li T, Liu H, Wang Y, Zheng J, Liu H, Bi Z, Xu F (2020) Resequencing of 145 landmark cultivars reveals asymmetric sub-genome selection and strong founder genotype effects on wheat breeding in China. *Mol Plant* 13:1733–1751
- He Y, Wang Q, Zeng J, Sun T, Yang, Guang-xiao HE, Guang Y (2015) Current status and trends of wheat genetic transformation studies in China. *J Integr Agric* 14:438–452
- Hickey LT, Hafeez AN, Robinson H, Jackson SA, Leal-Bertioli SC, Tester M, Gao C, Godwin ID, Hayes BJ, Wulff BB (2019) Breeding crops to feed 10 billion. *Nat Biotechnol* 37:744–754
- Hovmöller MS, Walter S, Bayles RA, Hubbard A, Flath K, Sommerfeldt N, Leconte M, Czembor P, Rodriguez-Algaba J, Thach T, Hansen JG, Lassen P, Justesen AF, Ali S, de Vallavieille-Pope C (2015) Replacement of the European wheat yellow rust population by new races from the centre of diversity in the near-Himalayan region. *Plant Pathol* 65:402–411
- Huang X, Wei X, Sang T, Zhao Q, Feng Q, Zhao Y, Li C, Zhu C, Lu T, Zhang Z (2010) Genome-wide association studies of 14 agronomic traits in rice landraces. *Nat Genet* 42:961–967
- Huang F, Qureshi JA, Meagher RL Jr, Reising DD, Head GP, Andow DA (2014) Cry1F resistance in fall armyworm *Spodoptera frugiperda*: single gene versus pyramided Bt maize. *PLoS One* 9:e112958
- Huerta-Espino J, Singh R, German S, McCallum B, Park R, Chen WQ, Bhardwaj S, Goyeau H (2011) Global status of wheat leaf rust caused by *Puccinia triticina*. *Euphytica* 179:143–160
- Igarashi S, Utimada C, Igarashi L, Kazuma A, Lopes R (1986) *Pyricularia* sp. em trigo. I. Ocorrencia de *Pyricularia* sp. no Estado do Parana. *Fitopatol Bras* 11:351–352
- Islam MT, Croll D, Gladieux P, Soanes DM, Persoons A, Bhattacharjee P, Hossain MS, Gupta DR, Rahman MM, Mahboob MG, Cook N, Salam MU, Surovy MZ, Sancho VB, Maciel JLN, NhaniJunior A, Castroagudin VL, Reges JTA, Ceresini PC, Ravel S, Kellner R (2016) Emergence of wheat blast in Bangladesh was caused by a South American lineage of *Magnaporthe oryzae*. *BMC Biol* 14:84
- Jahier J, Abelard P, Tanguy M, Dedryver F, Rivoal R, Khatkar S, Bariana HS, Koebner R (2001) The *Aegilops ventricosa* segment on chromosome 2AS of the wheat cultivar ‘VPM1’ carries the cereal cyst nematode resistance gene *Cre5*. *Plant Breed* 120:125–128
- Jamil S, Shahzad R, Ahmad S, Fatima R, Zahid R, Anwar M, Iqbal MZ, Wang X (2020) Role of genetics, genomics, and breeding approaches to combat stripe rust of wheat. *Front Nutr* 7:580715

- Jiang C, Kan J, Ordon F, Perovic D, Yang P (2020) Bymovirus-induced yellow mosaic diseases in barley and wheat: viruses, genetic resistances and functional aspects. *Theor Appl Genet* 133: 1623–1640
- Jin Y, Szabo LJ, Pretorius ZA, Singh RP, Ward R, Fetch T (2008) Detection of virulence to resistance gene Sr24 within race TTKS of *Puccinia graminis* f. sp. *tritici*. *Plant Dis* 92:923–926
- Jupe F, Witek K, Verweij W, Sliwka J, Pritchard L, Etherington GJ, Maclean D, Cock PJ, Leggett RM, Bryan GJ (2013) Resistance gene enrichment sequencing (RenSeq) enables reannotation of the NB-LRR gene family from sequenced plant genomes and rapid mapping of resistance loci in segregating populations. *Plant J* 76:530–544
- Kaiser N, Douches D, Dhingra A, Glenn KC, Herzig PR, Stowe EC et al (2020) The role of conventional plant breeding in ensuring safe levels of naturally occurring toxins in food crops. *Trends Food Sci Technol* 100:51–66
- Kaur N (2008) Allele mining and sequence diversity at the wheat powdery mildew resistance locus Pm3. Doctoral dissertation, University of Zurich
- Khan S, Anwar S, Yu S, Sun M, Yang Z, Gao Z (2019) Development of drought-tolerant transgenic wheat: achievements and limitations. *Int J Mol Sci* 20:3350
- Kim SH, Qi D, Ashfield T, Helm M, Innes RW (2016) Using decoys to expand the recognition specificity of a plant disease resistance protein. *Science* 351:684–687
- Kis A, Hamar É, Tholt G, Bán R, Havelda Z (2019) Creating highly efficient resistance against wheat dwarf virus in barley by employing CRISPR/Cas9 system. *Plant Biotechnol J* 17:1004–1006
- Kisten L, Tolmay VL, Mathew I, Sydenham SL, Venter E (2020) Genome-wide association analysis of Russian wheat aphid (*Diuraphis noxia*) resistance in *Dn4* derived wheat lines evaluated in South Africa. *PLoS One* 15:e0244455
- Kocheshkova AA, Kroupin PY, Bazhenov MS, Karlov GI, Pochtovyy AA, Upelniak VP (2017) Pre-harvest sprouting resistance and haplotype variation of *ThVp-1* gene in the collection of wheat-wheatgrass hybrids. *PLoS One* 12:e0188049
- Kokhmetova A, Sehgal D, Ali S, Atishova M, Kumarbayeva M, Leonova I, Dreisigacker S (2021) Genome-wide association study of tan spot resistance in a hexaploid wheat collection from Kazakhstan. *Front Genet* 11:581214
- Kolmer JA (2005) Tracking wheat rust on a continental scale. *Curr Opin Plant Biol* 8:441–449
- Kumar D, Dutta S, Singh D, Prabhu KV, Kumar M, Mukhopadhyay K (2017) Uncovering leaf rust responsive miRNAs in wheat (*Triticum aestivum* L.) using high-throughput sequencing and prediction of their targets through degradome analysis. *Planta* 245(1):161–182
- Kumar D, Kumar A, Chhokar V, Gangwar OP, Bhardwaj SC, Sivasamy M, Prasad SV, Prakasha TL, Khan H, Singh R, Sharma P (2020) Genome-wide association studies in diverse spring wheat panel for stripe, stem, and leaf rust resistance. *Front Plant Sci* 11:748
- Kumar A, Sharma A, Sharma R, Srivastava P, Choudhary A (2021a) Exploration of wheat wild relative diversity from Lahaul valley: a cold arid desert of Indian Himalayas. *Cereal Res Commun*. <https://doi.org/10.1007/s42976-021-00166-w>
- Kumar A, Sharma A, Sharma R, Choudhary A, Srivastava P, Kaur H, Padhy AK (2021b) Morphophysiological evaluation of *Elymus semicostatus* (Nees ex Steud.) Melderis as potential donor for drought tolerance in Wheat (*Triticum aestivum* L.). *Gen Res Cop Evol* 69(1):411–430. <https://doi.org/10.1007/s10722-021-01241-1>
- Kumar A, Choudhary A, Kaur H, Aggarwal SK, Mehta S (2022a) Smut and bunt diseases of wheat: biology, identification, and management. In: *New horizons in wheat and barley research*. Springer, Singapore, pp 107–131
- Kumar A, Choudhary A, Kaur H, Mehta S (2022b) A walk towards wild grasses to unlock the clandestine of gene pools for wheat improvement: a review. *Plant Stress* 3:100048
- Kuraparthy V, Sood S, Chhuneja P, Dhaliwal H, Kaur S, Bowden R, Gill B (2007) A cryptic wheat-translocation with leaf rust resistance gene. *Crop Sci* 47(5)
- Langner T, Kamoun S, Belhaj K (2018) CRISPR crops: plant genome editing toward disease resistance. *Annu Rev Phytopathol* 56:479–512

- Leonard KJ, Szabo LJ (2005) Stem rust of small grains and grasses caused by *Puccinia graminis*. *Mol Plant Pathol* 6:99–111
- Li J, Zhang Y, Zhang Y, Yu P-L, Pan H, Rollins JA (2018) Introduction of large sequence inserts by CRISPR-Cas9 to create pathogenicity mutants in the multinucleate filamentous pathogen *Sclerotinia sclerotiorum*. *MBio* 9:e00567-18
- Li F, Wen W, Liu J, Zhang Y, Cao S, He Z, Rasheed A, Jin H (2019) Genetic architecture of grain yield in bread wheat based on genome-wide association studies. *BMC Plant Biol* 19:168
- Li H, Dong Z, Ma C, Xia Q, Tian X, Sehgal S, Koo DK, Friebe B, Ma P, Liu W (2020a) A spontaneous wheat-*Aegilops longissima* translocation carrying Pm66 confers resistance to powdery mildew. *Theor Appl Genet* 133:1149–1159
- Li W, Deng Y, Ning Y, He Z, Wang GL (2020b) Exploiting broad-spectrum disease resistance in crops: from molecular dissection to breeding. *Annu Rev Plant Biol* 71:575–603
- Li J, Li Y, Ma L (2020c) Recent advances in CRISPR/Cas9 and applications for wheat functional genomics and breeding. *aBiotech* 2:375–385. <https://doi.org/10.1007/s42994-021-00042-5>
- Li J, Jiao G, Sun Y, Chen J, Zhong Y, Yan L, Jiang D, Ma Y, Xia L (2020d) Modification of starch composition, structure and properties through editing of TaSBEIIa in both winter and spring wheat varieties by CRISPR/Cas9. *Plant Biotechnol J* 19:937–951
- Liang C, Zeng YZ, Hong XL, Hong XL, LiPu D, Huijun X, Zhiyong X (2008) Overexpression of *TIERF1* enhances resistance to sharp eyespot in transgenic wheat. *J Exp Bot* 59:4195–4204
- Lin Q, Zong Y, Xue C, Wang S, Jin S, Zhu Z, Wang Y, Anzalone AV, Raguram A, Doman JL (2020) Prime genome editing in rice and wheat. *Nat Biotechnol* 38:582–585
- Liu HJ, Yan J (2019) Crop genome-wide association study: a harvest of biological relevance. *Plant J* 97:8–18
- Liu X, Yang L, Zhou X, Zhou M, Lu Y, Ma L, Ma H, Zhang Z (2013) Transgenic wheat expressing *Thinopyrum intermedium* MYB transcription factor TiMYB2R-1 shows enhanced resistance to the take-all disease. *J Exp Bot* 64:2243–2253
- Liu W, Koo DH, Xia Q, Li C, Bai F, Song Y, Friebe B, Gill BS (2017) Homoeologous recombination-based transfer and molecular cytogenetic mapping of powdery mildew-resistant gene Pm57 from *Aegilops searsii* into wheat. *Theor Appl Genet* 130:841–848
- Liu Y, Guo Y, Zhou Y (2018) Poverty alleviation in rural China: policy changes, future challenges and policy implications. *China Agric Econ Rev* 10:241–259
- Liu Y, Luo W, Linghu Q, Abe F, Hisano H, Sato K, Kamiya Y, Kawaura K, Onishi K, Endo M et al (2021) In planta genome editing in commercial wheat varieties. *Front Plant Sci* 12:648841
- Lujan Basile SM, Ramirez IA, Crescente JM, Conde MB, Demichelis M, Abbate P, Rogers WJ, Pontaroli AC, Helguera M, Vanzetti LS (2019) Haplotype block analysis of an Argentinean hexaploid wheat collection and GWAS for yield components and adaptation. *BMC Plant Biol* 19:553
- Ma K, Li X, Li Y, Wang Z, Zhao B, Wang B, Li Q (2021) Disease resistance and genes in 146 wheat cultivars (Lines) from the Huang-Huai-Hai Region of China. *Agronomy* 11:1025
- Mago R, Verlin D, Zhang P, Bansal U, Bariana H, Jin Y, Ellis J, Hoxha S, Dundas I (2013) Development of wheat-*Aegilops speltoides* recombinants and simple PCR-based markers for Sr32 and a new stem rust resistance gene on the 2S#1 chromosome. *Theor Appl Genet* 126:2943–2955
- Mago R, Zhang P, Vautrin S, Simkova H, Bansal U, Luo MC, Rouse M, Karaoglu H, Periyannan S, Kolmer J, Jin Y, Ayliffe MA, Bariana H, Park RF, McIntosh R, Dolezel J, Bergès H, Spielmeier W, Lagudah ES, Ellis JG, Dodds PN (2015) The wheat Sr50 reveals a rich diversity at a cereal disease resistance locus. *Nat Plants* 15:186
- Maqbool A, Saitoh H, Franceschetti M, Stevenson CEM, Uemura A, Kanzaki H, Kamoun S, Terauchi R, Banfield MJ (2015) Structural basis of pathogen recognition by an integrated HMA domain in a plant NLR immune receptor. *elife* 4:e08709
- Mascher M, Jost M, Kuon JE, Himmelbach A, Assfalg A, Beier S, Scholz U, Graner A, Stein R (2014) Mapping-by sequencing accelerates forward genetics in barley. *Genome Biol* 15:R78

- Mehta S, Lal SK, Sahu KP, Venkatapuram AK, Kumar M, Sheri V, Varakumar P, Vishwakarma C, Yadav R, Jameel MR, Ali M, Achary VMM, Reddy MK (2020) CRISPR/Cas9-edited rice: a new frontier for sustainable agriculture. In: New frontiers in stress management for durable agriculture. Springer, Singapore, pp 427–458
- McCallum BD, Hiebert CW, Cloutier S, Bakkeren G, Rosa SB, Humphreys DG, Marais GF, McCartney CA, Panwar V, Rampitsch C, Saville BJ, Wang X (2016) A review of wheat leaf rust research and the development of resistant cultivars in Canada. *Can J Plant Pathol* 38:1–18
- McDonald BA, Linde C (2002) Pathogen population genetics, evolutionary potential, and durable resistance. *Annu Rev Phytopathol* 40:349–379
- Miedaner T, Juroszek P (2021) Climate change will influence disease resistance breeding in wheat in Northwestern Europe. *Theor Appl Genet* 134:1771–1785
- Mujeeb-Kazi A, Munns R, Rasheed A, Ogbonnaya FC, Ali N, Hollington P, Dundas I, Saeed N, Wang R, Rengasamy P, Saddiq MS (2019) Breeding strategies for structuring salinity tolerance in wheat. *Adv Agron* 155:121–187
- Muñoz IV, Sarrocco S, Malfatti L, Baroncelli R, Vannacci G (2019) CRISPR-Cas for fungal genome editing: a new tool for the management of plant diseases. *Front Plant Sci* 10:135. <https://doi.org/10.3389/fpls.2019.00135>
- Murray GM, Brennan JP (2009) Estimating disease losses to the Australian wheat industry. *Australas Plant Pathol* 38:558–570
- Olivera Firpo P, Newcomb M, Szabo L, Rouse MN, Johnson JL, Gale SW, Luster D, Hodson D, Cox JA, Burgin L (2015) Phenotypic and genotypic characterization of race TKTF of *Puccinia graminis* f. sp. *tritici* that caused a wheat stem rust epidemic in southern Ethiopia in 2013/14. *Phytopathology* 105:917–928
- Olivera Firpo P, Newcomb M, Flath K, Sommerfeldt-Impe N, Szabo L, Carter M, Luster D, Jin Y (2017) Characterization of *Puccinia graminis* f. sp. *tritici* isolates derived from an unusual wheat stem rust outbreak in Germany in 2013. *Plant Pathol* 66:1258–1266
- Pardey P, Beddow J, Kriticos D, Hurley T, Park R, Duveiller E, Sutherst R, Burdon J, Hodson D (2013) Right-sizing stem-rust research. *Science* 340:147–148
- Pasquariello M, Berry S, Burt C (2020) Yield reduction historically associated with the *Aegilops ventricosa* 7D^V introgression is genetically and physically distinct from the eyespot resistance gene *Pch1*. *Theor Appl Genet* 133:707–717
- Paul NC, Park S-W, Liu H, Choi S, Ma J, MacCready JS, Chilvers MI, Sang H (2021) Plant and fungal genome editing to enhance plant disease resistance using the CRISPR/Cas9 System. *Front Plant Sci* 12:700925
- Periyannan S, Milne RJ, Figueroa M, Lagudah ES, Dodds PN (2017) An overview of genetic rust resistance: from broad to specific mechanisms. *PLoS Pathog* 13:e1006380
- Pretorius ZA, Singh RP, Wagoire WW, Payne TS (2000) Detection of virulence to wheat stem rust resistance gene Sr31 in *Puccinia graminis* f. sp. *tritici* in Uganda. *Plant Dis* 84:203
- Pretorius Z, Bender C, Visser B, Terefe T (2010) First report of a *Puccinia graminis* f. sp. *tritici* race virulent to the Sr24 and Sr31 wheat stem rust resistance genes in South Africa. *Plant Dis* 94:784
- Prins R, Groenewald JZ, Marais G, Snape J, Koebner R (2001) AFLP and STS tagging of Lr19, a gene conferring resistance to leaf rust in wheat. *Theor Appl Genet* 103:618–624
- Qi T, Zhu X, Tan C, Liu P, Guo J, Kang Z (2018) Host-induced gene silencing of an important pathogenicity factor P s CPK 1 in *Puccinia striiformis* f. sp. *tritici* enhances resistance of wheat to stripe rust. *Plant Biotechnol J* 16:797–807
- Qi T, Guo J, Liu P, He F, Wan C, Islam MA (2019) Stripe rust effector PstGSRE1 disrupts nuclear localization of ROS-promoting transcription factor TaLOL2 to defeat ROS-induced defense in wheat. *Mol Plant* 12:1624–1638
- Raffan S, Sparks C, Huttly A, Hyde L, Martignago D, Mead A, Hanley SJ, Wilkinson PA, Barker G, Edwards KJ et al (2021) Wheat with greatly reduced accumulation of free asparagine in the grain, produced by CRISPR/Cas9 editing of asparagine synthetase gene TaASN2. *Plant Biotechnol J* 19(8):1602–1613

- Rai R, Das BK, Bhagwat SG (2017) Development and validation of scar marker for stem rust resistance gene Sr26 in wheat (*Triticum aestivum* L.). *Biol Syst Open Access* 6:181
- Rasool G, Ullah A, Jan A, Waris M, Tariq MA, Ahmad Q (2021) Morphological evaluation of wheat genotypes for grain yield under arid environment of Balochistan. *Pure Appl Biol* 10: 1441–1449
- Razzaq A, Kaur P, Akhter N, Wani SH, Saleem F (2021) Next-generation breeding strategies for climate-ready crops. *Front Plant Sci* 12:620420
- Rong W, Qi L, Wang J, Du L, Xu H, Wang A, Zhang Z (2013) Expression of a potato antimicrobial peptide SN1 increases resistance to take-all pathogen *Gaeumannomyces graminis* var. *tritici* in transgenic wheat. *Funct Integr Genomics* 13:403–409
- Rong W, Qi L, Wang A, Ye X, Du L, Liang H, Xin Z, Zhang Z (2014) The ERF transcription factor TaERF3 promotes tolerance to salt and drought stresses in wheat. *Plant Biotechnol J* 12:468–479
- Różewicz M, Wzyńska M, Grabiński J (2021) The most important fungal diseases of cereals—problems and possible solutions. *Agronomy* 11:714
- Sack GM (2020) Editing *Fusarium graminearum* using CRISPR/Cas9. Honors Program Theses, p 431
- Sanchez-Martin J, Steuernagel B, Ghosh S, Herren G, Humi S, Adamski N, Vrana J, Kubaláková M, Krattinger SG, Wicker T (2016) Rapid gene isolation in barley and wheat by mutant chromosome sequencing. *Genome Biol* 17:221
- Satheesh V, Zhang H, Wang X, Lei M (2019) Precise editing of plant genomes—prospects and challenges. In: Seminars in cell and developmental biology, vol 96. Academic Press, pp 115–123
- Schenke D, Cai D (2020) Applications of CRISPR/Cas to improve crop disease resistance: beyond inactivation of susceptibility factors. *Science* 23:101478. <https://doi.org/10.1016/j.isci.2020.101478>
- Schumann GL, D’Arcy CJ (2009) Essential plant pathology. APS Press, St. Paul, MN
- Segretin ME, Pais M, Franceschetti M, Chaparro-Garcia A, Bos JIB, Banfield MJ, Kamoun S (2014) Single amino acid mutations in the potato immune receptor R3a expand response to *Phytophthora* effectors. *Mol Plant-Microbe Interact* 27:624–637
- Shabeer A, Bockus WW (1988) Tan spot effects on yield and yield components relative to growth stage in winter wheat. *Plant Dis* 72:599–602
- Shahriar SA, Islam MN, Chun CNW, Rahim MA, Paul NC, Uddain J, Siddiquee S (2021) Control of plant viral diseases by CRISPR/Cas9: resistance mechanisms, strategies and challenges in food crops. *Plan Theory* 10:1264
- Shakeel A, Xiangjin W, Zhonghua S, Peisong H, Shaoqing T (2020) CRISPR/Cas9 for development of disease resistance in plants: recent progress, limitations and future prospects. *Brief Funct Genom* 19:26–39
- Shakeel A, Liqun T, Rahil S, Amos M, Gundra SR, Shakra J, Chen W, Zhonghua S, Gaoneng S, Xiangjin W, Peisong H, Magdy M, Shikai H, Shaoqing T (2021) CRISPR-based crop improvements: a way forward to achieve zero hunger. *J Agric Food Chem* 69:8307–8323
- Sheikh SK, Vishal G, Devanshi P, Sonali A, Dechan C, Saima F, Rafakat H (2021) Epidemiology of stripe rust of wheat: a review. *Int J Curr Microbiol App Sci* 10:1158–1172
- Simón MR, Börner A, Struik PC (2021) Editorial: fungal wheat diseases: etiology, breeding, and integrated management. *Front Plant Sci* 12:671060
- Singh S, Franks CD, Huang L (2004) *Lr41*, *Lr39*, and a leaf rust resistance gene from *Aegilops cylindrica* may be allelic and are located on wheat chromosome 2DS. *Theor Appl Genet* 108: 586–591
- Singh RP, Hodson DP, Huerta-Espino J, Jin Y, Bhavani S, Njau P, Herrera-Foessel S, Singh PK, Singh S, Govindan V (2011) The emergence of Ug99 races of the stem rust fungus is a threat to world wheat production. *Annu Rev Phytopathol* 49:465–481
- Singh RP, Hodson DP, Jin Y, Lagudah ES, Ayliffe MA, Bhavani S, Rouse MN, Pretorius ZA, Szabo LJ, Huerta-Espino J, Basnet BR, Lan C, Hovmøller MS (2015) Emergence and spread of

- new races of wheat stem rust fungus: continued threat to food security and prospects of genetic control. *Phytopathology* 105:872–884
- Singh V, Singh G, Chaudhury A, Ojha A, Tyagi BS, Chowdhary AK, Sheoran S (2016) Phenotyping at hot spots and tagging of QTLs conferring spot blotch resistance in bread wheat. *Mol Biol Rep* 43:1–11
- Singh M, Nara U, Kumar A, Thapa S, Chandan J, Singh H (2021a) Enhancing genetic gains through marker-assisted recurrent selection: from phenotyping to genotyping. *Cereal Res Commun.* <https://doi.org/10.1007/s42976-021-00207-4>
- Singh M, Nara U, Kumar A, Choudhary A, Singh H, Thapa S (2021b) Salinity tolerance mechanisms and their breeding implications. *J Gen Eng Biotech* 19:173
- Singh A, Mehta S, Yadav S, Nagar G, Ghosh R, Roy A, Chakraborty A, Singh IK (2022) How to cope with the challenges of environmental stresses in the era of global climate change: an update on ROS stave off in plants. *Int J Mol Sci* 23:1995
- Steuernagel B, Periyannan SK, Hernández-Pinzón I, Witek K, Rouse MN, Yu G et al (2016) Rapid cloning of disease-resistance genes in plants using mutagenesis and sequence capture. *Nat Biotechnol* 34(6):652–655
- Su Z, Bernardo A, Tian B, Chen H, Wang S, Ma H, Cai S, Liu D, Zhang D, Li T (2019) A deletion mutation in TaHRC confers Fhb1 resistance to Fusarium head blight in wheat. *Nat Genet* 51: 1099–1105
- Tang S, Hu Y, Zhong S, Luo P (2018) The potential role of powdery mildew-resistance gene Pm40 in Chinese wheat-breeding programs in the Post-Pm21 Era. *Engineering* 4:500–506
- Tehseen MM, Kehel Z, Sansaloni CP, Lopes MDS, Amri A, Kurtulus E, Nazari K (2021) Comparison of genomic prediction methods for yellow, stem, and leaf rust resistance in wheat landraces from Afghanistan. *Plan Theory* 10:558
- Tembo B, Mulenga RM, Sichilima S, M'siska KK, Mwale M, Chikoti PC (2020) Detection and characterization of fungus (*Magnaporthe oryzae* pathotype *Triticum*) causing wheat blast disease on rain-fed grown wheat (*Triticum aestivum* L.) in Zambia. *PLoS One* 15:e0238724
- Thind AK, Wicker T, Simkova H, Fossati D, Moullet O, Brabant C, Vrana J, Dolezel J, Krattinger SG (2017) Rapid cloning of genes in hexaploid wheat using cultivar-specific long-range chromosome assembly. *Nat Biotechnol* 35:793–796
- Tyagi S, Kumar R, Kumar V, Won SY, Shukla P (2021) Engineering disease resistant plants through CRISPR-Cas9 technology. *GM Crops & Food* 12:125–144
- Varga E, Wiesenberger G, Hametner C, Ward TJ, Dong Y, Schöfbeck D, McCormick S, Broz K, Stückler R, Schuhmacher R, Krska R, Kistler HC, Berthiller F, Adam G (2015) New tricks of an old enemy: isolates of *Fusarium graminearum* produce a type A trichothecene mycotoxin. *Environ Microbiol* 17:2588–2600
- Verma AK, Mandal S, Tiwari A, Monachesi C, Catassi GN, Srivastava A, Gatti S, Lionetti E, Catassi C (2021) Current status and perspectives on the application of CRISPR/Cas9 gene-editing system to develop a low-gluten. *Non-Transgenic Wheat Variety Foods* 10:2351
- Wang Y, Cheng X, Shan Q, Zhang Y, Liu J, Gao C et al (2014) Simultaneous editing of three homoeoalleles in hexaploid bread wheat confers heritable resistance to powdery mildew. *Nat Biotechnol* 32:947–951. <https://doi.org/10.1038/nbt.2969>
- Wang H, Sun S, Ge W, Zhao L, Hou B, Wang K, Lyu Z, Chen L, Xu S, Guo J (2020) Horizontal gene transfer of Fhb7 from fungus underlies Fusarium head blight resistance in wheat. *Science* 368:eaba5435
- Wellings CR (2011) Global status of stripe rust: a review of historical and current threats. *Euphytica* 179:129–141
- Williamson VM, Thomas V, Ferris H, Dubcovsky J (2013) An *Aegilops ventricosa* translocation confers resistance against root-knot nematodes to common wheat. *Crop Sci* 53:1412–1418
- Worku D, Zerihun T, Daniel K, Habtemariam Z, Dawit A, Wanyera R (2016) Development of wheat germplasm for stem rust resistance in eastern Africa. *Afr Crop Sci J* 24:25–33
- Wulff BBH, Moscou MJ (2014) Strategies for transferring resistance into wheat: from wide crosses to GM cassettes. *Front Plant Sci* 5:692

- Yan F, Zheng Y, Zhang W (2006) Obtained transgenic wheat expressing *pac1* mediated by *Agrobacterium* is resistant against Barley yellow dwarf virus-GPV. *Chin Sci Bull* 51:2362–2368
- Zaidi SS, Mahas A, Vanderschuren H, Mahfouz MM (2020) Engineering crops of the future: CRISPR approaches to develop climate-resilient and disease-resistant plants. *Genome Biol* 21: 289
- Zaynab M, Sharif Y, Fatima M, Afzal MZ, Aslam MM, Raza MF et al (2020) CRISPR/Cas9 to generate plant immunity against pathogen. *Microb Pathog* 141:103996. <https://doi.org/10.1016/j.micpath.2020.103996>
- Zhang Z, Liu X, Wang X, Zhou M, Zhou X, Ye X, Wei X (2012) An R2R3 MYB transcription factor in wheat, TaPIMP1, mediates host resistance to *Bipolaris sorokiniana* and drought stresses through regulation of defense- and stress-related genes. *New Phytol* 196:1155–1170
- Zhang Q, Wang Q, Wang X, Liu J, Li M, Huang L, Kang Z (2013) Target of ta-miR408, a chemocyanin-like protein gene (TaCLP1), plays positive roles in wheat response to high-salinity, heavy cupric stress and stripe rust. *Plant Mol Biol* 83:433–443
- Zhang Y, Bai Y, Wu G, Zou S, Chen Y, Gao C, Tang D (2017a) Simultaneous modification of three homoeologs of TaEDR1 by genome editing enhances powdery mildew resistance in wheat. *Plant J* 91:714–724
- Zhang Y, Bai Y, Wu G, Zou S, Chen Y, Gao C, Tang D (2017b) Simultaneous modification of three homoeologs of TaEDR1 by genome editing enhances powdery mildew resistance in bread confers heritable resistance to powdery mildew. *Nat Biotechnol* 32:947–951
- Zhang Y, Geng H, Cui Z, Wang H, Liu D (2021) Functional analysis of wheat NAC transcription factor, *TaNAC069*, in regulating resistance of wheat to leaf rust fungus. *Front Plant Sci* 12: 604797
- Zhao TJ, Zhao SY, Chen HM, Zhao QZ, Hu ZM, Hou BK, Xia GM (2006) Transgenic wheat progeny resistant to powdery mildew generated by *Agrobacterium* inoculum to the basal portion of wheat seedling. *Plant Cell Rep* 25:1199–1204