Powdery Mildew of Wheat: Research Progress, Opportunities, and Challenges

5

Vijay Rana, Aashima Batheja, Ravi Sharma, Amit Rana, and Priyanka

5.1 Introduction

Crops have always been exposed to the perils of various biotic and abiotic stresses to varying degrees. Unfortunately, global climate change is expected to increase the incidence and severity of novel biotic stress factors, virulence evolvement, and broadening of the host range. Resistance response to pests and pathogens has a major role to play in safeguarding the yield potential of high yielding varieties.

Wheat (*Triticum aestivum* L.) is one of the most valuable food crops, playing a critical role in global food supply and defense, but its development is constantly threatened by a variety of diseases (Ma et al. 2014; Zhang et al. 2017a, b). The biotrophic fungus *Blumeria graminis* f. sp. *tritici* (Bgt) causes powdery mildew, which is one of the most severe diseases restricting wheat production in many regions of the world. *Blumeria graminis*, also known as grass powdery mildew, is a fungus that affects grass plants in the Poaceae family. Because of its economic impact on cereal crops (especially wheat and barley), it is considered one of the most important fungal pathogens, and it serves as a model system for studying biotrophic pathogens (Dean et al. 2012). Although the management of powdery mildew in realistic agriculture can vary depending on its economic significance, chemical control of the most common fungal diseases has been widely considered to be uneconomic (Wellings and Luig 1984). The ever growing world population

V. Rana (✉)
Rice and Wheat Research Centre, CSK Himachal Pradesh Krishi Vishvavidyalaya, Malan, Himachal Pradesh, India

Department of Genetics and Plant Breeding, CSK Himachal Pradesh Krishi Vishvavidyalaya, Palampur, Himachal Pradesh, India

A. Batheja · R. Sharma · A. Rana · Priyanka
Department of Genetics and Plant Breeding, CSK Himachal Pradesh Krishi Vishvavidyalaya, Palampur, Himachal Pradesh, India

P. L. Kashyap et al. (eds.), *New Horizons in Wheat and Barley Research*,
https://doi.org/10.1007/978-981-16-4134-3_5

demands well-organized plant disease management and control in agricultural production systems to ensure food security and safety (FAO et al. 2018). An effective and efficient mechanism for early warning and fast response is very essential to control phytopathogenic fungi. In this context, novel and effective diagnostic methods to minimize fungal plant disease are of utmost importance. Molecular assays can overcome many shortcomings of the conventional and serological methods in fungal diagnostics (Hariharan and Prasannath 2021). Given the expansion of powdery mildew's host range, a better understanding of the underlying genetics of reproductive barriers and self- versus non–self-identification between species of fungal plant pathogens could help predict hybridization events in various agroecosystems. The availability of large genome data sets will greatly support future research, and genome data will be a valuable resource when combined with experimental methods for analyzing hybrid fungal organisms. Over the last few decades, breeding achievements for disease resistance are likely to be equally important as breeding achievement for increased yield potential (Byerlee and Moya 1993). To maintain global food security by reducing the incidence of disease epidemics, great efforts are required to breed wheats with diverse and durable resistance. By reducing reliance on pesticides for disease and pest control, it also helps to protect the atmosphere and farmer's income. However, the most important thing to know is that host resistance might not be enough to control wheat powdery mildew disease; sound agricultural practices and judicious use of fungicides should also be considered. Looking at the ever growing economic importance of powdery mildew, information on various aspects pertaining to the pathogen study, host resistance, and integrated disease management is reviewed herewith.

To summarize, linkage drag, fungicidal resistance, fast jump and expansion in host range due to increased pathogenic variability are among the potential challenges for managing powdery mildew. On the other hand, advancements in the molecular diagnostic techniques for pathogen identification, cultivar development, artificial intelligence algorithms, and speed breeding protocols offer vast opportunities to tackle powdery mildew fungus in future.

5.2 Global Distribution and Host Range of Powdery Mildew Fungus

Wheat powdery mildew is found all over the world, although it is most prevalent in the northern hemisphere. It was found to be economically harmful in colder, coastal, or semi-continental climates until the Green Revolution. However, due to the introduction of intensive processing techniques, wheat powdery mildew has become a problem even in some hotter, drier areas in recent decades. This is largely due to the use of semi-dwarf cultivars, higher population densities, nitrogen fertilizers and irrigation, which result in thicker, more compact and more humid canopies (Bennett 1984; Cunfer 2002). The disease is more prevalent in areas where there is a lot of rain and the temperature is relatively low (Bennett 1984). Powdery mildew has been found in UK, Russia, Germany, Japan, Africa, and much of West Asia (Bennett

1984). Cooler areas of China, Japan, and Central Asia, as well as North and South America harbor powdery mildew as a common disease (Roelfs 1977; Saari and Wilcoxson 1974). The disease is more extreme in warmer, humid areas with mild winters, such as parts of South America and the southeastern United States. Powdery mildew is less common in areas where rain is regular and heavy because the spores are washed away from the leaves (Merchan and Kranz 1986). Powdery mildew is becoming increasingly problematic in India, especially in the northern and southern hills along with some areas in the northwest plain zone.

Regarding host range, powdery mildews (Ascomycota, Erysiphales) are known to infect over 10,000 dicot and monocot plant species around the world (Braun and Cook 2012). Many powdery mildew species cause economically significant diseases in agricultural and horticultural crops like wheat, barley, vegetable species, fruits, grapevine, etc. (Glawe 2008). Some forms of this fungus also affect various forest plant species (Marcais and Desprez-Loustau 2014). Many parts of the world have faced invasion by some powdery mildews (Kiss 2005; Desprez-Loustau et al. 2010), leading to threat to plant health and biosecurity (Desprez-Loustau et al. 2010). *Blumeria graminis* infecting cereals and *Erysiphe necator* infecting grapevine, two important powdery mildew species, have served as model species in plant pathology research (Gadoury et al. 2012; Bindschedler et al. 2016). On the other hand, in wild plant pathosystems (Susi et al. 2015), interactions between *Podosphaera plantaginis* and its host *Plantago lanceolata* have long been the focus of many studies.

B. graminis has eight formae speciales that are each specialized on particular host species among the wild and cultivated grasses. However, the host range of *B. graminis* cultures isolated from cereals in Israel is wider than that of isolates from elsewhere in the world (Eshed and Wahl 1970). This likely reflects the greater diversity of *B. graminis* hosts in the Middle East, which is believed to be the center of origin and diversity of the wild ancestors and relatives of cultivated cereals (Wyand and Brown 2003).

Braun (1987) discovered 18 genera and 435 species of the powdery mildews, which are able to infect a wide variety of hosts from several tree species to herbs. Up to 9838 species among 1617 genera, 169 families, and 44 orders of angiosperm plants have been found to be the host of powdery mildews (Amano 1986). Thus, the powdery mildew fungus is one of the most significant plant pathogens. Host range of these is exclusively limited to angiosperms and they have never infected ferns or gymnosperms.

5.2.1 Yield Losses and Adverse Effects

The wheat powdery mildew, *Blumeria graminis* (DC.) E.O. Speer, f. sp. *tritici* Em. Marchal (Bgt) (syn. *Erysiphe graminis* (DC) f. sp. *tritici*), is the sixth most important fungal pathogen in wheat, according to Dean et al. (2012), and is responsible for the eighth highest yield loss due to pests and pathogens worldwide (Savary et al. 2019). Powdery mildew may occur year-round in many wheat-producing regions, with output losses of up to 35%, 62%, and 40% in Russia, Brazil, and

China, respectively (Mehta 2014). Attributes of Bgt, such as short life cycle, airborne spores equipped for voyaging significant distances, and above all sexual recombination for producing new virulences, advance quick spread and variation.

The relationship of mildew severity to yield loss depends on the crop growth stage, methodology used for disease assessment, timing, canopy position, and intensity of epidemic pressure. Several studies have elucidated this relationship in experimental field settings. Large and Doling (1962, 1963) found the best growth stage for relating yield loss in winter wheat to mildew severity (measured as total photosynthetic leaf area covered by mildew pustules) was at full heading. The grain yield loss was found to be proportional to twice the square root of severity, using a data set in which mildew severity from natural epidemics in unprotected plots ranged from 0% to 16%. However, Dutch researchers noted an effect of canopy position (Rabbinge et al. 1985). They observed that if preflowering infections were in upper canopy levels or distributed uniformly throughout the canopy, even low severity (approximately 4% of leaf area covered by mildew) could cause as much as a 10% yield loss, with the disproportionate impact attributable to reductions in assimilation and transpiration rates. The fungus reduces the amount of photosynthates available in leaves, lowers the leaf assimilation index, and has a negative impact on grain yield components (Bowen et al. 1991; Henry and Kettlewell 1996; Samobor et al. 2005). Infection during the tillering, stem elongation, and booting phases has a significant impact on yield, particularly when it occurs early (Bowen et al. 1991), resulting in lower kernel weight and yield.

Grain yield losses associated with wheat powdery mildew infection can exceed upto 40%, with the most extreme losses occurring before or after flowering, when the flag leaf becomes infected (Royse et al. 1980; Li et al. 2011; Alam et al. 2013). *Blumeria graminis tritici* has been confirmed to reduce wheat yield by 10–15% in most cases, and up to 50% in extreme cases, according to recent studies (Jia et al. 2018; Singh and Sharma 2020).

5.2.2 Symptoms, Disease Cycle, and Epidemiology

Powdery mildew occurs as thick, white powdery fungal fruiting bodies on the leaf surface, as well as on the awns and glumes under favorable conditions. The symptoms usually progress from lower to upper leaves, but infection can happen at any time during the season depending on weather conditions. Rapidly developing tissue is more vulnerable to infection, so plants in their early stages of development and after nitrogen application are more likely to have a more severe infection. Fungal colonies grow in size and eventually merge. The region around the lesion, as well as the leaf's reverse side, turns yellow to brown. Older infections turn grey and may develop black fruiting bodies, known as chasmothecia (formerly known as cleistothecia), that appear as black specks. Infections that are moderate to severe are able to cause necrosis. From a distance, a powdery mildew-infected crop seems yellow and exhibits symptoms similar to that from water logging or nutrient deficiency.

Powdery mildew has a fast infection period and develops millions of spores (conidia), allowing it to spread quickly through the crop. The cycle of spore germination, infection, and eventual spore development can be completed in as little as 5 days under ideal conditions (cold and humid). With changing temperatures, there is significant variation in spore production and the latent period (time between infection and spore formation). Optimum temperature range of 15–22 °C is required for disease development. Lower temperatures (5–10 °C) cause the infection cycle to take 2–3 times longer than at 20 °C, resulting in delayed symptom expression and reduced spore formation.

Infection and sporulation are stalled at temperatures above 25 °C. If the infection has taken hold, the white dense powdery mildew conidia are dispersed across the crop by the wind as a secondary infection. The disease thrives in humid, mild weather with a moist canopy. Since the fungus does not need wet leaves to infect them, rain is not needed for disease transmission, but it does promote canopy humidity. Infection becomes even more common when the relative humidity rises to 90%, but does not occur when the leaf surfaces are wet (e.g., in a rain shower). Heavy rain can wash spores from the leaf surface, slowing disease progression temporarily.

When environmental conditions are unfavorable, infection process is decelerated. These entail periods of low canopy humidity and temperatures above 25 °C, as well as dry and warm weather conditions. Experiments have shown that exposure to 25 °C for 6–12 h will defer disease development by 4–6 days and curtail severity by 30–50%. Exposing to 25 °C for more than 24 h dissuades disease development. The fungus endures the winter in the form of cleistothecia on wheat straw or mycelium on infected wheat. Under cold, humid conditions, spores germinate and infect plants. The two forms of pathogenic inoculum for infection are asexual conidia and sexual ascospores. A specialized germ tube is formed when conidia or ascospores adhere to a photosynthetically active wheat leaf surface, and it elongates to form a thread-like hypha with appressoria in as little as 2 h (Acevedo-Garcia et al. 2017). The digitate hypha then produces a penetration peg and grows into a haustorium, allowing the host epidermal cell to be breached (Glawe 2008). Bgt can thrive in the absence of a living crop due to the ascospores produced by chasmothecia/cleistothecia. Jankovics et al. (2015) characterized the mechanism of ascosporic infection in Bgt. The outbreak process is aided even further by mild temperatures (10–22°C) (Beest et al. 2008).

Powdery mildew can live between seasons by growing on volunteer wheat plants (green bridges) and wheat stubble. The presence of green wheat during the year in a given area offers an avenue for biotrophic pathogens such as rusts and powdery mildew to infect new emerging crops, resulting in higher levels of disease inoculum spreading at the start of the season. In some areas, favorable summer/autumn weather can allow for the production and persistence of regrowth. After autumn rains, the fungus lives as fruiting bodies on wheat stubbles (from previously infected crops) that release spores. Once a crop is affected, disease can be transmitted over great distances through light, airborne spores from fluffy white outbreaks on leaves.

5.2.3 Pathogenic Variation and Evolutionary Analysis in *Blumeria Graminis*

The classification of *B. graminis* in numerous *formae speciales* was presented for the first time by Marchal (1902) and it is utilized to characterize "forms" that are morphologically not discernable but infect different plant species (Schulze-Lefert and Panstruga 2011). According to this definition, a forma speciales does not necessarily represent a distinct evolutionary unit (heredity). However, the specialization on different hosts implies, at least in theory, barriers to gene flow between different ff. spp. and, therefore, defines ff. spp. as separately evolving lineages, which is the only necessary property of a species according to the unified species concept (de Queiroz 2007). The advent of next-generation sequences has provided researchers the ways that how species evolves and attempts to reconstruct the tree of life with huge amount of data. One consequence of this has been the full recognition of the difference between gene trees and species trees and of the processes that cause it (incomplete lineage sorting and lateral gene flow) (Posada 2016). These processes have different relevance in different systematic groups and at different timescales in the same group. Menardo et al. (2017a, b) have suggested to reconstruct evolutionary histories with genomics data using a diverse set of methods that are suited for lineages with a different level of divergence and isolation. The application of these methods to the grass powdery mildew *B. graminis* has allowed these researchers to disentangle a complex evolutionary trajectory that includes coevolution between pathogen and host, host jumps, and fast radiations. In the recent times, *B. graminis* has evolved eight distinct *formae speciales* (ff. sp.) that display strict host specialization.

During the past few years, powdery mildew has emerged on triticale, the artificial intergeneric hybrid between wheat and rye in the early 2000s in many locations, probably due to a host range expansion of the wheat forma species, *Blumeria graminis* f. sp. *tritici.* Many triticale cultivars have been found to be highly susceptible to powdery mildew, mainly in seedling stage, revealing a probably narrow genetic basis for powdery mildew resistance genes (Pm). Moreover, as *Blumeria graminis* is an obligate biotrophic fungus, it is very time consuming and difficult to maintain powdery mildew isolates for a nonspecialized laboratory and evolution of populations can occur. Interspecific crossing of wheat, resistant to powdery mildew in seedling stage, and rye has been initiated to introduce potentially interesting genes for resistance in triticale. Troch et al. (2014) utilized *B. graminis* isolates sampled from triticale, wheat, and rye from different breeding regions in Europe. Pathogenicity tests showed that isolates collected from triticale are highly pathogenic on most of the tested triticale cultivars. Moreover, these isolates were also able to infect several wheat cultivars (their previous hosts), although a lower aggressiveness was observed compared to isolates collected from wheat. Phylogenetic analysis of nuclear gene regions identified two statistically significant clades, which to a certain extent correlated with pathogenicity. No differences in virulence profiles were found among the sampled regions, but the distribution of genetic variation demonstrated to be geography dependent. A multilocus haplotype network showed that haplotypes

pathogenic on triticale are distributed at different sites in the network, but always clustered at or near the tips of the network. This study revealed a genetic structure in *B. graminis* with population differentiation according to geography and host specificity. In addition, evidence is brought forward demonstrating that the host range expansion of wheat isolates to the new host triticale occurred recently and multiple times at different locations in Europe.

5.2.4 Conventional and Modern Methods for Pathogen Identification

In the field of phytopathogenic fungal diagnosis, several advancements have been made. Traditional diagnosis of fungal diseases relied on visible morphological structures such as sclerotia, conidia, or mycelia found on the outer surfaces of flora or by the symptoms produced after infection by the fungal pathogens (Nezhad 2014; Tor and Woods-Tor 2017). These widely used traditional approaches including isolation, culturing, reinoculation, and biochemical as well as microscopic techniques are believed to be the foundation for diagnosis of fungal diseases (Tan et al. 2008; Sharma and Sharma 2016). These methods are time consuming and requires deep knowledge and experience in plant fungal taxonomy and pathology (Pryce et al. 2003; McCartney et al. 2003; Sharma et al. 2017). Diagnostic approaches based on antigen-antibody binding have poor affinity, sensitivity in assays, and possible interference caused by contaminants (Meng and Doyle 2002). Further, due to high inconsistency and phenotypic serological plasticity of fungi also leads to ineffective detection of fungal plant pathogens (Luchi et al. 2020). As a result, it is critical to introduce and improve innovative and efficient diagnostic methods to combat plant fungal diseases. Hence, plant-fungal diagnosis has shifted toward molecular methods which are rather more useful in pathogen identification and quantification. Moreover, molecular assays can solve the limitations of traditional and serological approaches.

In context to early plant disease detection, polymerase chain reaction developed in the mid-1980s has proved to be a fundamental technique in molecular biology. PCR allows small amounts of the DNA fragments to be amplified in a semi-conservative way (Mullis and Faloona 1987) and determination of taxonomical status of fungal isolates. Detection techniques are mainly based on the presence of specific fragments of fungal DNA or the amplicons. A primer pair was developed by Zeng et al. (2008) to amplify *B. graminis* f. sp. *tritici* DNA. Chen et al. (2015) used BF-F1/R PCR primers to create a single 464-bp product for multiplex detection of three pathogens. Later, a nested PCR assay was designed by Zeng et al. (2010). Its sensitivity was increased by using external and internal primer pairs. The internal transcribed spacer (ITS) DNA marker is commonly used for fungal identification, but only three of four powdery mildew samples yield a clear result. In contrast to ITS, some genes provide improved identification, according to a search for new markers (Kashyap et al. 2017). Others fail because of problems with amplification and sequencing, as well as a lack of insightful variability. Some of the powdery

mildew species are easy to see but hard to identify. There is room for improvement in current identification and phylogenetic reconstruction methods. With varying degrees of success, working protocols for amplification and sequencing of seven genes (actin, tubulin, calmodulin, Chs, elongation factor 1- [EF1-], Mcm7, and Tsr1) have been established. When used alone and in conjunction with ITS, Mcm7 proves to be the most useful for phylogenetic reconstruction of closely related, phylogenetically young, powdery mildew species. As a result, Elingham et al. (2019) recommended that Mcm7 in addition to the ITS be used as the most appropriate candidate gene for powdery mildew diagnostics. Even though molecular diagnostic approaches have advanced significantly in recent years, there is still a long way to go in terms of their development and application in plant diseases. Aside from the aforementioned methods and technologies, studies using artificial intelligence for plant disease detection have begun to emerge (Singh and Sharma 2020).

5.3 Identification of Resistance to Wheat Powdery Mildew

Genes for resistance to wheat powdery mildew, whether qualitative or quantitative are termed Pm genes. Artificial inoculations in controlled environments of greenhouses or growth chambers are mostly used to carry out genetic studies on race-specific Pm genes. Isolates are multiplied under most appropriate conditions in a growth chamber and, thereafter, used to inoculate wheat seedlings growing under greenhouse conditions (Hua et al. 2009; Li et al. 2009). This method ensures the elimination of variation in disease reaction response that can be observed due to the heterogeneity of the pathogen population in the field, but has limitation of interpretation of results to a single isolate or to a small sample of isolates. Because *B. graminis* f. sp. *tritici* is an obligate parasite, propagation of inoculum can only be done on living plant tissues. Individual isolates with known virulence spectrum are usually maintained on detached segments of leaves of universally mildew-susceptible wheat variety. The leaves are floated on agar medium amended with a low concentration of the fungicide benzimidazole, which slows leaf senescence (Parks et al. 2008). Isolates can also be increased on seedlings grown in pots enveloped in plastic bags with a small opening at the bottom for gas exchange. Powdery mildew spores are short lived but have a short generation time (approximately 1 week) and can reproduce in very large quantities (Bushnell 2002).

5.3.1 Types of Resistance

Genetic resistance is believed to be the most useful, cost-effective and environmentally sustainable method of controlling powdery mildew. Different plant resistance levels to a particular pathogen species are determined largely by how the pathogen interacts with the host, which can be broad spectrum (e.g., quantitative basal resistance) or race specific (R gene-based resistance). In this sense, race-specific resistance is often related to life-long immunity and reflects resistance at all times,

while quantitative resistance is typically effective only after seedling stage. There are, however, certain instances in which such laws do not apply. The nucleotide-binding site leucine-rich repeat (NLR) type receptors are a well-known class of resistance proteins encoded by plant R genes (Deyoung and Innes 2006; Jones and Dangl 2006). Wheat powdery mildew resistance gene, *Pm21,* generates a standard NLR protein, but it confers broad-spectrum Bgt resistance at both seedling and adult plant levels (He et al. 2018). Some genes, such as the adult-plant resistance (APR) gene, LR22a, are involved in quantitative resistance. However, this gene also encodes an NLR protein (Thind et al. 2017). Furthermore, in wheat lines carrying Pm6 and Pm8, decoupling of race-specific resistance and life-long resistance was observed, with resistance present at the adult plant stage but not at seedling stage (Golzar et al. 2016). Since few Pm genes have been sequenced and understanding of the genetic basis underlying quantitative resistance to disease is still in its early stages, resistance modes included in resistance breeding schemes (Ning and Wang 2018) are commonly referred to as race-specific resistance or broad-spectrum resistance.

In plants, reactive oxygen species (ROS) play an important role in their response to biotic stress. The disparity in subcellular localization of H_2O_2 and O_2 between two powdery mildew susceptible and resistant wheat cultivars was found to be correlated with different downregulation of the genes accounting for superoxide dismutase and catalase. These findings indicated that reactive oxygen species (ROS) are involved in the process of cell death in wheat roots caused by the powdery mildew fungus.

5.3.2 Race-Specific Resistance

The existence of a major resistance gene (R gene) and cognate pathogen avirulence gene (Avr gene) causes race-specific resistance (Flor 1971), and this has proven to be the underlying theory for resistance breeding in wheat for several decades (Wang et al. 2005; Lillemo et al. 2010; Shamanin et al. 2019). Regardless of plant level, the resistance (R) gene codes for a receptor that is activated by a pathogen effector. The dominant R gene and dominant Avr gene are predicted to produce a resistant outcome, while the interaction of a recessive allele in one or both of the host and pathogen leads to susceptibility. Only six (*Pm2*, *Pm3*, *Pm8*, *Pm17*, *Pm21*, and *Pm60*) of the collection of powdery mildew resistance (R) genes (*Pm* genes and temporarily assigned genes) and alleles reported in the wheat genome have been cloned so far, all encoding NLR class proteins. (Yahiaoui et al. 2004; Cao et al. 2011; Hurni et al. 2013; Sánchez-Martín et al. 2016; Xing et al. 2017; He et al. 2018; Singh et al. 2018; Zou et al. 2018; Kang et al. 2020). The host still has complete resistance to the pathogen as a result of the gene-for-gene interaction. When the prevailing pathogen genotype alters, however, R gene resistance is no longer reliable. As a result, race-specific resistance genes often trigger "boom–bust" disease cycles over time, with the disease being dominated by a new gene for a period of time before being resolved by adaptation in the plant pathogen. Strategies based on gene pyramiding with a variety of *Pm* genes simultaneously, regional distribution, or

temporal allocation of R genes are suggested for robust breeding to extend the durability of race-specific resistance (Li et al. 2014; Burdon et al. 2014). Because of the genetic variation in the pathogen population, the concurrent existence of various pathotypes in natural surroundings increases the risk of disease outbreak. As a result, pyramided genotypes can fail to stop pathogenic intrusion for extended periods of time and ultimately become ineffective once these genes are overcome. In plant breeding, allele mining has been proposed as a way to bring value to gene stacking (Bhullar et al. 2010b). Genetic variation in a phenotype or trait is caused by allelic diversity at a resistance locus. For example, combining lines with different alleles of a single resistance gene (*Pm3*) has demonstrated to be an effective technique for the successful and long-term use of race-specific genes (Brunner et al. 2012; Ma et al. 2016), which may be an evolutionary advantage to selection by particular pathotypes (Yahiaoui et al. 2006). Allele mining of *Pm3* gene present in wheat on chromosome 1AS resulted in the identification of 20 functional alleles. Seventeen of them have been cloned. These 17 alleles share 97% of the homology (Yahiaoui et al. 2006; Bhullar et al. 2010a). Comparative analysis between *Pm3* loci of wheat and two rye (*Secale cereale*)-derived powdery mildew resistance genes *Pm17* and *Pm8* suggests that *Pm17* and *Pm8* of the 1RS translocation are evidently allelic and are orthologous to *Pm3* (Singh et al. 2018). In addition, allele mining of *Pm17*/*Pm8* is a powerful indicator of the enhancement of the wheat powdery mildew gene pool by introgression of various rye germplasm alleles.

Evolutionary study suggested that *Pm3* alleles originally come from *Pm3CS*, a susceptible allele in domesticated tetraploid wheat and widely found in bread wheat cultivars (Yahiaoui et al. 2006). Transgenic lines with *Pm3* allelic series gave greater resistance to powdery mildew in field tests compared to parental lines with only one *Pm3* allele (Koller et al. 2018). This increase in resistance came from an allelic conjunction and an additive interaction of alleles.

5.3.3 Quantitative (Broad-Spectrum) Resistance

Arbitrary terminology for quantitative resistance includes the terms "partial resistance," "horizontal resistance," "background resistance," "slow-mildewing," or "APR" to represent resistance in plants after seedling stage (Bennett 1984; Tucker et al. 2007). Thus, unlike race-specific resistance, quantitative resistance has very distinct characteristics. This type of resistance does not often result in a total absence of infection; instead, it lessens fungal sporulation and duration of infection (Poland et al. 2009). Quantitative trait locus (QTL) mapping is an effective method of detecting quantitative resistance to powdery mildew. Over 100 Bgt QTLs have indeed been mapped to homoeologous groups from various molecular mapping studies, some of which are positioned at the same marker intervals (Kang et al. 2020). New QTL identification is still predicted to boost with the development of a high-resolution genetic map aided by genome-wide genotyping markers. The single nucleotide polymorphisms (SNPs) array provides a high-performance platform for the molecular breeding of quantitative traits and is effective for the discovery of

genetic variants. They have been used to map the disease resistance loci and identify four QTLs in the elite wheat line Zhou8425B (Jia et al. 2018).

A fully sequenced and annotated wheat genome (Appels et al. 2018) will also help in the future to explore certain functional gene groups underlying powdery mildew QTLs mapped to a similar region. Most studies have found that quantitative resistance is more durable and robust than qualitative resistance to pathogen evolution, provided that there is almost no selection pressure on the pathogen (Liu et al. 2001; Li et al. 2014). Some powdery mildew APR genes provide broad efficacy to multiple pathogens, a trait much desired by breeders.

Isolation of the APR genes, *Pm38* and *Pm46,* found a single gene encoding the ATP-binding cassette (ABC) transporter (Krattinger et al. 2009) and the hexose transporter (Moore et al. 2015), respectively, at the multipathogenic resistance locus, which imparts dual resistance to wheat leaf rust and strip rust along with powdery mildew. Besides these, many other ground-breaking findings highlight the relevance of ABA and sugar signaling in modulating plant immune systems not mentioned in the zigzag model. The complex genetic basis makes it difficult for breeders to manipulate quantitative resistance. If quantitative resistance has an impact on basal nonhost defense, then it is fair to expect that it will be more durable (Mundt 2014). Johnson (1981) assumed that the forecasting of durability is complicated to implement because the interpretation is made after the allocation of the cultivar to a favorable environment. As a result, a plant breeder does not know how a cultivar will perform in the long term until a multiyear field trial is conducted.

Multifaceted genetic interactions of race-specific resistance and quantitative resistance to powdery mildew are normally found to co-exist in a given cereal cultivar (Miedaner and Flath 2007). Some studies have already reported that the promising durability of qualitative R genes can be boosted when combined with quantitative resistance (Brun et al. 2010). This provides a commitment for breeding cultivars with long-lasting resistance, taking advantage of both types of resistance, but yielding far beyond additive benefits. But the assessment of the genetic effects in the blending of both types of resistance in a cultivar is difficult because quantitative resistance can only be evaluated when the host lacks qualitative resistance genes (Miedaner and Flath 2007; Burdon et al. 2014).

5.3.4 Recessive Resistance

Resistance genes or QTLs have been considered to confer resistance to disease, but susceptibility genes have also been identified to control disease reactions in plants. Silencing of these susceptibility factors has also been proven to contribute to resistance to powdery mildew in monocots and dicots (Consonni et al. 2006; Wang et al. 2014; Appiano et al. 2015; Pessina et al. 2016). *MlO* (Mildew-Locus-O) is a very well-explored type of powdery mildew susceptibility gene. It was first reported in barley toward *Blumeria graminis* f. *hordei* (Bgh) in 1942. The recessive mutation of the *MlO* gene is observed as an efficient and durable source of resistance (*MlO* resistance) to Bgt. In barley, the *mlo*-mutated gene has conferred resistance to

most Bgh isolates for more than 30 years (Jorgensen 1992). However, hardly any natural incidence of a *mlo* gene has been noticed in wheat (Acevedo-Garcia et al. 2017).

Recently, *TaMlo* mutants have been produced on the basis of different technologies, all showing good resistance to Bgt (Wang et al. 2014; Acevedo-Garcia et al. 2017). *Mlo* genes are largely conserved in the plant kingdom, with comparative studies showing that wheat and barley have conserved similarity in the genome structure. Similarly, host-specific pathogens Bgt and Bgh also coevolved with each host and showed gene collinearity (Mayer et al. 2011; Oberhaensli et al. 2010). The functional annotation of barley *Mlo* genes should be able to assist in the exploration of wheat mlo-based resistance, as *TaMlo* shows approximately 88% similarity to barley (Elliott et al. 2002).

Powdery mildew-specific resistance separates *MlO* from another type of negative regulator, enhanced disease resistance 1 (EDR1) (Zhang et al. 2017b), a mutation that also causes powdery mildew resistance but exhibits more general resistance (Huckelhoven 2005). EDR1 resistance is another type of disease resistance mechanism, where mutation also causes resistance to powdery mildew. Zhang et al. (2017b) created *Taedr1* mutants by editing wheat EDR1 with regularly interspersed short palindromic repeats/CRISPR-associated 9 (CRISPR/Cas9) technologies. Bgt resistance exhibited by the mutant plants, thus, generated was found to be independent of mildew-induced cell death. This study clearly highlights the possibility of using EDR1 as an ideal target for improving resistance to powdery mildew through the use of new genome-editing tools.

5.4 Breeding and Deployment of Wheat Powdery Mildew Resistance

5.4.1 Management Strategies: Deployment of Wheat Powdery Mildew Resistance

Due to the significant yield-limiting economic effects of powdery mildew, the improvement of disease resistance is given due importance in most wheat breeding programs worldwide. During the 1996 survey, it was reported that powdery mildew resistance was one of the top four genetic disease resistance priorities in 115 winter and voluntary wheat breeding programs worldwide (Braun et al. 1997). Powdery mildew fungi of cereals are considered by the Fungicide Resistance Action Committee (FRAC) to be plant pathogens at high risk of developing fungicide resistance (FRAC 2005). It is, therefore, particularly important to ensure a broad and effective genetic basis for resistance in cultivars to this disease. Breeding of resistant cultivars is considered to be the most economically sound and environmentally safe method of eliminating the use of fungicides and reducing crop losses due to powdery mildew. The most common breeding strategy was the use of major genes conferring hypersensitive resistance types. This form of resistance, also known as race-specific resistance, follows the gene-for-gene model (Flor 1955), in which a corresponding

avirulence gene (Avr gene, now often referred to as elicitor) is present in the pathogen for each resistance gene (R gene) in the host plant. The interaction between the host R gene and the pathogen Avr gene determines whether there will be a compatible (susceptible) or incompatible (resistant) reaction in the host.

Temporal and spatial continuity in the use of cultivars with race-specific resistance genes generally provides immunity or near disease immunity, but exerts selection pressure on the pathogen population. This causes the pathogen to develop corresponding virulence, which reduces the life span of these cultivars to a few years. This scenario occurred with most commercially grown wheat varieties (McDonald and Linde 2002). Increased virulence and changes in virulence frequency are strongly influenced by resistance genes borne by cultivars grown in a particular area. Major genes can confer more long-lasting resistance to disease if they are deployed using disruptive directional selection. Simultaneous deployment of different *Pm* genes using cultivar mixtures (Mundt 2002), isolines with different resistance genes (Zhou et al. 2005), or pyramiding different major genes into a single cultivar (Liu et al. 2000) increases the number of mutations needed in the pathogen population to overcome all existing host resistance genes.

Use of cultivar mixtures should be the ideal target for the control of powdery mildew due to the relatively shallow dispersal gradient of the mildew pathogen and the large number of pathogen generations per crop season. Manthey and Fehrmann (1993) reported that the levels of infection with powdery mildew, leaf rust, and striped rust were significantly reduced with the use of cultivar mixtures and the greatest reduction in disease development was observed for powdery mildew. Zhou et al. (2005) have developed near-isogenic lines (NILs) with powdery mildew resistance using molecular markers. Amplified fragment length polymorphisms (AFLPs) were used to assess the similarity of NILs to their recurrent parent, and AFLPs and Pm-linked microsatellite markers were used to select powdery mildew resistance.

Pyramiding multiple resistance genes in local cultivars is an effective strategy to increase the durability of powdery mildew resistance. Three powdery mildew resistance gene combinations *Pm2* + *Pm4a*, *Pm2* + *Pm21*, *Pm4a* + *Pm21*, and *Pm4a* + *Pm21* have been successfully integrated into the elite wheat cultivar "Yang158" by means of markedly aided pyramiding (Liu et al. 2000). In another example, Murphy et al. (2009) reported 13 two-gene and 6 three- and four-gene pyramids, developed using a combination of marker-assisted selection and duplicate haploid technologies. The combination of various resistance genes in a single genetic background is expected to provide broad-spectrum resistance through individual gene action and complementation between resistance genes. However, the detection and screening of several resistance genes in the same population at the same time as conventional methods are hardly applicable in practice. Recently, Koller et al. (2018) reported that the combined effects of enhanced total transgene expression level and allele-specificity combination in transgenic allele-pyramided *Pm3* wheat lines resulted in improved powdery mildew field resistance without negative pleiotropic effects. All four allele-pyramided lines exhibited strongly enhanced powdery mildew resistance in the field compared to the parental lines.

5.4.2 Mapping of Powdery Mildew Resistance Genes

In 1930, Australian researcher Waterhouse discovered the first powdery mildew (Pm) resistance gene in wheat in the wheat variety "Thew" (Zeller 1973). New powdery mildew resistance genes have been discovered in common wheat and wheat relatives since then. Meanwhile, the inheritance properties of the powdery mildew resistance genes and chromosome positions have been extensively studied (Bhullar et al. 2010a, b; Brunner et al. 2012; Hanusova et al. 1996). Over 91 Pm resistance genes have been identified so far, with 61 loci mapped to them. Apart from these, new genes are continually been searched and described in common wheat and its different relatives (Hao et al. 2015; Li et al. 2017, 2019a, b, c; Tan et al. 2019; Zhang et al. 2017a, b). These genes provide protection for the wheat crop at the seedling stage or at the adult plant stage. However, only a few of them have been widely used in the development of disease-resistant wheat cultivars. For example, Pm8 was introduced from rye in the form of wheat rye 1BL:1RS chromosome translocation. Wheat cultivars such as Kavkaz, Lovrin 13, and Aurora, all having *Pm8* gene have been extensively used as parental lines in wheat improvement programs due to their efficacy against powdery mildew, high yielding ability, and broad genetic base from the time they were first introduced into China in the 1970s. *Pm8* has been incorporated into local wheat genotypes, resulting in the production of a number of commercial wheat cultivars that are locally adapted. Another important Pm gene used in wheat improvement programs is *Pm21*, which is derived from *Haynaldia villosa* L. (Li et al. 2007). With the exception of the fewest, most known Pm genes, especially those derived from closely or distantly related wheat species which have not been used in the wheat breeding programs due to the presence of linkage drag, resulting in decreased agronomic importance. Strong efforts are needed to improve their agronomic scores, increase their yield potential, and eliminate other undesirable traits. As a result, breeders prefer to use Pm genes identified from improved genetic backgrounds with promising agronomic performance. Several *Pm* genes have been identified in Chinese wheat cultivars, such as Yumai 66 (Hu et al. 2008), Zhoumai 22 (Xu et al. 2010), Liangxing 66 (Huang et al. 2012), and Tangmai 4 (Xie et al. 2017). The *Pm* genes in the widely cultivated Jimai 22 (*PmJM22*) and Liangxing 99 (*MlLX99*) wheat cultivars were localized on 2BL chromosome (Yin et al. 2009; Zhao et al. 2013). The *MlLX99* was permanently designated as *Pm52* (McIntosh et al. 2014). A saturated generic linkage map of *Pm52* has recently been established (Wu et al. 2019), which allows the target gene to be precisely detected. *Pm52* was effective against 81% of 123 Bgt isolates from different regions of China (Zou et al. 2017) and 94% of another 49 Bgt isolates from Northern China (Ma et al. 2018).

Various types of mapping populations such as F_2 population, $F_{2:3}$ populations, backcross (BC), recombinant inbreed lines (RILs), near-isogenic lines (NILs), double haploid (DH), and inbred lines (ILs) can be used for mapping purposes. $F_{2:3}$ population is the result of the generation of single-generation F_2 individuals. Like the F_2 populations, they are also of a mortal nature. Neu et al. (2002) developed a population of F_2 to map the *Pm1a* allele of the *Pm1* gene. The *Pm2c* gene was

mapped to the F_2 population (Xu et al. 2015). Dong et al. (2020) used the F_2 population to map the *Pm57* gene in *Aegilops searsii*. Genes *Pm59*, *Pm63*, *Pm64*, and *Pm65* have been mapped using populations of F_2 and $F_{2:3}$ (Tan et al. 2018; Li et al. 2019a, b, c; Tan et al. 2019; Zhang et al. 2019). The backcross (BC) population is formed by crossing the F_1 hybrid with one of its parents. They also need less time to generate. BC population has been used to map several powdery mildew resistance genes, such as *Pm4c*, *Pm43*, and *Pm2b* (Hao et al. 2008; He et al. 2009; Ma et al. 2015). Recombinant inbreed lines (RILs) are the result of continuous inbreeding of individual members of the F_2 population until complete homozygosity is achieved. They are immortal in nature and are important for the purposes of QTL mapping. However, they require a number of seasons to develop.

Chhuneja et al. (2012) mapped two powdery mildew resistance genes, *PmTb7A*.2 (new allele of *Pm1*) and *PmTb7A*.1 in *T. boeoticum* acc. *pau5088*, using the RIL population. The *Pm49* gene has also been mapped using the population mapping of the RILs by Piarulli et al. (2012). Hao et al. (2015) used RILs population to map the *Pm54* gene in soft red winter wheat. Similarly, near-isogenic lines (NILs) can also be generated by repeated backcrossing of the F_1 hybrid with the recurrent parent. Such lines may be helpful in tagging genes for powdery mildew resistance, which are generally monogenic. For example, Tao et al. (2000) mapped *Pm6* gene on the chromosome 2BL using NILs population. Nematollahi et al. (2008) successfully used NILs population for mapping of *Pm5d* gene. *Pm4e* gene has also been mapped with NILs mapping population (Ullah et al. 2018).

Mapping of resistance genes facilitates in locating a particular gene on the chromosome. There are a large number of powdery mildew resistance genes in wheat, which have been mapped using different molecular markers. These markers tend to cosegregate with the gene of interest. With the development of markers tightly linked with the gene, we can screen population for marker which ultimately linked to the resistance gene that aids in marker-assisted selection. Already many powdery mildew resistance genes have been labelled with molecular markers. Singrun et al. (2003) found that SSR and AFLP marker, GWM344-null–S13M26–372, was linked to an allele of *Pm1* gene, *Pm1e,* with a genetic distance of 0.9 cM and 0.2 cM, respectively. Ma et al. (2014) used F_2 population for tagging of Pm4a powdery mildew resistance gene using SSR markers and reported that *Xgwm356*, SSR marker, was closely linked to the gene and can be used for marker-assisted selection. Nematollahi et al. (2008) developed NILs population for screening of markers linked to the allele of *Pm5* gene, *Pm5d,* and observed that *Xgwm611* and *Xgwm577* were at genetic distance of 2.1 cM and 2.0 cM from gene, respectively. Luo et al. (2009) reported that the close flanking SSR marker, *Xgwm297,* with genetic distance of 0.4 cM will enable marker-assisted transfer of *Pm40* gene into wheat breeding populations. The closely linked molecular marker, BF146221, congregated with *Pm42* gene (Hua et al. 2009). *Pm6* was found to be closely linked with STS markers; *CINAU127*, distally at 1.1 cM, and *CINAU123*, proximally at 0.1 cM distance (Qin et al. 2011). The Pm46 gene was located on the 5DS chromosome and flanked by SSR markers *Xgwm205* and *Xcfd81* at 18.9 cM apart (Gao et al. 2012). *MlIW172* resistance gene was found closely linked to the *Xpsr680*

RFLP probe derived from the *Xmag2185* STS marker and the BE405531 and BE637476 EST markers (Ouyang et al. 2014).

Bulked segregant analysis showed that multiple simple sequence repeat (SSR) markers, *Xgwm499* and *Xwmc759,* flanked the *Pm53* gene with 0.7 cM proximally (Petersen et al. 2015). Tan et al. (2018) developed STS markers – *Xmag1759* and *Xmag1714* – that are tightly linked to *Pm59* gene with a genetic distance of 0.4 cM on the distal side and 5.7 cM on the proximal side. *Pm61* was positioned in a 0.71 cM genetic interval and can also be observed in a high-throughput scale by the *Xicscx497* and *Xicsx538* SSR markers (Hu et al. 2019). Recently, *Pm57* was physically mapped on the long arm of $2S^{s}$#1chromosome of *Aegilops searsii* and was flanked by markers *X67593* and *X62492* (Dong et al. 2020). These markers will allow the efficient utilization of genes to the wheat breeding program, thus contributing to its genetic diversity.

5.5 Challenges

The current populace of 7.6 billion individuals on the planet is assessed to rise to 10 billion by 2050. With quick populace development, the world has grown exponentially in cities and the extent of nourishment producers for food consumers has dropped drastically. This has put weight on food generation around the world, but escalated, proficient agricultural production has met these needs. There is, however, a genuine concern that the anticipated increment in demand for planted crops up to 70% over the following 30 to 40 years cannot be met with expanded efficiency utilizing current crop varieties and cultivating practices.

Moreover, the Earth's climate has undergone major changes since the industrial revolution and is anticipated to change even more in the near future (Pachauri et al. 2014). For illustration, the worldwide mean surface air temperature has expanded by 0.74 ± 0.18 °C over a 100-year period (1906–2005) and is anticipated to rise by an extra 1.0–3.7 °C by the end of the twenty-first century, owing to the aggregation of nursery gasses (Anderson et al. 2016; Deryng et al. 2014; Huang et al. 2017; Jiang and Fu 2012; Pachauri et al. 2014; Solomon et al. 2007). Climate change too has been applying a noteworthy effect on the event and epidemics of crop pests and infections (Coakley et al. 1999; Fischer et al. 1995; Goudriaan and Zadoks 1995; Rosenzweig and Parry 1994; Rosenzweig et al. 2001).

In this context, wheat powdery mildew (caused by *Blumeria graminis* f. sp. *tritici*) has ended up becoming one of the foremost vital wheat diseases due to changing climate conditions, vulnerability of developed varieties, extensive irrigation, and utilization of nitrogen fertilizers (Cao et al. 2010; Cao et al. 2015; Shen et al. 2015). The frequency dispersion of *B. graminis* f. sp. *tritici* segregates with distinctive temperature sensitivities shows that the pathogen populaces have been impacted by selection pressure from changing temperature. In this way, given the seriousness of wheat powdery mildew, the association of pathogens and climate alterations, and current understanding of the conditions beneath which wheat powdery mildew flourishes, it is imperative to explain the impacts of climate alterations

on plagues of wheat powdery mildew. Plant growth at higher nitrogen accessibility may result in expanded disease severity (Mitchell et al. 2003) since the utilization of nitrogen fertilizer may result in a denser canopy and a more sticky microclimate (Bremner 1995). Moreover, this issue ought to be considered to decide the relationship between wheat powdery mildew plagues and changing climate under the biological systems utilizing high nitrogen.

Biodiversity preservation is another major challenge confronting cereal breeders within the twenty-first century. High yield and other desirable agronomic characteristics are the main needs of advanced wheat breeding programs, which is frequently related to a chance of losing hereditary differences for disease resistance. In conventional farming, agriculturists plant a variety of crops that ordinarily have an expansive supply of interesting genotypes. The large-scale development of high yielding varieties and their monoculture has driven an undesirable misfortune in crop hereditary diversity. Conventional crops have the most elevated gene diversity and as they wane, those genes disappear. These hereditary diversity losses can be seen all over the world in areas that actualized green revolution farming strategies. Modern bread wheat (*Triticum aestivum* L.) varieties ought to have high yields, high protein substance, as well as high resistance to biotic and abiotic stresses. High-yielding varieties of bread wheat seem to account for up to 90% of wheat production around the world within the twenty-first century. In any case, only a restricted number of local varieties, a number of which are closely interrelated, can be utilized as breeding materials, which limits down the diversity of gene pool of bread wheat. For this reason, closely related taxa of T. aestivum are progressively utilized for advancement of new varieties with alluring agronomic characteristics, high dietary esteem, handling quality, as well as resistance to the economically critical parasitic pathogens. Hexaploid spelt (*Triticum spelta* L.) one of the closely related taxa, for all intents and purposes, having no crossing obstructions with bread wheat, which empowers the generation of fertile and steady hybrids characterized by superior grain quality and resistance to pathogens compared to bread wheat.

Two primary avenues for expanding crop efficiency are, namely, the arrangement of genetically predominant crop varieties and other, by selection of better management practices, which ought to be tended in parallel to provide a step change in efficiency comparative to what was accomplished through green revolution. Green revolution depicts the colossal increment of grain yield related with improved genetics and application of plant protection chemicals and mineral fertilizers. Whereas it took nearly 10,000 years for people to create 1 billion tons of grain universally, the green revolution led to multiplying of that amount in just 40 years between 1960 and 2000. The appearance of smaller, more stable varieties with a higher gather record went accompanied by a few positive impacts, counting a progressed allotment of supplements and assimilates to the grains and a reduction in leftover plant biomass.

Intercropping is supplanted by monocropping, a wide difference of species is replaced by a small number of commercial assortments. As a result, the awesome genetic diversity inside the same crop species is replaced by a narrow hereditary range of fiscally lucrative varieties. The net effect of these and other practices has

been an enormous uprooting of innate seed varieties, such that within the case of most major crops now, the larger part of indigenous cultivars are not developed. Hence, due to a limited genetic base of the current Indian wheats with regard to the resistance range (most of the high-yielding wheat assortments infer their resistance to rusts and fine buildup from the 1BL/1RS translocation) and intensive cultivation practices, there has been an increment in the frequency of rusts and more prominent severity of powdery mildew and other already minor maladies. Hence, green revolution brought modern challenges to sustain its growth under unused challenges of genetic defenselessness to maladies and disease management with environmental contemplations.

5.5.1 Linkage Drag Associated with Introgression of Exotic Resistance Alleles Using Conventional Breeding

Routine breeding is still the foundation within the trim enhancement pipeline. It is conducted by crossing plants with characteristics of intrigued and selecting the offsprings with the ideal combination of characteristics. In any case, linkage drag leading to the presentation of outside chromosomal segments containing resistance can come with pleiotropic impacts since harmful qualities related to poor agronomic performance in yield or quality will also be introgressed at the side the quality of interest. Yield penalties of resistance in wheat have been detailed for Pch1 (Johnson 1992; Groos et al. 2003) and Pm16 (Chen et al. 2005). A chromosome fragment from *Aegilops ventricosa* has carried both the eyespot resistance quality Pch1 and yield-reducing qualities in wheat (Doussinault et al. 1983; Groos et al. 2003). This potential "linkage drag" incredibly puts confinements on the coordinated use of *Pm* qualities in breeding programs.

In addition, one of the major bottlenecks of plant breeding is the time it takes to create a progressed trim assortment. In this case, routine breeding strategies take numerous eras and time (ordinarily 6 years for conventional breeding of self-pollinating crops) to assess phenotypes and get the target recombination of genes, which is clearly time devouring (Cowling 2013). Indeed so, significant benefactor DNA material can still be found alongside genes of interest in eras after different backcrosses (Young and Tanksley 1989). The issue of linkage drag is exacerbated in breeding self-pollinating crops, where levels of linkage disequilibrium were found to be 200 times higher than in out-crossing crops (Rostoks et al. 2006). Additionally, the rate at which foreign segments recombine with wheat chromosomes is lower than when a wheat homoeologous partner is utilized. For this reason, confinement of resistance genes by routine map-based cloning has run into more challenges. Such challenge in hereditary illustration has been illustrated in cloning of Pm21 on the 6VS arm, beginning from the Triticeae grass *D. villosum* (Chen et al. 1995). Recombination hindrance of remote chromosome 6VS through a map-based cloning technique was not attainable for Pm21 (Qi et al. 1998). More noteworthy exactness in mapping the physical area of resistance genes is undoubtedly vital for distinguishing candidate genes, and the position of embedded alien segments within

the wheat genome too accounts for effective improvement of the crop (Dundas et al. 2007).

The improvement of cytogenetic stocks made a difference to find Pm21 and recognized a serine/threonine kinase gene Stpk-V upgrading powdery mildew resistance (Cao et al. 2011). However, it was dubious in case Stpk-V gene that whether a candidate gene or set of genes at the Pm21 locus is responsible for developing resistance. This speculation was upheld by the proven fact that Stpk-V silencing did not totally compromise resistance of Pm21 (Cao et al. 2011). Later work advance substantiates the theory where two commonplace NLR qualities, DvRGA2 (He et al. 2018) and NLR1-V (Xing et al. 2018), were found as candidates for Pm21 and are likely allelic. Subsequently, plant breeders and analysts around the world are creating unused advances and approaches to assist speed up of the productivity of crop breeding.

5.5.2 Fungicide Resistance

Cereal mildews have an inherently high resistance risk because of their remarkable ability to adapt to fungicide treatments. Currently, resistance in mildew to quinone outside inhibitors (QoIs) is high across Northern and Western Europe. Following an initial shift toward reduced sensitivity, the sensitivity pattern to the morpholines and DMIs has remained stable for several years. Isolates with reduced sensitivity to quinoxyfen have been found in Europe with reports of reduced performance. Isolates with reduced sensitivity to metrafenone have been found but field performance remained good. Good resistance management strategies should be followed by applying fungicide before the disease becomes severe, rotating fungicides, and not using more than two sprays of any product per season. But the initial genetic changes (or "gateway" mutations) in wheat powdery mildew strains will always be a threat leading to fungicide resistance issues in powdery mildew management.

5.5.3 Fast Jump: Expansion of the Host Range Due to Pathogen Diversity

Climate change is a generic term that explains the recent and forecasted change in multiple environmental factors. Most of them, including atmospheric CO_2 concentration, temperature, and the frequency and amount of precipitation, affect plant growth. Beyond the temperature optimum, which is very crop and variety specific, higher temperatures result in heat stress, which is considered a major cause of wheat yield loss in developing countries. It has been estimated that each °C increase leads to a decrease in global wheat production by 6%. Increasing temperature can also indirectly affect crop yields due to an increased occurrence of pests and diseases.

5.6 Prospects for Broadening the Genetic Basis of Host Resistance

Need to feed a rapidly growing population in the face of visibly changing climate has raised concerns for global food security. In times of rapid population growth and visibly changing climate, the rate of improvement of genetic yield potential and resistance against fast evolving plant pathogens has to be increased beyond current rate achieved by the ongoing breeding programs to protect global food security. While plant breeding has been very successful and has delivered today's highly productive crop varieties, the rate of genetic improvement must double to meet the estimated future demands. For this, a set of new approaches are needed to accelerate the crop breeding process.

In a broader sense, any breeding program can be broadly classified into three main processes: (1) the creation of new genetic variation, (2) the selection of best individuals based on set objective of improvement, and (3) the evaluation, multiplication, and release of improved crop varieties. The conventional way of creating new genetic variation is to attempt targeted crossing between selected individuals to create desirable segregants and further to identify genetically superior individuals from typically large populations of genotypes. Longer generation times taken in conventional breeding represent a major bottleneck for crop breeding, apart from multiple breeding cycles, especially due to time-consuming line fixation. For self-pollinating crops (i.e., wheat), usually six to eight generations are expected for genetically heterogeneous breeding lines to reach fixation (Lenaerts et al. 2019). Further, after release of a variety, the adoption of poor or suboptimal management practices in farmers' fields results in a yield "gap," where the potential yields of varieties are not realized. Therefore, closing the yield gap between potential and realized yields is considered a challenging and high-priority goal for enhancing productivity and global food security.

For most important crop species, modern selection strategies have been developed that incorporate genome information based on next-generation DNA sequencing technologies in the breeding process. Modern plant breeding programs have become highly multidisciplinary involving genetics, biochemistry, physiology, bioinformatics, molecular biology, statistics, agronomy, and economics as well. Advances in DNA sequencing technologies have revolutionized plant breeding research, opening up the "genomics era" of crop improvement. Very cost-efficient genotyping platforms to "DNA fingerprint" plants have been developed and whole-genome reference DNA sequences are available for most important crop species. Single nucleotide polymorphisms (SNPs) have become the markers of choice because of being ubiquitous in plant genomes and very easy and cost-efficient to score. It has, therefore, become common practice in modern crop breeding to genotype large populations of plants with several thousands of markers on a routine basis. Whole-genome sequencing data are becoming increasingly available. Large amounts of genotype data are being increasingly used for various purposes using the latest statistical genetics approaches.

5.6.1 Utilizing Exotic Sources for Resistance

High yield and other desirable agronomic traits are the most important priorities of recent wheat breeding programs, which are often related to a risk of losing genetic diversity for disease resistance. Wheat relatives possess untapped diversity for mildew resistance. In this context, interspecific hybridization for introgressing disease resistance genes from wild distant relatives is effective for breeding more resilient cultivars. Among close and wild relatives of *Triticum aestivum*, rye and *Dasypyrum villosum*, respectively, are used for transferring a spread of resistance genes against mildew and rust fungi (Graybosch 2001; Chen et al. 2013; Li et al. 2018). Genes for resistance to mildew (Pm8 and Pm17), as an example, and rust (Sr31, Lr26, and Yr9) on chromosome 1RS of "Petkus" rye are successfully introduced into commercial wheat cultivars worldwide (Jiang et al. 1994; Kim et al. 2004). For *Triticum aestivum*, wild wheat, one among the progenitor species, is additionally an upscale donor of diversity of resistance to varied diseases and may be exploited for trait improvement (Huang et al. 2016). Wild species and primitive forms including wild wheat are the source of the many confirmed Pm genes. Incorporating Pm genes from wild sources into commercial cultivars has been made possible as wild wheat is crossable with both hexaploid (*Triticum aestivum*) and tetraploid durum (Rong et al. 2000; Elkot et al. 2015). Easy crossability of untamed emmer with both hexaploid *Triticum aestivum* and tetraploid durum has made it possible to include Pm genes into commercial cultivars (Rong et al. 2000; Elkot et al. 2015). On the opposite hand, landraces of bread wheat are genetically more polymorphic sources of disease resistance thanks to cultivation for thousands of years under natural environments (Talas et al. 2011; Li et al. 2016), and are rich reservoirs of adaptive traits to abiotic stressors (Reynolds et al. 2007). Compared to distant relatives, landraces are ready for direct crossing of interesting traits into new cultivars. A group of wheat landraces have exhibited highly significant resistance to mildew, formally designated as Pm2c (Xu et al. 2015), Pm3b (Yahiaoui et al. 2004), Pm5d (Hsam et al. 2001), Pm5e (Huang and Roder 2003), Pm24a (Huang et al. 2000), Pm24b (Xue et al. 2012), Pm47 (Xiao et al. 2013), Pm59 (Tan et al. 2018), Pm61 (Sun et al. 2018), Pm63 (Tan et al. 2019), and PmQ (Li et al. 2020). However, PmQ and Pm63 isolated from two different landraces, from Iran and China, are found to be located during a similar genomic region, in order that they could also be allelic. Among others, pyramiding multiple resistance genes into local cultivars is an efficient strategy to extend the sturdiness of mildew resistance. Identification of latest sources of resistance to diversify the resistance base of existing cultivars in wheat is often achieved expeditiously within the north-western Himalayan regions like states of Himachal Pradesh, where the second wheat crop is often taken in summer within the dry temperate zone. There is a requirement to specialize in utilization of diverse sources of slow mildewing resistance to Bgt. Clues might be taken from genetic analyses of durable resistance in *Puccinia graminis* diseases which indicate that effective disease control is often achieved by combining three to five minor, slow rusting genes during a single cultivar. Such resistance is predicted to supply sufficient protection to farmers' crop against all pathotypes over an extended

period. Efforts will also be needed to use molecular markers in order to identify chromosomal regions containing genes for slow mildewing resistance present within the diverse sources.

5.6.2 Marker-Assisted Selection and Precision Phenotyping

Molecular marker may be a fragment of DNA that is readily detected and whose inheritance is often monitored easily. They are located near a gene or gene of interest and are used to identify particular locations where the sequences differ among varieties. They have been successfully used to map mildew resistance genes in wheat. The identification of molecular markers linked to resistance genes could facilitate marker-assisted selection. A perfect DNA marker should generate polymorphisms indicating slight changes within the genome of two different genotypes. It should be codominant and have multiple alleles to supply adequate resolution of genetic differences among individuals/lines. As many agronomically important traits are polygenic/quantitative in nature, like yield and disease resistance, QTL mapping is used to get marker-trait association (Collard and Mackill 2008). Valuable markers are then utilized in marker-assisted breeding to screen individuals. MAS shortens the breeding cycle and has many advantages in selecting disease-resistant plants compared to phenotyping (Tanweer et al. 2015). With QTL-MAS, many genes and alleles are often introduced to commercially favored cultivars. MAS also can be combined with genomic selection (Nakaya and Isobe 2012) to form the breeding cycle simpler and efficient. Unlike traditional MAS, which mainly selects for QTLs with modest-to-large effects, an upgraded sort of MAS named genomic selection captures all minor-effect QTLs also, identifying individuals with high genomic estimated breeding value (GEBV) for the chosen traits (Desta and Ortiz 2014). It relies on genomic prediction of the likelihood of every individual to possess a superior phenotype; therefore, GEBV-based selection reduces the number of generations required (Bassi et al. 2016). Accurate, precise phenotyping plays an increasingly pivotal role for the choice of resistant genotypes and, more generally, for a meaningful dissection of the quantitative genetic landscape that underlines the resistance pattern. Evaluation of quantitative resistance requires reliable phenotyping data, and accurate genotype-phenotype association is critical for candidate gene identification. However, disease estimation by commonly adopted visual scoring is extremely subjective and error prone (Poland and Nelson 2011), and within the case of a large-scale screening, this method greatly limits efficiency and accuracy of phenotyping. MAS is essentially conducted alongside linkage mapping in family-based populations, genome-wide association mapping in natural diversity populations, and joint linkage association mapping using both sorts of populations of these mapping methods to process which requires both genotypic and phenotypic data. Obtaining reliable phenotype data is pivotal for identifying true trait-associated markers. Within the case of mildew APR, the phenotype is usually disease severity, measured either as disease index (i.e., 0–9 scale) or as percentage disease at a selected adult stage. However, the resistance response might change as plants

mature, which is seen in some powdery mildewed cereals including wheat (Carver and Adaigbe 1990; Duggal et al. 2000). This was also observed in QTL mapping of mildew resistance in mungbean, during which a QTL was found for resistance effective 85 days after sowing, while no resistance was expressed 20 days earlier (Young et al. 1993). Multiyear and environment field trials are necessary for QTL detection because it is common for a QTL identified during one year-environment scenario to not appear in another year-environment combination.

For durable resistance breeding, resistance QTLs with consistent performance over several years, environments, and plant growth would be more valuable. Given the character of the phenotypic expression of slow mildewing, the timing of scoring the phenotypes is vital for assessing the extent of resistance. Disease severity at one time point is not the sole component concerning resistance; the length of the latent period, survival percentage, and area under the disease progress curve (AUDPC) even have potential in discovery of resistance loci through these traits, very probably controlled by overlapping QTLs (Wang et al. 1994; Muranty et al. 2009; Chung et al. 2010). Inspired by this, future QTL mapping could address more of those resistance-relevant components. QTL mapping clarifies significant markers that are beyond an assigned threshold, mentioned as logarithm of odds (LOD) in linkage mapping and p value in genome-wide association studies. However, not every QTL exceeding these criteria may be a true candidate region because it could be a false positive. In linkage mapping, QTLs of mildew resistance in wheat always function with additive effects, but in some mapping studies epistatic interactions between these QTLs also appear (Goldringer et al. 1997). This confounds evaluation of QTLs because the existence of epistasis can mask latent genetic variation for quantitative traits (Mackay 2014). Development of high-throughput phenotyping technologies (crop phenomics) provides a useful set of tools for assisting precision breeding (Zhao et al. 2019). Some image-based technologies like fluorescence imaging and spectral imaging have already been demonstrated as promising diagnostic tools in detecting wheat mildew (Yuan et al. 2012; Zhang et al. 2012; Ajigboye et al. 2016).

5.6.3 Advances in High-Throughput Genotyping Technologies and Genomics

Development and application of molecular markers in crop breeding are impactful in parental selection, genetic diversity estimation, and reducing linkage drag and, thus, of paramount importance in genetic mapping and gene discovery (Rasheed et al. 2017). The genome-wide molecular markers derived from modern technologies like array- and sequencing-based genotyping have overcome the scarcity of genetic markers, and facilitated the identification of resistance genes or QTLs in mapping experiments. For instance, array-based SNP platforms improve the marker coverage and mapping resolution, and may more efficiently and accurately target R genes or define genomic regions related to quantitative traits. SNPs are important contributors to phenotypic variation (Saxena et al. 2014), and therefore, the use of a high-throughput SNP array in wheat is rapid, where a series of fixed SNP arrays were

produced in wheat from 9 K to 820 K (Cavanagh et al. 2013; Wang et al. 2014; Winfield et al. 2016; Allen et al. 2017). Alternatively, an ever-increasing throughput of next-generation sequencing (NGS) technologies is often wont to assess genome-wide diversity. It is possible to rapidly identify causal variants during a single step by using NGS (Schneeberger 2014). Embedded in genetic mappings, high-density SNP genotyping arrays and NGS have helped a substantial number of studies to molecularly detect mildew resistance genes/QTLs during a wheat panel (Liu et al. 2017a, b; Chao et al. 2019).

In spite of this, the wheat genome (~17Gb in size) remains too enormous to figure out using NGS processing especially as it is just too cumbersome due to massive size of wheat genome. To deal with this difficulty, different approaches are developed to scale back such complexity in large-genome species like wheat. Rapid isolation of resistance in wheat has been facilitated greatly with the advances in DNA sequencing and bioinformatics technologies. Exome capture and sequencing is one such approach, which greatly reduces sequencing volume and costs, while giving detailed coverage of gene coding regions or sufficient mapping information of a genomic interval containing causal gene (Mo et al. 2018). Exome capture assays are used for identification of candidate genes for plant height and resistance to leaf and yellow rust in wheat mutants (Hussain et al. 2018; Mo et al. 2018). With the prior map information of the targeted gene and isolation of individual chromosomes, targeted chromosome-based cloning via long-range assembly (TACCA) is often used. The success of this approach has been demonstrated by the isolation of Lr22a, a wheat leaf rust R gene (Thind et al. 2017). Construction of high-density maps is often bypassed by some novel isolation techniques that use mutational genomics for resistance gene cloning. Combined with chemical mutagenesis, another fine mapping-independent strategy employing exome capture and sequencing was developed to focus on NLR-type resistance genes for cloning (MutRenSeq) (Steuernagel et al. 2016). This group of researchers applied MutRenSeq for isolation of two R genes (Sr22 and Sr45) that confer stem rust resistance in wheat. More recently, a speed cloning approach using high-throughput DNA sequencing (AgRenSeq) for NLR gene enrichment was reported to spot and isolate four wheat stem rust R genes from the wheat wild progenitor *Aegilops tauschii* (Arora et al. 2019), the D genome donor of bread or hexaploid wheat.

These state-of-the art genomic technologies effectively catch up on the reduced recombination during introgression of foreign sources of disease resistance to wheat (Wulff and Moscou 2014), paving the way for fast-track identification of resistance loci and, therefore, the utilization of crop's wild relatives. The entire reference genome of hexaploid wheat (Chinese Spring) recently became publicly available (Appels et al. 2018), providing vast potential for discovery of untapped genetic resources by enabling the alignment of genetic and physical maps. Realizing the importance of genome diversity in wheat for crop improvement, ongoing sequencing efforts have also been applied to different wheat cultivar. The so-called wheat pangenome allows identification of novel genes and alleles absent within the single reference accession (Sanchez-Martin and Keller 2019). Available pangenomes of the wild relatives of wheat is of paramount relevance in wheat resistance breeding,

which facilitates identifying orthologues for the rationale that wild relative-derived R genes are usually suppressed by their orthologues in domesticated wheat (Sanchez-Martin and Keller 2019). The arrival of NGS technologies has begun to provide insights into genetic diversity for optimizing crop improvement, and also set in motion, the new landscape of pathogen study, pathogenomics, an emerging genomics era. Field pathogenomics has revolutionized crop pathogen surveillance and diagnostics, and by increasing understanding of pathogen biology, population structure, and pathogenesis offers the prospect to predict emerging epidemics (Hubbard et al. 2015; Möller and Stukenbrock 2017). This approach allows researchers to get sequencing data directly from field samples of diseased plant tissues. Moreover, it can trace pathogen evolution to tell development of suitable wheat lines with both strong and long-lasting resistance.

5.6.4 Potential of New Breeding Technologies and Transgenic Approaches

Over the past decades, a vast number of technologies have emerged, which will accelerate plant breeding efforts. Among them, genomic selection, as an example, has emerged to be a really promising modern selection strategy that comes with genome-wide DNA marker information, during which statistical models or machine learning algorithms are deployed to link genomic polymorphisms to phenotypic variation. This enables breeders to predict genotype performance as soon as DNA marker profiles are often generated (i.e., at seedling stage) employing a genomic estimated breeding value (GEBV) for every genotype. Using this approach, the time until selection decisions are being made is significantly decreased, which results in increased genetic gain per unit of your time. Till date, genomic selection has led to tremendous increases in genetic gain in animal breeding with great promises for crop improvement also. Among others, methodologies like gene editing technology are fast evolving and protocols are refined for many major crop species. In CRISPR gene editing systems, guide RNA directs the Cas9 enzyme to the target DNA site and cuts the DNA. This will be wont to activate or deactivate alleles of a target gene to reinforce plant performance, for example, through improving disease resistance or drought tolerance.Despite the promise of gene editing and powerful support from the scientific literature regarding safety and sustainability, many countries have employed strict legal restrictions favoring rejection of genetically modified food. On the other hand, a really widely used and accepted breeding method is mutation breeding, which uses chemicals or radiation to induce random mutations throughout the genome rather than genetically engineered (targeted) mutation. This is often why the bulk of the plant science community contends that mutations induced using genome editing, where no foreign DNA is introduced, should be considered a non-GM tool.

5.6.5 Genetic Engineering

Plant transformation has the advantage of having the ability to interrupt interspecific crossing barriers and provides an alternative to standard breeding methods for disease resistance that potentially can expand the available gene pool. However, the procedure is restricted to genes already cloned; extensive testing is required to make sure stability and heritability of the transgene and transformation can sometimes have a negative effect on agronomic performance (Campbell et al. 2002). Wheat, like other cereals, presents the extra challenge of not being amenable to Agrobacterium-mediated transformation (Wu et al. 2003). In comparison to biolistic procedures, Agrobacterium transformation has the benefits of providing a more precise insertion of the transgene, greater stability, and lower copy number (Meyer and Giroux 2007). Significant progress has been made in improving transformation procedures in wheat, both on biolistics (Srivastava et al. 1999) and Agrobacterium-mediated gene transfer (Khanna and Daggard 2003; Wu et al. 2003). Particle bombardment was used successfully to get transgenic wheat expressing a barley seed class II chitinase (Bliffeld et al. 1999) and a tobacco β–1,3-glucanase gene was transferred to wheat seedlings via Agrobacterium transformation (Zhao et al. 2006). In both cases, increased resistance to mildew was reported. Incorporating monogenic resistance to mildew by means of gene splicing faces an equivalent challenge as conventional breeding regarding resistance durability. Transforming wheat with several antifungal proteins to enhance mildew resistance was attempted by Oldach et al. (2001). The researchers used three proteins: the antifungal protein AgAFP from *Aspergillus giganteus*, a barley class II chitinase, and sort I ribosome inactivating protein (RIP). They found that simultaneous expression of the AgAFP and, therefore, the barley chitinase enhanced mildew resistance quantitatively, whereas the RIP gene had no effect on this disease. An alternate strategy being explored is that the use of gene splicing to control defense signaling pathways so as to activate multiple defense genes and induce the systemic acquired resistance (SAR) (Stuiver and Custers 2001). The NPR1 gene from Arabidopsis, a key regulator of SAR, was wont to engineer wheat plants with improved resistance to Fusarium blight (caused by *Gibberella zeae*) (Makandar et al. 2006). Genetic modification (GM) and genome editing are often utilized to expand the genetic tools within the hands of researchers to enhance disease resistance. GM delivers genetic improvement for wheat breeding because it enables faster transfer of resistance genes from another species compared to standard crossing and overcomes sexual barriers. Transgenic wheat lines expressing antifungal barley seed class II chitinase and exhibiting enhanced resistance against mildew (Bliffeld et al. 1999) are samples of the effectiveness of GM. Polyploid nature of *Triticum aestivum* essentially makes it challenging to get stable inheritance of traits developed by DNA editing tools to induce mutations. The advances in forward screening make it feasible. Genome editing via sequence-specific nucleases (SSN) with introduction of transcription activator-like effector nuclease (TALENs) together simultaneously edited three MLO homoeoalleles within the same wheat individual; resistance during this triple mutant is complete and heritable (Wang et al. 2014). However, TaMlo modifications caused leaf

chlorosis in plants. Limitations of the mlo mutant include the common observation of coupling to undesirable traits for instance, spontaneous leaf decay, which has been a symbol of yield penalty, the potential of enhancing sensitivity to another pathogens, and also as reduced plant size (Jarosch et al. 1999; Zheng et al. 2013; McGrann et al. 2014; Acevedo-Garcia et al. 2017). The good potential of the CRISPR/Cas9 technique for improving disease resistance makes it perhaps the best known and most generally adopted genome editing tool (Hilscher et al. 2017). CRISPR/Cas9 is demonstrated to achieve success in enhancing mildew resistance of wheat (Wang et al. 2014), tomato (Nekrasov et al. 2017), and rice blast resistance (Wang et al. 2016). It had been adapted from a naturally occuring genome editing system in bacteria, through single-guide (sg) RNA-mediated DNA mutation to manipulate and encode the new traits in plants (Knott and Doudna 2018). CRISPR/Cas9 technology does not involve the insertion of a gene from a special organism; rather, it involves gene/genome editing. Evidence of edited plant progeny freed from CRISPR genes indicated a possible strategy for producing nontransgenic crops (Char et al. 2017; Chen et al. 2018). Recently, progress in targeting induced local lesions in genomes (TILLING) technology has been applied in wheat for the assembly of economic powdery mildew-resistant varieties. TILLING combines high-throughput genotyping for mutations with traditional chemical mutagenesis, which is more efficient to spot single nucleotide mutations in regions of interest (McCallum et al. 2000). The orthologue of barley Mlo are created using TILLING, as several combinations of mutant alleles of TaMlo are carried by partially resistant bread wheat lines (Acevedo-Garcia et al. 2017). Hence, there is no evident abnormality in plant growth due to the loss-of-function of TaMlo homoeologues which overcame the disturbance of pleiotropic phenotypes.

5.6.6 Transgenic-Based Resistance

Failure in transgenic plants has often been addressed, like poor or maybe no expression or inheritance of a transgene (Kumar et al. 2016). Also, transgene expression might be suffering from environment. For instance, field conditions are generally more complicated than a controlled environment, and in this sense, more genetic factors might be involved in biological and physiological activities and interact with transgene (Ueda et al. 2006). Moreover, uncontrolled transgene insertion might end in uncertain detrimental effects on plant growth and development. The subject surrounding genetic modification is usually related to concerns about potential hazards from transgenic plants; many countries, especially in Europe, have announced a ban on planting transgenic seeds. Release of strains employing a cisgenic approach is taken into similar risk as to standard breeding because cisgenic plants only have genes from an equivalent species or from a crossable relative (Schouten et al. 2006). It takes a breakthrough from introgression breeding because it directly transfers functional genes without multiple transfer steps that involve linkage of other genes (Jacobsen and Schouten 2007). Further, wheat breeding projects can use cisgenic methods, as wheat and progenitors and such relatives are

great sources of resistance genes. Despite the very fact that genome-edited plants are indistinguishable from those formed by natural or induced mutations (e.g., ethyl methanesulfonate) or conventional breeding (Duensing et al. 2018), many countries are still debating whether genome-edited crops should be subject to an equivalent regulation as genetically modified organisms (GMO). The importance of CRISPR/Cas9 as a transgenic approach lies in the need to develop transgenic lines to introduce the CRISPR/Cas9 into the genome of the target plant (Collinge 2018). However, transgenesis-free methods are developed for vegetatively propagated crops and perennials (Danilo et al. 2019). Moreover, methods to efficiently eliminate editing machinery and choose transgene-free CRISPR/Cas9-edited crop plants also are available for dry seeds (Aliaga-Franco et al. 2019). The regulatory requirements for genome-edited crops are currently controversial within the European Union because the European Court of Justice (ECJ) declared products of genome editing as GMOs in 2018 (ECJ 2018). This supported GMO legislation issued in 2001 (Official Journal of the ECU Communities 2001) did not consider CRISPR/Cas9 approaches. Consequently, scientists and breeders in Europe are urgently calling for the GMO ruling to be updated to a product-based evaluation instead of a process-based one (Collinge 2018; Schulman et al. 2019). Several countries outside Europe have excluded genome-edited crops from GMO regulations, like the USA, Argentina, and Japan (Schulman et al. 2019). US market pipeline already has a minimum of 20 genome-edited crops, stated to be exempted from GMO legislation (Schulman et al. 2019). In spite of the differences in regulatory approach, these new breeding technologies are believed to represent a sustainable solution to global agricultural challenges, crucial for reducing pesticides and securing food supply.

5.7 Need for Speed: An Intimidating Priority

Since the green revolution, steady increases in crop productivity have occurred; however, there is concern that yield improvement is beginning to plateau. The current rate of annual yield improvement for major crops ranges between 0.8 and 1.2%, which must be doubled in order to meet the highly increased future demand for plant-based products. In this context, new technology and advances in science offer new opportunities to further improve the efficiency of agriculture, while reducing its negative environmental impact, as well as enrich human diets with more nutritious foods. Without new approaches that help boost productivity of staple crops through genetic improvement, global food security will be severely compromised in the next two to three decades, given the current global consumer behavior. Rapid generation advances or in other terms shortening the fixation stage is an important component for reducing the time required to develop a new variety. "Speed Breeding" developed by Dr. Lee Hickey and colleagues provides a non-GM route to rapidly introgress or pyramid new trait variation. Speed breeding (SB) is an effective approach for rapid generation (Watson et al. 2018). SB creates rapid growth conditions by extending the photoperiod in a controlled-environment growth chamber (Ghosh et al. 2018). This method certainly speeds up the line fixation compared

with the process under typical glasshouse conditions. Extended photoperiod and controlled temperature regime can help to achieve up to six generations of spring wheat and durum wheat per year (Watson et al. 2018). Moreover, it can also be combined with genomic selection for accelerating crop improvement.

Most of the modern technologies have been proven to assist in the development of improved crop varieties. However, more efficient breeding strategies that effectively combine these technologies could lead to a step change to achieve rate of genetic gain. Ongoing investment from the public and private sectors is necessary to build and maintain capacity for sustained crop improvement to ensure the development of crops that are capable of feeding the world in the future.

5.8 Integrated Disease Management

Apart from the use of the disease-resistant varieties for any disease, crop monitoring is a key to control spread of powdery mildew. Powdery mildew is more difficult to control once it has established itself in crop canopies, so it is always advisable to monitor crops regularly from early tillering, to detect early symptoms, particularly in susceptible varieties. Powdery mildew severity can be exacerbated by high seeding rates, high nitrogen fertilization levels, and semi-dwarf growth habit. (Last 1954; Tompkins et al. 1992). High nitrogen levels escalate plant height and tillering, reducing the culm strength which leads to extended leaf wetness and increased lodging favorable for disease infection (Shaner and Finney 1977). Disease severity in the following wheat crop may be increased in the subsequent crops due to residual nitrogen from the previous wheat crop, which received high rates of nitrogen concentrations, and from legumes that contain nitrogen (Parmentier and Rixhon 1973). Volunteer plants can serve as inoculum source in reduced tillage systems. Potassium deficiency can make crops more vulnerable to infection in potassium-deficient soils but its application beyond need will not reduce disease risk. Hence, improper fertilization levels increase the susceptibility of the crop.

In winter barley, the use of cultivar mixtures to slow a powdery mildew outbreak has been studied (Wolfe 1984). The expected benefits include slowing the epidemic progression, reducing or eliminating the need for foliar fungicides, and thus, reducing the pathogen's ability toward fungicide resistance. Deploying greater number of resistance genes in both spring and winter wheat aims to diversify the population of *B. graminis* f. sp. *tritici,* while mixtures of cultivars containing different resistance genes slowed the progress of the powdery mildew epidemic and improved yield by 5% (Stuke and Fehrmann 1988). Cultivar mixtures have been used on a small scale despite being shown to be useful in many wheat-pathogen systems. The maturities of the cultivars in the mixture must be identical, and the end use must be considered, especially if the crop is to be sold through traditional grain marketing channels.

Powdery mildew infection can be reduced with seed dressing and in-furrow fungicides that are approved for the control of other wheat leaf diseases, however, they are not registered for this use. Young plants are the most vulnerable to the powdery mildew, so minimizing the risk of early disease onset can be helpful in

high-risk situations. Currently, no seed dressings or in-furrow fungicides for powdery mildew in wheat have been approved and scanty information is available regarding the integrated disease management approach, but some fungicides have been approved for powdery mildew in barley, including flutiafol in-furrow and fluquinconazole as seed dressing (Department of Primary industries and Regional Development 2020).

Applying registered fungicides can help limit infection in the upper canopy and heads, and is recommended in the more vulnerable varieties. It should be noted, however, that yield increases from a single fungicide have ranged from 0 to 25% in trials, with an average of about 10% (Department of Primary industries and Regional Development 2020). If the disease symptoms return after 2–3 weeks and the conditions remain optimal, a second fungicide application may be required. Early season infection development is regulated by seed-applied systemic fungicides, particularly in winter wheat. Excess tillering caused by mildew infection early in the season was reduced by triadimenol seed treatment, which led to a higher grain yield later in the season, particularly when high temperatures during grain filling reduced the severity of disease (Everts and Leath 1992; Frank and Ayers 1986; Leath and Bowen 1989). Difenoconazole also has systemic activity against powdery mildew. These fungicides have a wide spectrum of activity and may be economical seed treatments when they also contribute to reduction in smuts and other foliar pathogens (Leath and Bowen 1989). Powdery mildew is also treated with difenoconazole, which has systemic activity. These fungicides have a broad range of application and can be cost-effective crop treatments if they also help to reduce smuts and other foliar pathogens (Leath and Bowen 1989).

At present most control measures are based on the use of fungicides at the preflowering stage and in order to find new eco-compatible control methods against wheat powdery mildew, the biocontrol agents (BCAs) like yeasts *Rhodotorula glutinis* (isolate LS11) and *Cryptococcus laurentii* (isolate LS28) and the yeast-like fungus *Aureobasidium pullulans* (isolate LS30) were applied alone or in combination with a low dosage of common fungicides or with natural adjuvants. BCAs added in conjunction with certain adjuvants (i.e., calcium citrate, calcium chloride, calcium propionate, soybean oil, and humic acid) as well as a low dose of fungicides provided the best protection against powdery mildew. Furthermore, leaves treated with BCAs plus mineral salts had the highest amounts of antagonist population (De Curtis et al. 2007).

To prevent the development of fungicide resistance, wherever possible, fungicide mixtures containing several modes of action, such as cyproconazole and azoxystrobin, epoxiconazole and azoxystrobin, and epoxiconazole and pyraclostrobin, should be used. If environmental conditions are conducive to persistence, the first appearance of symptoms should be taken seriously and disease control practices must be implemented as soon as possible. Moreover, it is best to stop using the same fungicide or mode of action, such as demethylation inhibitor (DMI) fungicides, after the previous use. Rotation of the wheat crops with nonhost crops such as canola, barley, or legumes should be frequently practiced. The severity of powdery mildew can be influenced by fertilizer use. Plants become more

vulnerable to increased nitrogen fertilization, and dense crop canopies favor epidemic growth. Such crops would necessitate more intensive disease control and management. As a result, managing nitrogen application is critical for reducing the incidence of powdery mildew.

An integrated disease management system should be used with genetic resistance as the cornerstone of the program. Cultural management, including proper management of nitrogen fertilization, is essential to minimize risk of crop damage from powdery mildew. Rotate wheat crops with nonhost crops such as canola, barley, or legumes. Fungicides should be used in conjunction with a disease monitoring system employed from planting through the flowering stage of growth to estimate economic return.

5.9 Concluding Remarks

Molecular genetic research into various resistance forms for wheat powdery mildew is still ongoing. Exploration of underlying gene functions and interactions will be crucial in the future to achieve resilient and high levels of resistance. To diversify their resistance base, more focus will have to be placed on incorporating an array of resistance genes/QTLs into wheat cultivars. Wheat, as a polyploid, has a diverse gene pool that serves a variety of disease resistance sources for broadening the genetic base for powdery mildew resistance. Improvements in genetic techniques could speed up the detection and characterization of novel resistance genes. Current and upcoming methods and developments, including recent gene isolation techniques, would significantly accelerate the excavation of so-called "alien genes" (from cultivated or wild relatives). In plant pathogens, comparative genomics and population genomics provide new and effective ways to detect ongoing and past hybridization (Menardo et al. 2017a, b; Stukenbrock et al. 2012). Experiments on the genetics of reproductive barriers in model ascomycetes have also shed light on the genetics of these barriers (Dettman et al. 2007; Turner et al. 2011). Given the expansion of powdery mildew's host range, a better understanding of the underlying genetics of reproductive barriers and self- versus non–self-identification between species of fungal plant pathogens could help predict hybridization events in various agroecosystems. Therefore, there is a need to efficiently explore modern technologies to boost crop improvement in the face of more challenging production conditions, genetic barriers in alien introgression, and expanding host range of powdery mildew fungus in future. Examining the vast literature, great prospects could be foreseen with the advancements in the molecular diagnostic techniques for pathogen identification, cultivar development, artificial intelligence algorithms, and speed breeding protocols, which offer great opportunities to combat powdery mildew fungus in future. From the grower's point of view, the most important thing to know is that host resistance might not be enough to control wheat powdery mildew disease; sound agricultural practices and judicious use of fungicides should also be considered.

References

Acevedo-Garcia J, Spencer D, Thieron H, Reinstadler A (2017) MLO-based powdery mildew resistance in hexaploid bread wheat generated by a non-transgenic TILLING approach. Plant Biotechnol J 15(3):367–378. https://doi.org/10.1111/pbi.12631

Ajigboye OO, Bousquet L, Murchie EH, Ray RV (2016) Chlorophyll fluorescence parameters allow the rapid detection and differentiation of plant responses in three different wheat pathosystems. Funct Plant Biol 43:356–369

Alam MA, Xue F, Ali M, Wang C, Ji W (2013) Identification and molecular mapping of powdery mildew resistance gene PMG25 in common wheat originated from wild emmer (*Triticum turgidum* var. *dicoccoides*). Pak J Bot 45(1):203–208

Aliaga-Franco N, Zhang C, Presa S, Srivastava AK, Granell A, Alabadí D, Sadanandom A, Blázquez MA, Minguet EG (2019) Identification of transgene-free CRISPR edited plants of rice, tomato, and *Arabidopsis* by monitoring DsRED fluorescence in dry seeds. Front Plant Sci 10:1150

Allen AM, Winfield MO, Burridge AJ, Downie RC, Benbow HR, Barker GLA, Wilkinson PA, Coghill J, Waterfall C, Davassi A, Scopes G, Pirani A, Webster T, Brew F, Bloor C, Griffiths S, Bentley AR, Alda M, Jack P, Phillips AL, Edwards KJ (2017) Characterization of a wheat breeders array suitable for high-throughput SNP genotyping of global accessions of hexaploid bread wheat (*Triticum aestivum*). Plant Biotechnol J 15:390–401

Amano K (1986) Host range and geographical distribution of the powdery mildew fungi. Japan Scientific Societies Press, Tokyo, p 741

Anderson TR, Hawkin E, Jones PD (2016) CO_2, the greenhouse effect and global warming: from the pioneering work of Arrhenius and Callendar to today's earth system models. Endeavour 40: 178–187

Appels R, Eversole K, Feuillet C, Keller B, Rogers J, Stein N et al (2018) Shifting the limits in wheat research and breeding using a fully annotated reference genome. Science 361:1–13

Appiano M, Pavan S, Catalano D, Zheng Z, Bracuto V, Lotti C, Richard V, Luigi R, Yuling B (2015) Identification of candidate MLO powdery mildew susceptibility genes in cultivated Solanaceae and functional characterization of tobacco NtMLO1. Transgenic Res 24:847–858

Arora S, Steuernagel B, Gaurav K, Chandramohan S, Long Y, Matny O, Johnson R (2019) Resistance gene cloning from a wild crop relative by sequence capture and association genetics. Nat Biotechnol 37:139–143

Bassi FM, Bentley AR, Charmet G, Ortiz R, Crossa J (2016) Breeding schemes for the implementation of genomic selection in wheat (*Triticum* spp.). Plant Sci 242:23–36. https://doi.org/10.1016/j.plantsci.2015.08.021

Beest Te DE, Paveley ND, Shaw MW, Van den Bosch F (2008) Disease–weather relationships for powdery mildew and yellow rust on winter wheat. Phytopathology® 98(5):609–617. https://doi.org/10.1094/PHYTO-98-5-0609

Bennett FGA (1984) Resistance to powdery mildew in wheat: a review of its use in agriculture and breeding programmes. Plant Pathol 33:279–300

Bhullar NK, Mackay M, Keller B (2010a) Genetic diversity of the *Pm3* powdery mildew resistance alleles in wheat gene bank accessions as assessed by molecular markers. Diversity 2:768–786

Bhullar NK, Zhang ZQ, Wicker T, Keller B (2010b) Wheat gene bank accessions as a source of new alleles of the powdery mildew resistance gene Pm3: a large-scale allele mining project. BMC Plant Biol 10:88

Bindschedler LV, Panstruga R, Spanu PD (2016) Mildew-omics: how global analyses aid the understanding of life and evolution of powdery mildews. Front Plant Sci 7:123

Bliffeld M, Mundy J, Potrykus I, Futterer J (1999) Genetic engineering of wheat for increased resistance to powdery mildew disease. Theor Appl Genet 98:1079–1086

Bowen KL, Everts KL, Leath S (1991) Reduction in yield of winter wheat in North Carolina due to powdery mildew and leaf rust. Phytopathology 81:503–511

Braun HJ, Ekiz H, Eser V, Keser M, Ketata H, Marcucci G et al (1997) Breeding priorities of winter wheat programs. In: Braun F, Altay WE, Kronstad SP, Beniwal SPS, McNab A (eds) Wheat: prospects for global improvement, vol 6. Kluwer Academic Publishers, Dordrecht, pp 553–560

Braun U (1987) A monograph of the Erysiphales (powdery mildews). Beih Nova Hedwigia 89:1–700

Braun U, Cook RTA (2012) Taxonomic manual of the *Erysiphales* (powdery mildews). CBS-KNAW Fungal Biodiversity Centre, Utrecht

Bremner JM (1995) Recent research on problems in the use of urea as a nitrogen fertilizer. Nutr Cycl Agroecosyst 42:321–329

Brun H, Chevre AM, Fitt BDL, Powers S, Besnard AL, Ermel M, Marquer B, Eber F, Renard M, Andrivon D (2010) Quantitative resistance increases the durability of qualitative resistance to *Leptosphaeria maculans* in *Brassica napus*. New Phytol 185:285–299

Brunner S, Stirnweis D, Quijano CD, Buesing G, Herren G, Parlange F et al (2012) Transgenic Pm3 multilines of wheat show increased powdery mildew resistance in the field. Plant Biotechnol J 10:398–409

Burdon JJ, Barrett LG, Rebetzke G, Thrall PH (2014) Guiding deployment of resistance in cereals using evolutionary principles. Evol Appl 7:609–624

Bushnell WR (2002) The role of powdery mildew research in understanding host-parasite interaction: past, present and future. In: Berlanger RR, Bushnell WR, Dik AJ, Carver TLW (eds) The powdery mildews, a comprehensive treatise. APS Press, St Paul, pp 1–12

Byerlee D, Moya P (1993) Impacts of international wheat breeding research in the developing world, 1996–1990. CIMMYT, Mexico

Campbell MA, Fitzgerald HA, Ronald PC (2002) Engineering pathogen resistance in crop plants. Transgenic Res 11:599–613

Cao A, Xing L, Wang X, Yang X, Wang W, Sun Y et al (2011) Serine/threonine kinase gene Stpk-V, a key member of powdery mildew resistance gene Pm21, confers powdery mildew resistance in wheat. Proc Natl Acad Sci U S A 108:7727–7732

Cao X, Luo Y, Zhou Y, Fan J, Xu X, West JS, Duan X, Cheng D (2015) Detection of powdery mildew in two winter wheat plant densities and prediction of grain yield using canopy hyperspectral reflectance. PLoS One 10(3):e0121462. https://doi.org/10.1371/journal.pone.0121462

Cao XR, Zhou YL, Duan XY, Song YL, He WI, Ding KJ, Wang BT, Xia XC (2010) Postulation of wheat powdery mildew resistance genes in 101 wheat cultivars (lines) from major wheat regions in China. J Triticeae Crops 30:948–953

Carver TLW, Adaigbe ME (1990) Effect of oat host genotype, leaf age and position and incubation humidity on germination and germling development by *Erysiphe graminis* f. sp. *avenae*. Mycol Res 94:18–26

Cavanagh CR, Chao S, Wang S, Huang BE, Stephen S, Kiani S et al (2013) Genome-wide comparative diversity uncovers multiple targets of selection for improvement in hexaploid wheat landraces and cultivars. Proc Natl Acad Sci U S A 110:8057–8062

Chao KX, Su WW, Wu L, Su B, Li Q, Wang B et al (2019) Molecular mapping of a recessive powdery mildew resistance gene in wheat cultivar Tian Xuan 45 using bulked segregant analysis with polymorphic single nucleotide polymorphism relative ratio distribution. Phytopathology 109:828–838

Char SN, Neelakandan AK, Nahampun H, Frame B, Main M, Spalding MH et al (2017) An agrobacterium-delivered CRISPR/ Cas9 system for high-frequency targeted mutagenesis in maize. Plant Biotechnol J 15:257–268

Chen LZ, Li W, Katin-Grazzini L, Ding J, Gu X, Li Y et al (2018) A method for the production and expedient screening of CRISPR/Cas9-mediated non-transgenic mutant plants. Hortic Res 5:13

Chen PD, Qi LL, Zhou B, Zhang SZ, Liu DJ (1995) Development and molecular cytogenetic analysis of wheat–Haynaldia villosa 6VS/6AL translocation lines specifying resistance to powdery mildew. Theor Appl Genet 91:1125–1128

Chen PD, You CF, Hu Y, Chen S, Zhou B, Cao A et al (2013) Radiation-induced translocations with reduced Haynaldia villosa chromatin at the Pm21 locus for powdery mildew resistance in wheat. Mol Breed 31:477–484

Chen S, Cao YY, Li TY (2015) Development of a specific SCAR marker to race 21C3CTH of *Puccinia graminis* f. sp. *tritici* in China. Int J Agric Biol 17:1200–1206

Chen XM, Luo YH, Xia XC, Xia LQ, Chen X, Ren ZL et al (2005) Chromosomal location of powdery mildew resistance gene Pm16 in wheat using SSR marker analysis. Plant Breed 124: 225–228

Chhuneja P, Kumar K, Stirnweis D, Hurni S, Keller B, Dhaliwal HS (2012) Identification and mapping of two powdery mildew resistance genes in *Triticum boeoticum* L. Theor Appl Genet 124:1051–1058. https://doi.org/10.1007/s00122-011-1768-4PMID:22198205

Chung CL, Longfellow JM, Walsh EK, Kerdieh Z, Van Esbroeck G, Balint-Kurti P et al (2010) Resistance loci affecting distinct stages of fungal pathogenesis: use of introgression lines for QTL mapping and characterization in the maize–Setosphaeria turcica pathosystem. BMC Plant Biol 10:103

Coakley SM, Scherm H, Chakraborty S (1999) Climate change and plant disease management. Annu Rev Phytopathol 37:399–426

Collard BC, Mackill DJ (2008) Marker-assisted selection: an approach for precision plant breeding in the twenty-first century. Philos Trans R Soc B Biol Sci 363:557–572. https://doi.org/10.1098/rstb.2007.2170

Collinge DB (2018) Transgenic crops and beyond: how can biotechnology contribute to the sustainable control of plant diseases? Biotechnology for plant disease control: GMOs and beyond. Eur J Plant Pathol 152:977–986

Consonni C, Humphry ME, Hartmann HA, Livaja M, Durner J, Westphal L et al (2006) Conserved requirement for a plant host cell protein in powdery mildew pathogenesis. Nat Genet 38:716–720

Cowling WA (2013) Sustainable plant breeding. Plant Breed 132:1–9

Cunfer BM (2002) Powdery mildew. In: Curtis BC, Rajaram S, Gomez Macpherson H (eds) Bread wheat: improvement and production. Food and Agriculture Organization of the United Nations, Rome, pp 301–308

Danilo B, Perrot L, Mara K, Botton E, Nogue F, Mazier M (2019) Efficient and transgene-free gene targeting using Agrobacteriummediated delivery of the CRISPR/Cas9 system in tomato. Plant Cell Rep 38:459–462

De Curtis F, Spina AM, Piedimonte D, Lima G, De Cicco V (2007) Biological and integrated control of wheat powdery mildew. J Plant Pathol 89:S38

Dean R, Van Kan JAL, Pretorius ZA, Kosack KEH, Pietro AD, Spanu PD, Rudd JJ, Dickman M, Kahmann R, Ellis J, Foster GD (2012) The top 10 fungal pathogens in molecular plant pathology. Mol Plant Pathol 13:414–430

Department of Primary industries and Regional Development (2020) Managing powdery mildew in wheat. https://www.agric.wa.gov.au/spring/managing-powdery-mildew-wheat?page=0%2C0. Accessed 29 Jan 2020

Deryng D, Conway D, Ramankutty N, Price J, Warren R (2014) Global crop yield response to extreme heat stress under multiple climate change futures. Environ Res Lett 9:034011

Desprez-Loustau ML, Courtecuisse R, Robin C, Husson C, Moreau PA, Blancard D (2010) Species diversity and drivers of spread of alien fungi (*Sensu lato*) in Europe with a particular focus on France. Biol Inv 12:157–172. https://doi.org/10.1007/s10530-009-9439

Desta ZA, Ortiz R (2014) Genomic selection: genome-wide prediction in plant improvement. Trends Plant Sci 19:592–601. https://doi.org/10.1016/j.tplants.2014.05.006

Dettman JR, Sirjusingh C, Kohn LM, Anderson JB (2007) Incipient speciation by divergent adaptation and antagonistic epistasis in yeast. Nature 447:585–588

Deyoung BJ, Innes RW (2006) Plant NBS-LRR proteins in pathogen sensing and host defense. Nat Immunol 7:1243–1249

Dong Z, Tian X, Ma C, Xia Q, Wang B, Chen Q, Sehgal SK, Friebe B, Li H, Liu W (2020) Physical mapping of Pm57, a powdery mildew resistance gene derived from *Aegilops searsii*. Int J Mol Sci 21:322

Doussinault G, Delibes A, Sanchezmonge R, Garciaolmedo F (1983) Transfer of a dominant gene for resistance to eyespot disease from a wild grass to hexaploid wheat. Nature 303:698–700

Duensing N, Sprink T, Parrott WA, Fedorova M, Lema MA, Wolt JD et al (2018) Novel features and considerations for ERA and regulation of crops produced by genome editing. Front Bioeng Biotechnol 6:79

Duggal V, Jellis GJ, Hollins TW, Stratford R (2000) Resistance to powdery mildew in mutant lines of the susceptible wheat cultivar Hobbit 'sib'. Plant Pathology 49(4):468–476. https://doi.org/10.1046/j.1365-3059.2000.00471.x

Dundas IS, Anugrahwati DR, Verlin DC, Park RF, Bariana HS, Mago R et al (2007) New sources of rust resistance from alien species: meliorating linked defects and discovery. Aust J Agr Res 58: 545–549

ECJ (2018) Judgment of 25 July 2018, Confédération Paysanne a.o., C- 528/16, ECLI:EU:C:2018: 583. https://curia.europa.eu/jcms/upload/docs/application/pdf/2018-07/cp180111en.pdf. Accessed 4 Feb 2020

Elingham O, David J, Culham A (2019) Enhancing identification accuracy for powdery mildews using previously underexploited DNA loci. Mycologia 111:1–15

Elkot AFA, Chhuneja P, Kaur S, Saluja M, Keller B, Singh K (2015) Marker assisted transfer of two powdery mildew resistance genes PmTb7A.1 and PmTb7A.2 from *Triticum boeoticum* (Boiss.) to *Triticum aestivum* (L.). PLoS One 10:e0128297

Elliott C, Zhou F, Spielmeyer W, Panstruga R, Schulze-Lefert P (2002) Functional conservation of wheat and rice MLO orthologs in defense modulation to the powdery mildew fungus. Mol Plant Microbe Interact 15:1069–1077

Eshed N, Wahl I (1970) Host ranges and interrelations *of Erysiphe graminis hordei*, *Erysiphe graminis tritici*, and *Erysiphe graminis avenae*. Phytopathology 60:628–634

Everts KL, Leath S (1992) Effect of early season powdery mildew on development, survival, and yield contribution of tillers of winter wheat. Phytopathology 82:1273–1278

FAO, IFAD, UNICEF, WFP, WHO (2018) The state of food security and nutrition in the world. Building climate resilience for food security and nutrition. FAO, Rome

Fischer G, Frohberg K, Parry ML, Rosenzweig C (1995) Climate change and world food supply, demand and trade. In: Rosenzweig C (ed) Climate change and agriculture: analysis of potential international impacts. American Society of Agronomy, Madison, pp 341–382

Flor HH (1955) Host-parasite interaction in flax rusts-its genetics and other implications. Phytopathology 45:680–685

Flor HH (1971) Current status of the gene-for-gene concept. Annu Rev Phytopathol 9:275–296

FRAC (2005) Pathogen risk list. Fungicide Resistance Action Committee, Limburgerhof, pp 1–5

Frank JA, Ayers JE (1986) Effect of triadimenol seed treatment on powdery mildew epidemics on winter wheat. Phytopathology 76:254–257

Gadoury DM, Cadle-Davidson L, Wilcox WF, Dry IB, Seem RC, Milgroom MG (2012) Grapevine powdery mildew (*Erysiphe necator*): a fascinating system for the study of the biology, ecology and epidemiology of an obligate biotroph. Mol Plant Pathol 13:1–16

Gao HD, Zhu FF, Jiang YJ, Wu JZ, Yan W, Zhang QF, Jacobi A, Cai SB (2012) Genetic analysis and molecular mapping of a new powdery mildew resistant gene *Pm46* in common wheat. Theor Appl Genet 125:967–973

Ghosh S, Watson A, Gonzalez-Navarro OE, Ramirez-Gonzalez RH, Yanes L, Mendoza-Suárez M, Simmonds J, Wells R, Rayner T, Green P et al (2018) Speed breeding in growth chambers and glasshouses for crop breeding and model plant research. Nat Protoc 13:2944–2963

Glawe DA (2008) The powdery mildews: a review of the world's most familiar (yet poorly known) plant pathogens. Annu Rev Phytopathol 46:27–51

Goldringer I, Brabant P, Gallais A (1997) Estimation of additive and epistatic genetic variances for agronomic traits in a population of doubled-haploid lines of wheat. Heredity 79:60–71

Golzar H, Shankar M, D'Antuono M (2016) Responses of commercial wheat varieties and differential lines to western Australian powdery mildew (*Blumeria graminis* f. sp. *tritici*) populations. Australas Plant Pathol 45:347–355

Goudriaan J, Zadoks JC (1995) Global climate change: modelling the potential responses of agro-ecosystems with special reference to crop protection. Environ Pollut 87:215–224

Graybosch RA (2001) Uneasy unions: quality effects of rye chromatin transfers to wheat. J Cereal Sci 33:3–16

Groos C, Robert N, Bervas E, Charmet G (2003) Genetic analysis of grain protein-content, grain yield and thousand-kernel weight in bread wheat. Theor Appl Genet 106:1032–1040

Hanusova R, Hsam SLK, Bartos P, Zeller FJ (1996) Suppression of powdery mildew resistance gene Pm8 in Triticum aestivum L. (common wheat) cultivars carrying wheat-rye translocation T1BL-1RS. Heredity 77:383–387

Hao Y, Liu A, Wang Y, Feng D, Gao J, Li X, Liu S, Wang H (2008) Pm23: a new allele of Pm4 located on chromosome 2AL in wheat. Theor Appl Genet 117:1205–1212

Hao Y, Parks R, Cowger C, Chen Z, Wang Y, Bland D, Murphy JP, Guedira M, Guedira GB, Johnson J (2015) Molecular characterization of a new powdery mildew resistance gene Pm54 in soft red winter wheat. Theor Appl Genet 128(3):465–476

Hariharan G, Prasannath K (2021) Recent advances in molecular diagnostics of fungal plant pathogens: a mini review. Front Cell Infect Microbiol 10:600234. https://doi.org/10.3389/fcimb.2020.600234

He H, Zhu S, Zhao R, Jiang Z, Ji Y, Ji J et al (2018) Pm21, encoding a typical CC-NBS-LRR protein, confers broad-spectrum resistance to wheat powdery mildew disease. Mol Plant 11:879–882

He R, Chang Z, Yang Z, Yuan Z, Zhan H, Zhang X, Liu J (2009) Inheritance and mapping of powdery mildew resistance gene Pm43 introgressed from Thinopyrum intermedium into wheat. Theor Appl Genet 118:1173–1180. https://doi.org/10.1007/s00122-009-0971-z

Henry RJ, Kettlewell PS (1996) Cereal grain quality, vol 488. Chapman & Hall, London

Hilscher J, Bürstmayr H, Stoger E (2017) Targeted modification of plant genomes for precision crop breeding. Biotechnol J 12:1600173

Hsam SLK, Huang XQ, Zeller FJ (2001) Chromosomal location of genes for resistance to powdery mildew in common wheat (*Triticum aestivum* L. em Thell.) 6. Alleles at the Pm5 locus. Theor Appl Genet 102:127–133

Hu JH, Li JT, Wu PP, Li YH, Qiu D, Qu YF, Xie JZ, Zhang HJ, Yang L, Fu TT, Yu YW, Li MJ, Liu HW, Zhu TQ, Zhou Y, Liu ZY, Li HJ (2019) Development of SNP, KASP, and SSR markers by BSR-RNA-Seq technology for saturation of genetic linkage map and efficient detection of wheat powdery mildew resistance gene Pm61. Int J Mol Sci 20:750

Hu TZ, Li HJ, Liu ZJ, Xie CJ, Zhou YL, Duan XY, Jia X, You MS, Yang ZM, Sun QX, Liu ZY (2008) Identification and molecular mapping of the powdery mildew resistance gene in wheat cultivar Yumai 66. Acta Agron Sin 34:545–550. (in Chinese)

Hua W, Liu Z, Zhu J, Xie C, Yang T, Zhou Y, Duan X, Sun Q, Liu Z (2009) Identification and genetic mapping of Pm42, a new recessive wheat powdery mildew resistance gene derived from wild emmer (*Triticum turgidum* var. *dicoccoides*). Theor Appl Genet 119:223–230. https://doi.org/10.1007/s00122-009-1031-4

Huang J, Zhao ZH, Song FJ, Wang XM, Xu HX, An DG, Li HJ (2012) Molecular detection of a gene effective against powdery mildew in wheat cultivar Liangxing 66. Mol Breed 30:1737–1745

Huang JP, Yu HP, Dai AG, Wei Y, Kang LT (2017) Drylands face potential threat under 2°C global warming target. Nat Clim Chang 7:417–422

Huang L, Raats D, Sela H, Klymiuk V, Lidzbarsky G, Feng L et al (2016) Evolution and adaptation of wild emmer wheat populations to biotic and abiotic stresses. Annu Rev Phytopathol 54:279–301

Huang XQ, Hsam SLK, Zeller FJ, Wenzel G, Mohler V (2000) Molecular mapping of the wheat powdery mildew resistance gene Pm24 and marker validation for molecular breeding. Theor Appl Genet 101:407–414

Huang XQ, Roder MS (2003) High-density genetic and physical mapping of the powdery mildew resistance gene Pm24 on chromosome 1D of wheat. In: Pogna HN, Romano M, Pogna EA, Galterio G (eds.), Proceedings of the 10th international wheat genetics symposium, Paestum, pp. 961–964

Hubbard A, Lewis CM, Yoshida K, Ramirez-Gonzalez RH, de Vallavieille-Pope C, Thomas J et al (2015) Field pathogenomics reveals the emergence of a diverse wheat yellow rust population. Genome Biol 16:23

Huckelhoven R (2005) Powdery mildew susceptibility and biotrophic infection strategies. FEMS Microbiol Lett 245:9–17

Hurni S, Brunner S, Buchmann G, Herren G, Jordan T, Krukowski P et al (2013) Rye Pm8 and wheat Pm3 are orthologous genes and show evolutionary conservation of resistance function against powdery mildew. Plant J 76:957–969

Hussain M, Iqbal MA, Till BJ, Rahman M (2018) Identification of induced mutations in hexaploid wheat genome using exome capture assay. PLoS One 13:e0201918

Jacobsen E, Schouten HJ (2007) Cisgenesis strongly improves introgression breeding and induced translocation breeding of plants. Trends Biotechnol 25:219–223

Jankovics T, Komaromi J, Fabian A, Jager K, Vida G, Kiss L (2015) New insights into the life cycle of the wheat powdery mildew: direct observation of ascosporic infection in *Blumeria graminis* f. sp. *tritici*. Phytopathology 105:797–804

Jarosch B, Kogel KH, Schaffrath U (1999) The ambivalence of the barley MLO locus: mutations conferring resistance against powdery mildew (*Blumeria graminis* f. sp, *hordei*) enhance susceptibility to the rice blast fungus *Magnaporthe grisea*. Mol Plant Microbe Interact 12: 508–514

Jia A, Ren Y, Gao F, Yin G, Liu J, Guo L et al (2018) Mapping and validation of a new QTL for adult-plant resistance to powdery mildew in Chinese elite bread wheat line Zhou8425B. Theor Appl Genet 131:1063–1071

Jiang DB, Fu YH (2012) Climate change over China with a 2°C GLOBAL warming. Chin J Atmos Sci 36:234–246

Jiang JM, Friebe B, Gill BS (1994) Recent advances in alien gene-transfer in wheat. Euphytica 73: 199–212

Johnson R (1981) Durable resistance: definition of, genetic control, and attainment in plant breeding. Phytopathology 71:567–568

Johnson R (1992) Past, present and future opportunities in breeding for disease resistance, with examples from wheat. Euphytica 63:3–22

Jones JDG, Dangl JL (2006) The plant immune system. Nature 444:323–329

Jorgensen JH (1992) Discovery, characterization and exploitation of MLO powdery mildew resistance in barley. Euphytica 63:141–152

Kang Y, Zhou M, Merry A, Barry K (2020) Mechanisms of powdery mildew resistance of wheat – a review of molecular breeding. Plant Pathol 69:601–617

Kashyap PL, Rai P, Kumar S, Chakdar H, Srivastava AK (2017) DNA barcoding for diagnosis and monitoring of fungal plant pathogens. In: Singh B, Gupta V (eds) Molecular markers in mycology. Fungal biology. Springer, Cham, pp 87–122. https://doi.org/10.1007/978-3-319-34106-4_5

Khanna HK, Daggard GE (2003) Agrobacterium tumefasciens-mediated transformation of wheat using a super binary vector and a polyamine supplemented regeneration medium. Plant Cell Rep 21:429–436

Kim W, Johnson JW, Baenziger PS, Lukaszewski AJ, Gaines CS (2004) Agronomic effect of wheat–rye translocation carrying rye chromatin (1R) from different sources. Crop Sci 44:1254–1258

Kiss L (2005) Powdery mildew as invasive plant pathogens: new epidemics caused by two north American species in Europe. Mycol Res 109:259–260

Knott GJ, Doudna JA (2018) CRISPR-Cas guides the future of genetic engineering. Science 361: 866–869

Koller T, Brunner S, Herren G, Hurni S, Keller B (2018) Pyramiding of transgenic Pm3 alleles in wheat results in improved powdery mildew resistance in the field. Theor Appl Genet 131:861–871

Krattinger SG, Lagudah ES, Spielmeyer W, Singh RP, Huerta Espino J, McFadden H et al (2009) A putative ABC transporter confers durable resistance to multiple fungal pathogens in wheat. Science 323:1360–1363

Kumar P, Akhtar J, Kandan A, Kumar S, Batra R, Dubey SC (2016) Advance detection techniques of phytopathogenic fungi: current trends and future perspectives. In: Kumar P, Gupta V, Tiwari A, Kamle M (eds) Current trends in plant disease diagnostics and management practices. Springer, Cham, pp 265–298. https://doi.org/10.1007/978-3-319-27312-9_12

Large EG, Doling DA (1962) The measurement of cereal mildew and its effect on yield. Plant Pathol 11:47–57

Large EG, Doling DA (1963) Effect of mildew on yield of winter wheat. Plant Pathol 12:128–130

Last FT (1954) The effect of time of application of nitrogenous fertiliser on powdery mildew on winter wheat. Ann Appl Biol 41:381–392

Leath S, Bowen KL (1989) Effects of powdery mildew, triadimenol seed treatment, and triadimefon foliar sprays on yield of winter wheat in North Carolina. Phytopathology 79:152–155

Lenaerts B, Collard B, Demont M (2019) Review: improving global food security through accelerated plant breeding. Plant Sci 287:110207. https://doi.org/10.1016/j.plantsci.2019.110207

Li C, Zhang N, Guan B, Zhou Z, Mei F (2019a) Reactive oxygen species are involved in cell death in wheat roots against powdery mildew. J Integr Agric 18(9):1961–1970

Li G, Chen P, Zhang S, Wang X, He Z, Zhang Y, Zhao H, Huang H, Zhou X (2007) Effects of the 6VS.6AL translocation on agronomic traits and dough properties of wheat. Euphytica 155:305–313

Li G, Cowger C, Wang X et al (2019b) Characterization of Pm65, a new powdery mildew resistance gene on chromosome 2AL of a facultative wheat cultivar. Theor Appl Genet 132:2625–2632. https://doi.org/10.1007/s00122-019-03377-2

Li G, Fang T, Zhang H, Xie C, Li H, Yang T et al (2009) Molecular identification of a new powdery mildew resistance gene Pm41 on chromosome 3BL derived from wild emmer (*Triticum turgidum* var. *dicoccoides*). Theor Appl Genet 119:531–539. https://doi.org/10.1007/s00122-009-1061-y

Li GQ, Carver BF, Cowger C, Bai GH, Xu XY (2018) Pm223899, a new recessive powdery mildew resistance gene identified in Afghanistan landrace PI 223899. Theor Appl Genet 131:2775–2783

Li GQ, Xu XY, Bai GH, Carver BF, Hunger R, Bonman JM (2016) Identification of novel powdery mildew resistance sources in wheat. Crop Sci 56:1817–1830

Li H, Dong Z, Ma C et al (2020) A spontaneous wheat-Aegilops longissima translocation carrying Pm66 confers resistance to powdery mildew. Theor Appl Genet 2020:1149. https://doi.org/10.1007/s00122-020-03538-8

Li H, Wang X, Song F, Wu C, Wu X, Zhang N, Zhon Y, Zhang X (2011) Response to powdery mildew and detection of resistance genes in wheat cultivars from China. Acta Agron Sin 37: 943–954

Li HH, Jiang B, Wang JC, Lu YQ, Zhang JP, Pan CL et al (2017) Mapping of novel powdery mildew resistance gene(s) from Agropyron cristatum chromosome 2P. Theor Appl Genet 130: 109–121. https://doi.org/10.1007/s00122-016-2797-9

Li SJ, Wang J, Wang KY, Chen JN, Wang K, Du LP et al (2019c) Development of PCR markers specific to Dasypyrum villosum genome based on transcriptome data and their application in

breeding Triticum aestivum-D. villosum 4 alien chromosome lines. BMC Genomics 20:289. https://doi.org/10.1186/s12864-019-5630-4
Li Z, Lan C, He Z, Singh RP, Rosewarne GM, Chen X et al (2014) Overview and application of QTL for adult plant resistance to leaf rust and powdery mildew in wheat. Crop Sci 54:1907–1925
Lillemo M, Skinnes H, Brown JKM (2010) Race specific resistance to powdery mildew in Scandinavian wheat cultivars, breeding lines and introduced genotypes with partial resistance. Plant Breed 129:297–303
Liu J, Liu D, Tao W, Li W, Wang S, Chen P et al (2000) Molecular marker facilitated pyramiding of different genes for powdery mildew resistance in wheat. Plant Breed 119:21–24
Liu N, Bai GH, Lin M, Xu XY, Zheng WM (2017a) Genomewide association analysis of powdery mildew resistance in US winter wheat. Sci Rep 7:11743
Liu SX, Griffey CA, Maroof MAS (2001) Identification of molecular markers associated with adult plant resistance to powdery mildew in common wheat cultivar Massey. Crop Sci 41:1268–1275
Liu WX, Koo DH, Xia Q, Li C, Bai F, Song Y et al (2017b) 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
Luchi N, Ioos R, Santini A (2020) Fast and reliable molecular methods to detect fungal pathogens in woody plants. Appl Microbiol Biotechnol 104:2453–2468
Luo PG, Luo HY, Chang ZJ, Zhang HY, Zhang M, Ren ZL (2009) Characterization and chromosomal location of Pm40 in common wheat: a new gene for resistance to powdery mildew derived from Elytrigia intermedium. Theor Appl Genet 18:1059–1064. https://doi.org/10.1007/s00122-009-0962-0
Ma P, Xu H, Li L, Zhang H, Han G, Xu Y et al (2016) Characterization of a new Pm2 allele conferring powdery mildew resistance in the wheat germplasm line FG-1. Front Plant Sci 7:546
Ma PT, Xu HX, Luo QL, Qie YM, Zhou YL, Xu YF, Han HM, Li LH, An DG (2014) Inheritance and genetic mapping of a gene for seedling resistance to powdery 13 mildew in wheat line X3986-2. Euphytica 200:149–157
Ma PT, Xu HX, Xu YF, Li LH, Qie YM, Luo QL, Zhang XT, Li XQ, Zhou YL, An DG (2015) Molecular mapping of a new powdery mildew resistance gene Pm2b in Chinese breeding line KM 2939. Theor Appl Genet 128:613–622
Ma PT, Xu HX, Xu YF, Song LP, Liang SS, Sheng Y, Han GH, Zhang XT, An DG (2018) Characterization of a powdery mildew resistance gene in wheat breeding line 10V-2 and its application in marker-assisted selection. Plant Dis 102:925–931
Mackay TFC (2014) Epistasis and quantitative traits: using model organisms to study gene-gene interactions. Nat Rev Genet 15:22–33
Makandar R, Essig JS, Schapaugh MA, Trick HN, Shah J (2006) Genetically engineered resistance to Fusarium head blight in wheat by expression of Arabidopsis NPR1. Mol Plant Microbe Interact 19:123–129
Manthey R, Fehrmann H (1993) Effect of cultivar mixtures in wheat on fungal diseases, yield and profitability. Crop Prot 12:63–68
Marcais B, Desprez-Loustau ML (2014) European oak powdery mildew: impact on trees, effects of environmental factors, and potential effects of climate change. Ann For Sci 71:633–642
Marchal E (1902) De la specialisation du paristisme chez l' *Erysiphe graminis*. Acad Sci Paris 135:210–212
Mayer KFX, Martis M, Hedley PE, Šimková H, Liu H, Morris JA et al (2011) Unlocking the barley genome by chromosomal and comparative genomics. Plant Cell 23:1249–1263
McCallum CM, Comai L, Greene EA, Henikoff S (2000) Targeting induced local lesions IN genomes (TILLING) for plant functional genomics. Plant Physiol 123:439–442
McCartney HA, Foster SJ, Fraaije BA, Ward E (2003) Molecular diagnostics for fungal plant pathogens. Pest Manag Sci 59:129–142. https://doi.org/10.1002/ps.575
McDonald BA, Linde C (2002) Pathogen population genetics, evolutionary potential, and durable resistance. Annu Rev Phytopathol 40:349–379

McGrann GRD, Stavrinides A, Russell J, Corbitt MM, Booth A, Chartrain L, Thomas WTB, Brown JKM (2014) A tradeoff between MLO resistance to powdery mildew and increased susceptibility of barley to a newly important disease, *Ramularia* leaf spot. J Exp Bot 65:1025–1037

McIntosh RA, Dubcovsky J, Rogers WJ, Morris C, Appels R, Xia XC (2014) Catalogue of gene symbols for wheat: 2013–2014 supplement. BMC Genomics 20:289

Mehta YR (2014) Wheat diseases and their management. Springer, Cham

Menardo F, Praz CR, Wicker T, Keller B (2017a) Rapid turnover of effectors in grass powdery mildew (Blumeria graminis). Genome Biol Evol 17(1):223. https://doi.org/10.1186/s12862-017-1064-2

Menardo F, Wicker T, Keller B (2017b) Reconstructing the evolutionary history of powdery mildew lineages (Blumeria graminis) at different evolutionary time scales with NGS data. Genome Biol Evol 9(2):446–456

Meng J, Doyle MP (2002) Introduction. Microbiological food safety. Microbes Infect 4:395–397. https://doi.org/10.1016/S1286-4579(02)01552-6

Merchán VM, Kranz J (1986) Untersuchungen über den Einfluß des Regens auf die Infektion des Weizens durch Erysiphe graminis DC f.sp. tritici Marchal. Z Pflanzenkr Pflanzenschutz 93:255–261

Meyer FD, Giroux MJ (2007) Wheat. In: Nagata T, Lorz H, Widholm JM (eds) Biotechnology in agriculture and forestry: transgenic crops IV. Springer, Berlin, pp 55–71

Miedaner T, Flath K (2007) Effectiveness and environmental stability of quantitative powdery mildew (*Blumeria graminis*) resistance among winter wheat cultivars. Plant Breed 126:553–558

Mitchell CE, Reich PB, Tilman D, Groth JV (2003) Effects of elevated CO2, nitrogen deposition, and decreased species diversity on foliar fungal plant disease. Glob Chang Biol 9:438–451

Mo YJ, Howell T, Vasquez-Gross H, De Haro LA, Dubcovsky J, Pearce S (2018) Mapping causal mutations by exome sequencing in a wheat TILLING population: a tall mutant case study. Mol Genet Genomics 293:463–477

Möller M, Stukenbrock EH (2017) Evolution and genome architecture in fungal plant pathogens. Nat Rev Microbiol 15:756–771

Moore JW, Herrera-Foessel S, Lan C, Schnippenkoetter W, Ayliffe M, Huerta-Espino J et al (2015) A recently evolved hexose transporter variant confers resistance to multiple pathogens in wheat. Nat Genet 47:1494–1498

Mullis KB, Faloona FA (1987) Specific synthesis of DNA *in vitro* via a polymerase-catalyzed chain reaction. Methods Enzymol 155:335–350. https://doi.org/10.1016/0076-6879(87)55023-6

Mundt CC (2002) Use of multiline cultivars and cultivar mixtures for disease management. Annu Rev Phytopathol 40:381–410

Mundt CC (2014) Durable resistance: a key to sustainable management of pathogens and pests. Infect Genet Evol 27:446–455

Muranty H, Pavoine MT, Jaudeau B, Radek W, Doussinault G, Barloy D (2009) Two stable QTL involved in adult plant resistance to powdery mildew in the winter wheat line RE714 are expressed at different times along the growing season. Mol Breed 23:445–461

Murphy JP, Maxwell JJ, Miranda LM, Lyerly JH, Parks WR, Srnic G et al (2009) Qualitative powdery mildew resistance mapping update. Eastern wheat workers/southern small grain workers-NCERA184 conference, Baltimore

Nakaya A, Isobe SN (2012) Will genomic selection be a practical method for plant breeding? Ann Bot 110:1303–1316

Nekrasov V, Wang CM, Win J, Lanz C, Weigel D, Kamoun S (2017) Rapid generation of a transgene-free powdery mildew resistant tomato by genome deletion. Sci Rep 7:482

Nematollahi G, Mohler V, Wenzel G, Zeller FJ, Hsam SLK (2008) Microsatellite mapping of powdery mildew resistance allele Pm5d from common wheat line IGV1-455. Euphytica 159(3):307–313

Neu C, Stein N, Keller B (2002) Genetic mapping of the Lr20– Pm1 resistance locus reveals suppressed recombination on chromosome arm 7AL in hexaploid wheat. Genome 45:737–744. https://doi.org/10.1139/g02-040

Nezhad AS (2014) Future of portable devices for plant pathogen diagnosis. Lab Chip 14:2887–2904. https://doi.org/10.1039/C4LC00487F

Ning YS, Wang GL (2018) Breeding plant broad-spectrum resistance without yield penalties. Proc Natl Acad Sci U S A 115:2859–2861

Oberhaensli S, Parlange F, Buchmann J, Jenny F, Abbott J, Burgis T, Spanu P, Keller B (2010) Comparative sequence analysis of wheat and barley powdery mildew fungi reveals gene colinearity, dates divergence and indicates host-pathogen co-evolution. Fungal Genet Biol 48: 327–341. https://doi.org/10.1016/j.fgb.2010.10.003

Official Journal of the European Communities (2001) Directive 2001/18/EC of the European Parliament and of the Council of 12 March 2001 on the deliberate release into the environment of genetically modified organisms and repealing council directive 90/220/EEC. Official Journal of the European Communities L 106/1

Oldach KH, Becker D, LOrz H (2001) Heterologous expression of genes mediating enhanced fungal resistance in transgenic wheat. Mol Plant Microbe Interact 14:832–838

Ouyang SH, Zhang D, Han J, Zhao X et al (2014) Fine physical and genetic mapping of powdery mildew resistance gene MlIW172 originating from wild emmer (*Triticum dicoccoides*). PLoS One 9:e100160

Pachauri RK, Allen MR, Barros VR, Broome J, Cramer W, Christ R, Church JA et al (2014) Synthesis report. Contribution of working groups I, II and III to the Fifth Assessment Report of the Intergovernmental Panel on Climate Change. Intergovernmental Panel on Climate Change, Geneva, Switzerland

Parks R, Carbone I, Murphy JP, Marshall D, Cowger C (2008) Virulence structure of the eastern U.S. wheat powdery mildew population. Plant Dis 92:1074–1082

Parmentier G, Rixhon L (1973) Influence des précédents culturaux sur l'infection öidienne du froment d'hiver. Parasitica 29:129–133

Pessina S, Lenzi L, Perazzolli M, Campa M, Dalla Costa L, Urso S et al (2016) Knockdown of MLO genes reduces susceptibility to powdery mildew in grapevine. Hortic Res 3:16016

Petersen S, Lyerly JH, Worthington ML, Parks WR, Cowger C, Marshall DS, Brown-Guedira G, Murphy JP (2015) Mapping of powdery mildew resistance gene Pm53 introgressed from *Aegilops speltoides* into soft red winter wheat. Theor Appl Genet 128:303–312

Piarulli L, Gadaleta A, Mangini G, Signorile MA, Pasquini M, Blanco A, Simeone R (2012) Molecular identification of a new powdery mildew resistance gene on chromosome 2BS from *Triticum turgidum* ssp. *dicoccum*. Plant Sci 196:101–106

Poland JA, Balint-Kurti PJ, Wisser RJ, Pratt RC, Nelson RJ (2009) Shades of gray: the world of quantitative disease resistance. Trends Plant Sci 14:21–29

Poland JA, Nelson RJ (2011) In the eye of the beholder: the effect of rater variability and different rating scales on QTL mapping. Phytopathology 101:290–298

Posada D (2016) Phylogenomics for systematic biology. Syst Biol 65:353–356

Pryce TM, Palladino S, Kay ID, Coombs GW (2003) Rapid identification of fungi by sequencing the ITS1 and ITS2 regions using an automated capillary electrophoresis system. Med Mycol 41(5):369–381. https://doi.org/10.1080/13693780310001600435

Qi LL, Wang SL, Chen PD, Liu DJ, Gill BS (1998) Identification and physical mapping of three Haynaldia villosa chromosome-6V deletion lines. Theor Appl Genet 97:1042–1046

Qin B, Cao A, Wang H, Chen T, You FM, Liu Y, Ji J, Liu D, Chen P, Wang X (2011) Collinearity-based marker mining for the fine mapping of Pm6, a powdery mildew resistance gene in wheat. Theor Appl Genet 123:207–218

Queiroz KD (2007) Species concepts and species delimitation. Syst Bot 56:879–886

Rabbinge R, Jorritsma ITM, Schans J (1985) Damage components of powdery mildew in winter wheat. Neth J Plant Pathol 91:235–247

Rasheed A, Hao YF, Xia XC, Khan A, Xu Y, Varshney RK et al (2017) Crop breeding chips and genotyping platforms: progress, challenges, and perspectives. Mol Plant 10:1047–1064

Reynolds M, Dreccer F, Trethowan R (2007) Drought-adaptive traits derived from wheat wild relatives and landraces. J Exp Bot 58:177–186

Roelfs AP (1977) Foliar fungal diseases of wheat in the People's Republic of China. Plant Dis Rep 61:836–841

Rong JK, Millet E, Manisterski J, Feldman M (2000) A new powdery mildew resistance gene: introgression from wild emmer into common wheat and RFLP-based mapping. Euphytica 115: 121–126. https://doi.org/10.1023/A:1003950431049

Rosenzweig C, Iglesias A, Yang XB, Epstein P, Chivian E (2001) Climate change and extreme weather events; implications for food production, plant diseases, and pests. Glob Change Hum Health 2:90–104

Rosenzweig C, Parry ML (1994) Potential impact of climate change on world food supply. Nature 367:133–138

Rostoks N, Ramsay L, MacKenzie K, Cardle L, Bhat PR, Roose ML et al (2006) Recent history of artificial outcrossing facilitates whole-genome association mapping in elite inbred crop varieties. Proc Natl Acad Sci U S A 103:18656–18661

Royse DJ, Gregory LV, Ayers JE, Cole H (1980) Powdery mildew of wheat: relation of yield components to disease severity. Can J Pl Pathol 2:131–136

Saari EE, Wilcoxson RD (1974) Plant disease situation of high-yielding dwarf wheats in Asia and Africa. Annu Rev Phytopathol 12:49–68

Samobor V, Vukobratovic M, Jost M (2005) Utjecaj napada pepelnice (Erysiphe graminis d.c. F.sp. tritici Marchal) na urod i fizikalne pokazatelje kakvoće zrna pšenice (Triticum aestivum ssp. vulgare) [effect of powdery mildew (Erysiphe graminis DC f. sp. tritici Marchal) attack on yield and physical parameters of wheat (Triticum aestivum spp vulgare) grain quality]. Poljoprivreda 11:30–37

Sanchez-Martin J, Keller B (2019) Contribution of recent technological advances to future resistance breeding. Theor Appl Genet 132:713–732

Sánchez-Martín J, Steuernagel B, Ghosh S, Herren G, Hurni S, Adamski N et al (2016) Rapid gene isolation in barley and wheat by mutant chromosome sequencing. Genome Biol 17:221–228

Savary S, Willocquet L, Pethybridge SJ et al (2019) The global burden of pathogens and pests on major food crops. Nat Ecol Evol 3:430–439

Saxena RK, Edwards D, Varshney RK (2014) Structural variations in plant genomes. Brief Funct Genomics 13:296–307

Schneeberger K (2014) Using next-generation sequencing to isolate mutant genes from forward genetic screens. Nat Rev Genet 15:662–676

Schouten HJ, Krens FA, Jacobsen E (2006) Cisgenic plants are similar to traditionally bred plants – international regulations for genetically modified organisms should be altered to exempt cisgenesis. EMBO Rep 7:750–753

Schulman AH, Oksman-Caldentey KM, Teeri TH (2019) European court of justice delivers no justice to Europe on genome-edited crops. Plant Biotechnol J 18:8–10

Schulze-Lefert P, Panstruga R (2011) A molecular evolutionary concept connecting nonhost resistance, pathogen host range, and pathogen speciation. Trends Plant Sci 16:117–125

Shamanin V, Shepelev S, Pozherukova V, Gultyaeva E, Kolomiets T, Pakholkova E et al (2019) Primary hexaploid synthetics: novel sources of wheat disease resistance. Crop Prot 121:7–10

Shaner G, Finney RE (1977) The effect of nitrogen fertilization on the expression of slow-mildewing resistance in Knox wheat. Phytopathology 67:1051–1056

Sharma P, Sharma S (2016) Paradigm shift in plant disease diagnostics: a journey from conventional diagnostics to nano-diagnostics. In: Current trends in plant disease diagnostics and management practices. Kumar P, Gupta V, Tiwari A, Kamle M (Cham: Springer): 237–264. https://doi.org/10.1007/978-3-319-27312-9_11

Sharma S, Rai P, Rai S, Srivastava M et al (2017) Genomic revolution in crop disease diagnosis: a review. In: Singh SS (ed) Plants and microbes in an ever changing environment. Nova Science Publishers, Hauppauge, pp 257–293

Shen XK, Ma LX, Zhong SF, Liu N, Zhang M, Chen WQ, Zhou YL, Li HJ, Chang ZJ, Li X, Bai GH, Zhang HY, Tan FQ, Ren ZL, Luo PG (2015) Identification and genetic mapping of the

putative Thinopyrum intermedium-derived dominant powdery mildew resistance gene PmL962 on wheat chromosome arm 2BS. Theor Appl Genet 128:517–528
Singh SP, Hurni S, Ruinelli M, Brunner S, Sanchez-Martin J, Krukowski P et al (2018) Evolutionary divergence of the rye Pm17 and Pm8 resistance genes reveals ancient diversity. Plant Mol Biol 98:249–260
Singh V, Sharma N, Singh S (2020) A review of imaging techniques for plant disease detection. Artif Intell Agric 4:229–242
Singrun CH, Hsam SLK, Hartl L, Zeller FJ, Mohler V (2003) Powdery mildew resistance gene Pm22 in cultivar Virest is a member of the complex Pm1 locus in common wheat (*Triticum aestivum* L. em Thell.). Theor Appl Genet 106:1420–1424
Solomon S, Qin D, Manning M, Marquis M, Averyt K, Tignor MMB, Miller HL Jr, Chen Z (2007) Climate Change 2007: the physical science basis. Contribution of working group I to the fourth assessment report of the intergovernmental panel on climate Change. Cambridge University Press, Cambridge, New York
Srivastava V, Anderson OD, Ow DW (1999) Single-copy transgenic wheat generated through resolution of complex integration patterns. Proc Nat Acad Sci USA 96:11117–11121
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 34:652–655
Stuiver MH, Custers JH (2001) Engineering disease resistance in plants. Nature 411:865–868
Stuke F, Fehrmann H (1988) Pflanzenpathologische Aspekte bei Sortenmischung im Weizenbau. J Plant Dis Prot 95:531–543
Stukenbrock EH, Christiansen FB, Hansen TT, Dutheil JY, Schierup MH (2012) Fusion of two divergent fungal individuals led to the recent emergence of a unique widespread pathogen species. Proc Natl Acad Sci 109:10954–10959
Sun H, Hu J, Song W, Qiu D, Cui L, Wu P, Zhang H, Liu H, Yang L, Qu Y, Li Y (2018) Pm61: a recessive gene for resistance to powdery mildew in wheat landrace Xuxusanyuehuang identified by comparative genomics analysis. Theor Appl Genet 131:2085–2097
Susi H, Barrès B, Vale PF, Laine A-L (2015) Co-infection alters population dynamics of infectious disease. Nat Commun 6:59–75
Talas F, Longin F, Miedaner T (2011) Sources of resistance to fusarium head blight within Syrian durum wheat landraces. Plant Breed 130:398–400
Tan CC, Li GQ, Cowger C, Carver BF, Xu XY (2018) Characterization of Pm59, a novel powdery mildew resistance gene in Afghanistan wheat landrace PI181356. Theor Appl Genet 131:1145–1152
Tan CC, Li GQ, Cowger C, Carver BF, Xu XY (2019) Characterization of Pm63, a powdery mildew resistance gene in Iranian landrace PI 628024. Theor Appl Genet 132:1137–1144
Tan DHS, Sigler L, Gibas CFC, Fong IW (2008) Disseminated fungal infection in a renal transplant recipient involving *Macrophomina phaseolina* and *Scytalidium dimidiatum*: case report and review of taxonomic changes among medically important members of the *Botryosphaeriaceae*. Med Mycol 46:285–292. https://doi.org/10.1080/13693780701759658
Tanweer FA, Rafii MY, Sijam K, Rahim HA, Ahmed F, Ashkani S et al (2015) Introgression of blast resistance genes (putative pi-b and pi-kh) into elite rice cultivar MR219 through marker-assisted selection. Theor Appl Genet 6:1002
Tao W, Liu D, Liu J, Feng Y, Chen P (2000) Genetic mapping of the powdery mildew resistance gene Pm6 in wheat by RFLP analysis. Theor Appl Genet 100:564–568. https://doi.org/10.1007/s001220050074
Thind AK, Wicker T, Simkova H, Fossati D, Moullet O, Brabant C et al (2017) Rapid cloning of genes in hexaploid wheat using cultivar-specific long-range chromosome assembly. Nat Biotechnol 35:793–796
Tompkins DK, Wright AT, Fowler DB (1992) Foliar disease development in no-till wheat: influence of agronomic practices on powdery mildew development. Can J Plant Sci 72:965–972

Tor M, Woods-Tor A (2017) Fungal and oomycete diseases. In: Thomas B, Murray BG, Murphy DJ (eds) Encyclopedia of applied plant sciences. Academic Press, New York, pp 77–82. https://doi.org/10.1016/B978-0-12-394807-6.00053-8

Troch V, Audenaert K, Wyand RA, Haesaert G, Höfte M, Brown JKM (2014) Formae speciales of cereal powdery mildew: close or distant relatives. Mol Plant Pathol 15:304–314

Tucker DM, Griffey CA, Liu S, Brown-Guedira G, Marshall DS, Maroof MAS (2007) Confirmation of three quantitative trait loci conferring adult plant resistance to powdery mildew in two winter wheat populations. Euphytica 155:1–13

Turner E, Jacobson DJ, Taylor JW (2011) Genetic architecture of a reinforced, postmating, reproductive isolation barrier between Neurospora species indicates evolution via natural selection. PLoS Genet 7:e1002204

Ueda A, Kathiresan A, Bennett J, Takabe T (2006) Comparative transcriptome analyses of barley and rice under salt stress. Theor Appl Genet 112:1286–1294

Ullah KN, Li N, Shen T et al (2018) Fine mapping of powdery mildew resistance gene Pm4e in bread wheat (*Triticum aestivum* L.). Planta 248:1319–1328. https://doi.org/10.1007/s00425-018-2990-y

Wang F, Wang C, Liu P, Lei C, Hao W, Gao Y et al (2016) Enhanced rice blast resistance by CRISPR/Cas9-targeted mutagenesis of the ERF transcription factor gene OsERF922. PLoS One 11:e0154027

Wang GL, Mackill DJ, Bonman JM, Mccouch SR, Champoux MC, Nelson RJ (1994) RFLP mapping of genes conferring complete and partial resistance to blast in a durably resistant rice cultivar. Genetics 136:1421–1434

Wang Y, Cheng X, Shan Q, Zhang Y, Liu J, Gao C, Qiu JL (2014) Simultaneous editing of three homoalleles in hexaploid bread wheat confers heritable resistance to powdery mildew. Nat Biotechnol 32:947–951

Wang ZL, Li LH, He ZH, Duan XY, Zhou YL, Chen XM et al (2005) Seedling and adult plant resistance to powdery mildew in Chinese bread wheat cultivars and lines. Plant Dis 89:457–463

Watson A, Ghosh S, Williams MJ, Cuddy WS, Simmonds J, Rey MD, Asyraf Md Hatta M, Hinchliffe A, Steed A, Reynolds D et al (2018) Speed breeding is a powerful tool to accelerate crop research and breeding. Nat Plants 4:23–29

Wellings CR, Luig NH. 1984. Wheat rusts, the old and the new. Australian Institute of Agricultural Science and Technology, Hawthorn, 15:5–15

Winfield MO, Allen AM, Burridge AJ et al (2016) High-density SNP genotyping array for hexaploid wheat and its secondary and tertiary gene pool. Plant Biotechnol J 14:1195–1206

Wolfe MS (1984) Trying to understand and control powdery mildew. Plant Pathol 33:451–466

Wu H, Sparks C, Amoah B, Jones HD (2003) Factors influencing successful agrobacteriummediated genetic transformation of wheat. Plant Cell Rep 21:659–666

Wu PP, Hu JH, Zou JW, Qiu D, Qu YF, Li YH, Li T, Zhang HJ, Yang L, Liu HW, Zhou Y, Zhang ZJ, Li JT, Liu ZY, Li HJ (2019) Fine mapping of the wheat powdery mildew resistance gene Pm52 using comparative genomics analysis and the Chinese spring reference genomic sequence. Theor Appl Genet 132:1451–1461

Wulff BBH, Moscou MJ (2014) Strategies for transferring resistance into wheat: from wide crosses to GM cassettes. Front Plant Sci 5:692

Wyand RA, Brown JKM (2003) Genetic and forma specialis diversity in *Blumeria graminis* of cereals and its implications for host-pathogen co-evolution. Mol Plant Pathol 4:187–198

Xiao MG, Song FJ, Jiao JF, Wang XM, Xu HX, Li HJ (2013) Identification of the gene Pm47 on chromosome 7BS conferring resistance to powdery mildew in the Chinese wheat landrace Hongyanglazi. Theor Appl Genet 126:1397–1403

Xie JZ, Wang LL, Wang Y, Zhang HZ, Zhou SH, Wu QH, Chen YX, Wang ZZ, Wang GX, Zhang DY, Zhang Y, Hu TZ, Liu ZY (2017) Fine mapping of powdery mildew resistance gene PmTm4 in wheat using comparative genomics. J Integr Agric 16:540–550

Xing L, Hu P, Liu J, Cui C, Wang H, Di Z et al (2017) NLR1-V, a CCNBS-LRR encoding gene, is a potential candidate gene of the wheat powdery mildew resistance gene Pm21. bioRxiv 2017: 114058

Xing L, Hu P, Liu J, Witek K, Zhou S, Xu J et al (2018) Pm21 from Haynaldia villosa encodes a CC-NBS-LRR protein conferring powdery mildew resistance in wheat. Mol Plant 11:874–878

Xu H, Yi Y, Ma P, Qie Y, Fu X, Xu Y et al (2015) Molecular tagging of a new broad-spectrum powdery mildew resistance allele Pm2c in Chinese wheat landrace Niaomai. Theor Appl Genet 128:2077–2084

Xu WG, Li CX, Hu L, Zhang L, Zhang JZ, Dong HB, Wang GS (2010) Molecular mapping of powdery mildew resistance gene PmHNK in winter wheat (*Triticum aestivum* L.) cultivar Zhoumai 22. Mol Breed 26:31–38

Xue F, Wang CY, Li C, Duan X, Zhou Y, Zhao N et al (2012) Molecular mapping of a powdery mildew resistance gene in common wheat landrace Baihulu and its allelism with Pm24. Theor Appl Genet 125:1425–1432

Yahiaoui N, Brunner S, Keller B (2006) Rapid generation of new powdery mildew resistance genes after wheat domestication. Plant J 47:85–98

Yahiaoui N, Srichumpa P, Dudler R, Keller B (2004) Genome analysis at different ploidy levels allows cloning of the powdery mildew resistance gene Pm3b from hexaploid wheat. Plant J 37: 528–538

Yin GH, Li GY, He ZH, Liu JJ, Wang H, Xia XC (2009) Molecular mapping of powdery mildew resistance gene in wheat cultivar Jimai 22. Acta Agron Sin 35:1425–1431

Young ND, Danesh D, Menanciohautea D, Kumar L (1993) Mapping oligogenic resistance to powdery mildew in mungbean with RFLPs. Theor Appl Genet 87:243–249

Young ND, Tanksley SD (1989) RFLP analysis of the size of chromosomal segments retained around the tm-2 locus of tomato during backcross breeding. Theor Appl Genet 77:353–359

Yuan L, Zhang J, Zhao J, Du S, Huang W, Wang J (2012) Discrimination of yellow rust and powdery mildew in wheat at leaf level using spectral signatures. In: Proceedings of the 1st international conference on agro-geoinformatics (agro-geoinformatics), Shanghai, China, pp. 5–9.

Zeller F (1973) 1B/1R wheat—rye chromosome substitutions and translocations. In: Proceedings of the 4th international wheat genetics symposium, Columbia, pp. 209–221

Zeng X, Luo Y, Zheng Y, Duan X, Zhou Y (2010) Detection of latent infection of wheat leaves caused by *Blumeria graminis* f. sp. *tritici* using nested PCR. J Phytopathol 158:227–235

Zeng XW, Luo Y, Zhou YL, Duan XY (2008) PCR detection of *Blumeria graminis* f. sp. *tritici* based on the sequences of rDNA. Acta Phytopathologica Sinica 38:211–214

Zhang D, Zhu K, Dong L, Liang Y, Li G et al (2019) Wheat powdery mildew resistance gene Pm64 derived from wild emmer (*Triticum turgidum* var. *dicoccoides*) is tightly linked in repulsion with stripe rust resistance gene *Yr5*. Crop J 7:761–770. https://doi.org/10.1016/j.cj.2019.03.0

Zhang H, Mittal N, Leamy LJ (2017a) Back into the wild—apply untapped genetic diversity of wild relatives for crop improvement. Evol Appl 10:5–24

Zhang JC, Pu RL, Wang JH, Huang WJ, Yuan L, Luo JH (2012) Detecting powdery mildew of winter wheat using leaf level hyperspectral measurements. Comput Electron Agric 85:13–23

Zhang Y, Bai Y, Wu G, Zou S, Chen Y, Gao C et al (2017b) Simultaneous modification of three homoeologs of TaEDR1 by genome editing enhances powdery mildew resistance in wheat. Plant J 91:714–724

Zhao CJ, Zhang Y, Du JJ, Guo XY, Wen WL, Gu SG et al (2019) Crop phenomics: current status and perspectives. Front Plant Sci 10:714

Zhao TJ, Zhao SY, Chen HM, Zhao QZ, Hu ZM, Hou BK et al (2006) Transgenic wheat progeny resistant to powdery mildew generated by agrobacterium inoculums to the basal portion of wheat seedling. Plant Cell Rep 25:1199–1204

Zhao ZH, Sun HG, Song W, Lu M, Huang J, Wu LF, Wang XM, Li HJ (2013) Genetic analysis and detection of the gene MlLX99 on chromosome 2BL conferring resistance to powdery mildew in the wheat cultivar Liangxing 99. Theor Appl Genet 126:3081–3089

Zheng Z, Nonomura T, Appiano M, Pavan S, Matsuda Y, Toyoda H, Wolters AMA, Visser RGF, Bai Y (2013) Loss of function in mlo orthologs reduces susceptibility of pepper and tomato to powdery mildew disease caused by Leveillula taurica. PLoS One 8:e70723

Zhou R, Zhu Z, Kong X, Huo N, Tian Q, Li C, Jin P, Dong Y, Jia J (2005) Development of near-isogenic lines for powdery mildew resistance. Theor Appl Genet 110:640–648

Zou JW, Qiu D, Sun YL, Zheng CX, Li JT, Wu PP, Wu XF, Wang XM, Zhou Y, Li HJ (2017) Pm52: effectiveness of the gene conferring resistance to powdery mildew in wheat cultivar Liangxing 99. Acta Agron Sin 43:332

Zou SH, Wang H, Li YW, Kong ZS, Tang DZ (2018) The NB-LRR gene Pm60 confers powdery mildew resistance in wheat. New Phytol 218:298–309