

Review Article

Advancements in Plant Breeding for Biotic Stress Resistance in Cereal Crops: A Comprehensive Overview.

Abstract

Current developments in plant breeding techniques used to improve cereals resistance against biotic stress. To overcome the problems provided by biotic stress, the focus is on investigating cutting-edge strategies and techniques that have transformed the area of cereal breeding. The creation of biotic stress-resistant varieties has been greatly accelerated by the introduction of Marker-Assisted Backcrossing (MABC), which enables the controlled transfer of advantageous genes from wild germplasm into elite cultivars. To better understand the genetic basis of resistance traits and support marker-assisted selection in breeding programs, Genome-Wide Association Studies (GWAS) have been useful in identifying genetic markers linked to biotic stress resistance. Researchers have been able to decipher intricate gene regulatory networks involved in plant responses against biotic stress using microarray technique; which leads to identifying critical genes and pathways underlying resistance mechanisms. New possibilities for precise genetic alterations in genomes, including as the introduction of novel resistance alleles using allele mining and the targeted disruption of susceptibility genes, have been made possible by genome editing tools like CRISPR/Cas9. Apart from these modern-day techniques, conventional methods such as mutation breeding are still being improved and combined with genomic technologies to create genetic variation and find new alleles that confer resistance to biotic stress. A promising method such as targeted gene silencing and RNA interference (RNAi) technology enables the suppression of genes linked to biotic stress susceptibility and also increases resistance. The improvement of cereal crop varieties resistant against biotic stress has advanced significantly due to the integration of these many breeding tactics and technologies. These new developments have the potential to significantly improve agricultural sustainability and food security by reducing yield losses from biotic stressors and supporting international efforts to improve crops. This review article enlightens the different conventional and advanced breeding techniques used against biotic stress found in cereal crops.

Keywords: Cereal crops, Biotic stress, MABC, CRISPR/Cas9, RNAi, and Microarray technique.

Introduction

A large proportion of the world's population feeds cereal grains like rice, wheat, and maize as their primary source of energy and nutrition for billions of people globally (Table 1). According to the FAO (Food and Agriculture Organisation) of the United Nations, global cereal production reached approximately 2.8 billion tonnes in 2021. According to FAO wheat accounts for approximately 20% of the world's caloric intake. Rice contributes around 21% of the global dietary energy supply as per the estimation of IRRI (International Rice Research Institute) Philippines. USDA (United States Department of Agriculture) states that maize accounts for approximately 15% of world caloric intake. Rice, wheat and maize account for two-thirds of the total and also make up more than 90% of world cereal production, (FAO).

Table 1: Global production and consumption of the major cereals

Crop	Production (million tons/year)			Consumption (million tons/year)			Major exporting countries
	2021/22	22/23	23/24	2021/22	22/23	23/24	
Wheat	780	803	789	784	794	806	Argentina, Australia, Canada, EU, Russia, Ukraine, USA
Rice	514	514	512	520	159	516	India, Pakistan, Thailand, USA, Vietnam
Maize	1224	1163	1223	1213	1181	1212	Argentina, Brazil, Ukraine, USA

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However, a variety of biotic stressors, such as infections raised by pathogens including fungus, bacteria, viruses and pests; pose a continual danger to these crops. The percentage losses caused by some major pathogens in Rice (*Xanthomonas O*; 30%, *Pyricularia O*, 10-30%, *Rhizoctonia solani*; 20%, etc (Savary, S et al., 2000), wheat (*Puccinia spp.*; 70%, *Fusarium graminearum* ; 10-50%, etc, (Singh, R. P et al., 2016), and Maize (*Chilo pertellus* ; 80%, *Sesamia inferans* ; 25.5-78.9%, *Antherigona soccata* ; 21.28%, *A. orientalis* ; 20%, fall army worm ; 73%, etc (Kumar P et al., 2018). To strengthen cereal crop's resistance to these risks and promote sustainable agriculture and global food security, breeding for biotic resistance has shown to be an essential approach. Considerable improvement has been achieved recently in decrypting the genetic keystones of biotic resistance and applying sophisticated breeding methods to create resistant cultivars. The molecular processes behind

plant-pathogen interactions have been elucidated by recent research, offering important new information on the identification and description of resistance genes in cereal crops. For example, in rice, breeding efforts have been transformed by identifying and using important resistance genes, such as Xa21 and Pi-ta, against bacterial blight and blast disease, respectively (Khan MA et al., 2015).

Phenotyping and high throughput genotyping technology have also sped up the process of finding resistant alleles and introducing them into elite germplasm. Breeders may now quickly identify genomic areas linked to resistance features and accelerate the creation of resistant cultivars using genome-wide association studies (GWAS) and genomic selection (Anilkumar C et al., 2022). Genetic resources from landraces and wild relatives in wheat have been essential in widening the genetic diversity for disease resistance. Traditional breeding and marker-assisted selection techniques have successfully transferred genes that confer resistance to wheat diseases such as wheat rusts and powdery mildew into elite genotypes. (Kang Y et al., 2020). Similarly, efforts have been focused on maize to improve resistance against severe diseases like northern leaf blight and maize fatal necrosis using available genetic variety and natural variation. The discovery and implementation of novel resistance genes in maize improvement pipelines have been made easier by the integration of genomic technologies with traditional breeding techniques (Ding J et al., 2023).

The introduction of novel pathogen strains, the stability of resistance genes, and the complicated genetic makeup of resistance features are some of the obstacles that remain in the way of biotic resistance breeding, despite notable advancements. To generate robust and sustainable cereal crop types, multidisciplinary techniques incorporating plant pathology, breeding, and genomics will be necessary to address these difficulties. Finally, new developments in the breeding of cereals for biotic resistance provide encouraging chances to reduce the negative effects of biotic stressors on the world's food supply. To provide food security and sustainable agriculture in the face of changing biotic challenges, research and development initiatives focused on improving cereal crops' genetic resilience must continue. Although there have been significant advancements in the last ten years in the creation and application of sustainable technologies to improve plant resistance against biotic stress but there is still a lacuna between controlled vs open field studies (Aghnoum R., et al (2010)). Over time, breeding programs have been changed since these programs utilize genomic tools instead of more traditional breeding methods. Many breeding programs have been benefited from the genetic information supplied through modern biotechnology such as allele mining and NGS platforms, that would not possible with only conventional breeding

techniques (Selvakumar, R., et al (2023)). Biotechnological "omics" technologies have greatly aided plant stress tolerance breeding by providing insight into genetic diversity, genotype variants, genetic maps, and other useful information related to the genetics of plant populations. This article offers a thorough summary of the most important tactics, difficulties, and potential future developments in the breeding of biotic resistance in cereal crops such as rice, wheat and maize etc.

a) Impact of biotic stressors on cereal crops

Many different types of organisms, including bacteria, fungus, viruses, and insects, can produce biotic stressors on plants. Numerous studies have demonstrated how biotic and abiotic stressors significantly lower cereal crop development and output. At several development phases (panicle formation, booting stage, and lactation stage), the bacterial leaf blight disease decreased rice production and grain quality (Noh et al. 2007). Sorghum's total seed weight, 100-seed weight, and seeds per panicle were all decreased by fusarium stalk rot and charcoal rot disease (Bandara et al. 2017). The most destructive *Magnaporthe oryzae* disease in cereals is blast disease. The growth of the leaf, stem, collar, node, neck, and panicle in all cereals is impacted by blast disease. Additionally, it has decreased the growth and production of all crops that are significant to the economy, including barley (Aghnoum et al. 2019), wheat (Cruz and Valent 2017), finger millet (*Eleusine coracana*) (Mbinda W et al., 2021), foxtail millet (*Setaria italica*) (Sharma et al. 2014), and rice (Kihoro et al. 2013). Barley and wheat yields were decreased by more than 40% due to yellow dwarf virus (Perry et al. 2000).

Several historical occurrences, such as potato blight in Ireland, coffee rust in Brazil (Rogers, 2004), and maize leaf blight in the USA (Ullstrup, 1972), resulted in total crop failure and starvation in the affected areas. Another instance of crop failure brought on by illnesses is the Great Bengal Famine of 1943. Millions of people died because of these incidents, and many more moved to other areas. According to Christou and Twyman (2004), biotic stressors such as insects and diseases significantly lower grain productivity. Specifically, just illnesses account for 10% of the world's food production, which results in 800 million people being hungry. In a similar vein, developing agricultural plants that are resistant to biotic stressors is challenging due to the lack of reliable resistance sources (Strange, 2005). On the other hand, plants are resistant to biotic stressors due to one or more genes. Therefore, plant breeders may use this genetic base to help agricultural plants become resistant to pest insects and illnesses. There are several breeding approaches that have been successfully utilized against biotic stress. These are categorized under conventional and advanced breeding approaches.

1. Conventional breeding approaches for biotic stress resistance

The availability of resistance sources determines the techniques and tactics used to induce and improve agricultural plant resistance to biotic stressors. Breeding tactics may be classified into traditional and contemporary ways. Conventional plant breeding techniques played a major part in the creation of biotic stress-tolerant cultivars. The different approaches employed for this goal are explained below.

1.1 Introduction of Exotic Lines

In the 1970s, a devastating corn leaf blight epidemic caused by the *Cochliobolus heterostrophus* pathogen wiped out corn crops in the southern United States. This was due to the lack of genetic diversity in the corn varieties grown in that region (Ullstrup, 1972). The epidemic was triggered by the emergence of a new race of pathogens called Race T, which possessed the T-cms virulence gene. To address this issue, a new type of corn, known as Texas cytoplasm, was introduced. Similarly, Shah et al. (1982) reported that potato germplasm imported from the USA, India, and the Netherlands showed promising resistance against potato leaf roll and blight diseases. This highlights the importance of introducing new genetic material to enhance the diversity and disease resistance of crop plants when local germplasm lacks these traits. Such introductions can be made through multinational companies or foreign gene banks. A recent and significant example is the introduction of Bt-cotton in Pakistan and India. As a result, a large area of the Pakistani cotton belt has been converted to transgenic Bt-cotton, replacing indigenous non-Bt cotton varieties (Sabir et al., 2011). The use of wild relatives also plays a major role in the cultivar development for biotic stress resistance (Table 2).

Table 2. Use of wild relatives in the development of biotic stress resilient cultivars:

Crop	Wild sp.	Trait	References
Wheat	<i>Triticum timopheevii</i>	Stem rust resistance	Kashyap, A et al., (2022)
	<i>Triticum turgidum</i>	Yellow rust resistance	Chhuneja et al., (2008)
	<i>Aegilops ventricosa</i>	Eye-spot resistance	Kashyap, A et al., (2022)
	<i>Aegilops geniculata</i>	powdery mildew resistance genes	Stoilova and Spetsov (2006)
	<i>T. turgidum var. dicoccoides</i>	Powdery mildew resistance	Blanco et al. (2008)
	<i>Aegilops tauschii</i>	Hessian fly resistance	Suszkiw (2005)
	<i>Triticum monococcum</i>	powdery mildew &	Yao et al., (2007)

		leaf rust	
	<i>Aegilops variabilis</i> .	nematode (<i>Heterodera avenae</i>) resistance	Barloy et al. (2007)
Rice	<i>Oryza longistaminata</i>	bacterial blight disease resistant	Khush et al. (1991)
	<i>Oryza nivara</i>	Grassy stunt virus resistance	Brar and Khush (1997)
	<i>O. brachyantha</i>	Yellow stem borer resistance	Behura et al. (2011)
	<i>Oryza rufipogon</i>	Brown plant hopper	Yang, M., et al (2020)
	<i>Oryza nivara</i>	Bacterial blight	Cheema, K.K., et al (2008)
Maize	<i>Tripsacum dactyloides</i>	Common Rust	Wani, S.H., et al (2022)
	<i>Zea diploperennis</i>	Maize Chlorotic Dwarf Virus	Wani, S.H., et al (2022)
	<i>Tripsacum dactyloides</i>	Northern Corn Leaf Blight, Maize weevil	Wani, S.H., et al (2022)
	<i>Zea mexicana</i>	Downy mildew, gray leaf spot	Wani, S.H., et al (2022)
	<i>Zea parviglumis</i>	Gray leaf spot, banded leaf and sheath blight	Wani, S.H., et al (2022)
Barley	<i>Hordeum bulbosum</i>	Stem rust resistance	Kashyap, A et al., (2022)
	<i>Hordeum vulgare</i>	spot blotch, leaf blotch and leaf scald	Kashyap, A et al., (2022)
Oat	<i>Avena strigosa</i>	multiple herbicide resistance	Lehnhoff et al., (2013),
	<i>A. barbata</i>	leaf rust resistance	Adhikari et al., (1999)

1.2 Hybridization and cultivar development

Hybridization is a technique to combine desirable genes from different sources, such as higher yield, disease resistance, and insect resistance, into a single plant variety. Plant breeders have successfully developed numerous disease-resistant hybrids and cultivars of various crop plants through conventional hybridization followed by selective breeding. One notable example is Lasani-2008, a wheat cultivar resistant to the Ug-99 stem rust pathotype. Pakistani plant breeders have developed Lasani-2008 variety, which exhibits high resistance to the Ug-99 race of stem rust (Singh et al., 2011).

The first step in this process is to identify the source of resistance for selecting the parental lines for crossing and developing resistant genotypes. The provided table lists various crop plant cultivars released world-wide for disease and insect resistance (Table 3).

Table3.Different cultivars of cereals around the world and their disease resistance.

Cereal crops	Cultivar	Place	Resistance to disease	reference
Rice	Koshihikari	Japan	Blast	Ishizaki K et al., (2005)
Rice	Gangyuan8	China	Rice sheath blight	Wang, Y et al., (2022)
Rice	Karnal Local (indica rice)	India	Yellow stem borer	Ali J, Wani SH (2021)
Rice	IR64	India	Blast	Ali J, Wani SH (2021)
Rice	Swarna	India	Bacterial blight	Ali J, Wani SH (2021)
Rice	Pusa Basmati-1	India	Blast, BLB	Ali J, Wani SH (2021)
Rice	IR8	IRRI (Philippines)	BLB	Khush, G.S., et al. (2005)
Wheat	Pusa Yashasvi	India (ICAR)	Yellow, Brown rust	Arun Gupta, et al., (2023)
Wheat	Karan Vrinda	India(ICAR)	Leaf rust	Arun Gupta, et al., (2023)
Wheat	Karan varuna	India (ICAR)	Leaf rust	Arun Gupta, et al., (2023)
Wheat	Pusa Ojaswi	India (ICAR)	Stem & Leaf rust	Arun Gupta, et al., (2023)
Wheat	PBW 826	India (PAU)	Wheat blast	Arun Gupta, et al., (2023)
Maize	NC250P	United states	Southern corn leaf blight	Belcher AR et al, (2012)
Maize	Ganga 7	India	Maize Rust	Naser M, et al., (2023)
Maize	Rajendra Hybrid	India	Maize rust	Naser M, et al.,

	makka -2			(2023)
Maize	Nyamula	IRRI (Phillipines)	Fall army worm	Xavier Chiriboga M, et al., (2021)
Maize	ZD05	Africa	Striga resistance	Rich PJ, Ejeta G (2018)

1.3 Backcross breeding

One of the most popular techniques for introducing a oligogene resistant to disease or insects into a high-yielding, vulnerable cultivar is backcross breeding. In this instance, the resistant cultivar is the donor, and the high-producing variety is the recipient. Researchers in India employed marker-assisted backcross breeding (MABC) to introduce blast resistance genes (xa13 and Xa21) from a donor variety into four popular Basmati rice cultivars (Pusa 3037, Pusa 3054, Pusa 3060, and Pusa 3066) (Singh G, et al., (2023)). This approach aimed to enhance blast resistance while retaining the desirable quality traits of Basmati rice.

1.4 Gene pyramiding (Multi line breeding)

Crop plant resistance is vertical or horizontal. Vertical resistance is regulated by a single gene and is short-lived because pathogen races evolve (Van derPlank, 1975). However, horizontal resistance is regulated by multiple genes and may withstand many pathogen races, making it persistent (Browning, 1969). Thus, gene pyramiding from numerous sources in single cultivars gives long-term resistance to biotic stressors (especially diseases) and has become a technique for plant breeders to generate disease-resistant cultivars against various pathogen races (**Fig 1**). Composite crosses, synthetics, and multiline breeding (Keneni et al., 2004) are used. Finckh et al. (2000) reported different features using gene pyramiding methods, especially of composite cross, and found that composite crosses give improved and lasting resistance against diseases and insect pests. Steffan et al. (2011) performed 218 crossings of 30 wheat types to integrate the bunt resistance genes in a single population and finally in a cultivar. Molecular markers were employed for analyzing the polymorphism in the F2 and F3 generations. After each crossing cycle, the populations were bulked and later investigations indicated transmission of resistance genes throughout this procedure. McDonald (2014) suggested that with the availability of molecular tools, composite crosses may be utilized to accumulate the R genes in populations.

Another viable method for developing horizontal resistance in agricultural plants is multiline breeding (Mundt 2014). Since several iso-lines are created in multiline breeding to improve a high-yield cultivar, it is also known as the "dirty crop" strategy. Multiline combinations consist of plants with similar morphologies but distinct genetic profiles; alternatively, a single variety may be employed (Keneni et al., 2012). By using established methodologies, Marshall and Pryor (1978) investigated the effectiveness of multilines for long-term durable resistance and concluded that multilines provide steady yield because they include a large number of resistant genes. Multiline cultivars are an effective strategy for managing insects and diseases. Multilines, which are combinations of iso-lines, are much more valuable in epidemiological settings since several resistance genes are at play. To generate powdery mildew-resistant wheat, Brunner et al. (2012) developed a novel method of imparting persistent resistance that blends traditional breeding with a cutting-edge transgenic technique. In their study, near-isogenic lines (NILs) with various resistance genes were combined to create multilines. Except for the single R gene, these NILs were produced with the identical genetic background. Using distinct locus Pm3 alleles, they created NILs of the same origin called Pm3a, Pm3c, Pm3d, Pm3f, or Pm3g based on the allele expressed in a given line. While all of these transgenic lines demonstrated enhanced resistance against powdery mildew the resistance increased to a greater extent than individual transgenic lines when a multiline including Pm3a, Pm3b, and Pm3d transgenic lines was created. Future studies will aim to generate agricultural plants with lasting resistance.

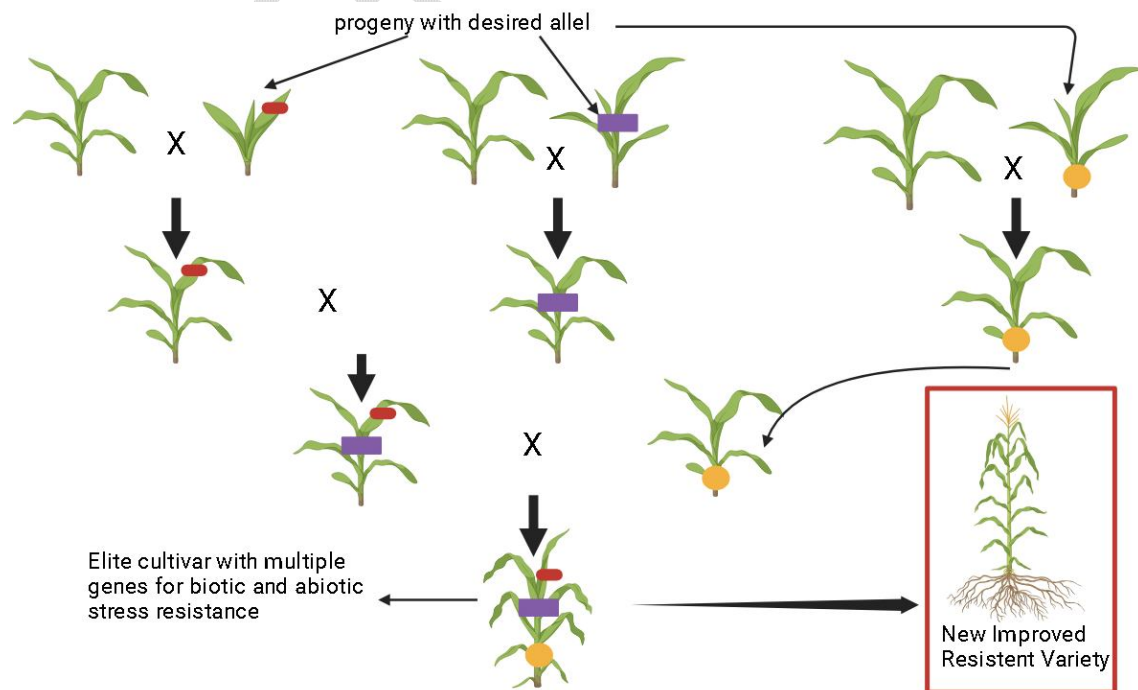


Fig 1 Stepwisessimultaneous transfer of genes into Maize crop using Gene pyramiding

2. Modern breeding methods for biotic stress resistance

The problems associated with classical breeding methods are the longer time required to develop resistance cultivars, more effort and labor requirements, and the transfer of non-desirable genes along with resistance genes. Therefore, there was a need to develop new and efficient modern methods to overcome the above-mentioned problems. With the advancement of molecular genetics knowledge, many modern methods have been developed for this purpose. The modernbreeding procedures to overcome the problems associated with traditional breeding strategies are given below.

2.1 Marker-Assisted Backcross Breeding for Resistance Traits

The MABC process includes molecular markers to introduce traits from a donor parent into a recurrent parent (often a popular variety). As a result, the product (variety/cultivar) keeps the entire genome of the recurrent parent, together with the gene of interest from the donor parent. In MABC, the introduction of DNA markers dramatically improves selection efficiency while shortening varietal development time by many years. This method may also be used to generate near-isogenic lines (NILs) or chromosomal segment substitution lines (CSSLs), which are commonly utilized for gene/QTL analysis and foreign gene introgressions (Varshney et al., 2013).

The steps of MABCare as follows(**Fig 2**).

1. Generating F1 by crossing recurrent and donor parents.
2. Backcrossing F1 with the recurrent parent for foreground and background selections.
3. Selfing of backcross generation to obtain the gene of interest in homozygous form.

The MABC breeding program effectively improved stress tolerance in rice by introducing bacterial blight resistance genes Xa13 and Xa21 into the parental lines of the superfine grain aromatic rice hybrid Pusa RH 10 (Singh et al., 2020). Similarly, a simultaneous but progressive transfer approach was used to transfer the blast resistance genes Pi-Kh and Piz5 from the donors Tetep and C101A51. However, the majority of breeders' desirable traits are regulated by several genes, such as resistance to multiple pathogen races. In such circumstances, the MABC technique is proven to be rather difficult in keeping the optimal gene combinations (Peleman & Van der Voort, 2003)

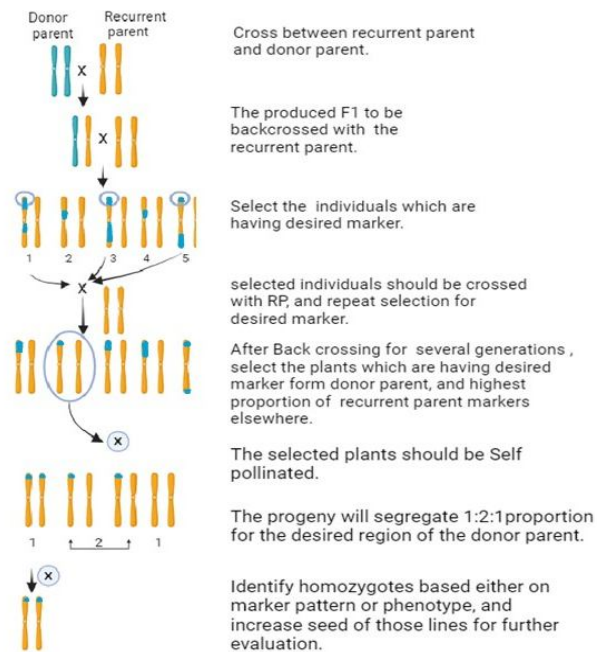


Fig 2 Workflow of marker-assisted backcross selection.

2.2 Mutation breeding

When natural sources of resistance are not readily available within germplasm, one possible approach is to induce heritable changes or mutations in crop plants and then identify rare mutants that are resistant to biotic stress. The discovery of new germplasms can be attributed to the identification of advantageous mutations, which are genetic changes caused by the application of chemicals or radiation (Suprasanna, P et al. 2015). Additionally, novel compounds such as benzothiadiazole (BTH) have been used in wheat for this purpose. According to the International Atomic Energy Agency, a leading organization involved in mutant database development, 3250 mutant varieties from various plant species have been officially released worldwide.

According to a study by Taheri et al. (2018), cereals make up 49.5% of the total, while ornamental plants and legumes account for 21.9% and 15%, respectively. Rp1-based Les Maize mutant provided protection against the *Puccinia sorghi* rust pathogen and *Cercosporazea maydis*, which causes gray leaf spot disease (Johal, 2007).

The development of the TILLING (targeting induced local lesions in genomes) method leads to the identification of beneficial mutations significantly, and these genome sequence data for

cereal crops can be used to identify new alleles in the germplasms that could help to improve important traits like yield, disease resistance, and nutritional value (Jankowicz-Cieslak, J et al. 2017). It allows for the quick detection of mutations in genes of interest within a mutagenized population (Kumar, A.P.K et al. 2017).

2.2.1 Tilling and Eco-Tilling

Claire McCallum and associates developed the TILLING technique in the late 1900s while working on *Arabidopsis* in their research (Borevitz, J.O et al. 2003). Although TILLING has exposed a useful technique for detecting induced mutations, naturally existing variants may be assessed using the EcoTILLING approach. To find novel allelic variants for upcoming molecular breeding, EcoTILLING has been applied to a variety of crops, such as *Arabidopsis*, rice, wheat, and sorghum (Jawher, M. et al. 2018). High-resolution melting (HRM), next-generation sequencing, and the LI-COR approach, which employs the enzyme CEL I for mutation identification, are the three main techniques for screening the mutant population utilizing TILLING (Blomstedt, C.K. et al. 2012). Out of all of these techniques, LI-COR (Dahmani-Mardas, F. et al. 2010) is the most recommended method for TILLING in plants. The following procedures are part of the standard approach for developing a TILLING platform in plants (Fig.3).

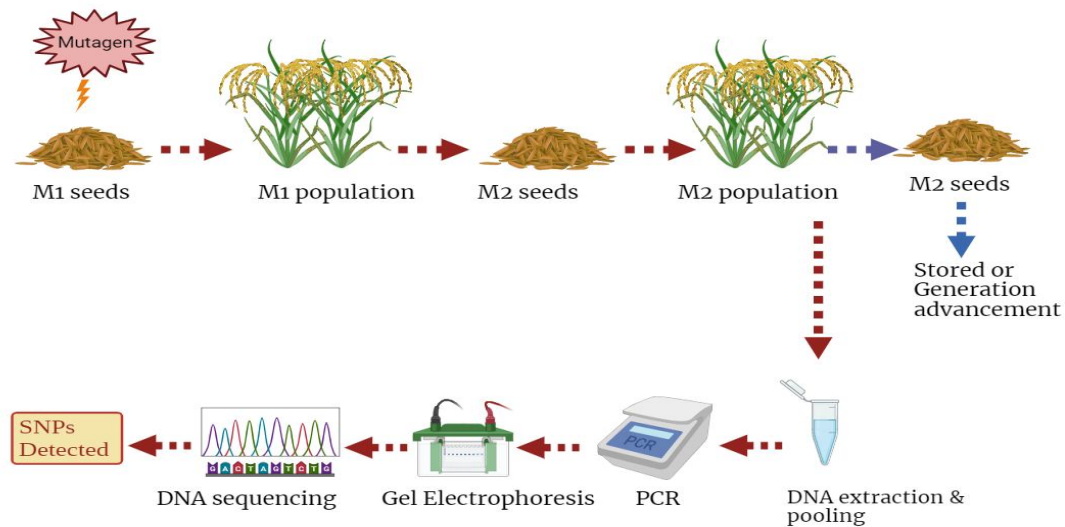


Fig 3. Standard approach for developing a TILLING platform in plants.

2.2.2 Applications of Tilling in Cereal Crops:

For the past eight decades, mutation breeding has played a significant role in the agricultural industry. The application of TILLING to mutant breeding utilizing radiation or chemical treatment for starch synthesis, for developing plant architecture has led to greater yielding of rice, Maize, and wheat (Chenet al, 2014)

2.2.3 Tilling to combat disease resistance

Multiple factors of living organisms' stress can impede wheat production, with one significant barrier being powdery mildew, stemming from *Blumeria graminis f. sp. Tritici*. Through TILLING, a technique identifying genetic variations, barley's Mlo gene equivalent in wheat, TaMlo, was analyzed. Among the three TaMlo homoeologs in wheat, sixteen mutations altering amino acids were discovered. Four mutant lines exhibiting resistance to powdery mildew were consequently generated, marking a notable stride in creating commercially viable, non-genetically modified wheat strains resistant to this fungal disease, as reported by Acevedo-Garcia et al. (2017). Similarly, in maize TILLING populations, two genes (ZmWAK-RLK1 and ZmWAK-RLK2) associated with northern corn leaf blight resistance were identified.

2.3 Transgenic approach

Resistance cannot be introduced via traditional hybridization when resistance genes are absent in a given species, even from its wild relatives and landraces. In this case, recombinant DNA technology is used to transfer resistant genes from another species to get past the genetic barriers. Different transformation technologies, such as gene cannon or particle bombardment, electroporation, floral dip (direct transformation methods), and Agrobacterium-mediated transformation (in direct transformation methods), are used to deliver foreign genes to agricultural plants. Even though appropriate biosafety procedures are performed while evaluating GMOs, their unnatural nature makes them risky. Between 1996 and 2003, the area planted with transgenic crops expanded 40 times globally, from 1.7 million hectares to 67.7 million hectares (Sathishkumar R, 2019).

2.3.1 RNAi-mediated gene silencing

RNAi silencing has been applied against viruses, bacteria, fungi, and nematodes for the development of biotic stress-resistant plants. The RNAi phenomenon was initially recognized in *Caenorhabditis Elegans*, a free-living worm (Fire, et al., 1998), wherein exogenously given

sense and antisense RNAs effectively silenced gene expression in this model nematode. Double-stranded RNA (dsRNA) molecules produce RNA interference (RNAi), a biological process that stops the production of certain genes by causing post-transcriptional gene silencing (PTGS) (Bosher JM, et al., 2000). It also plays a useful function in evaluating the alterations that take place in signaling networks (Tierney et al., 2005).

There are essentially three steps involved in RNAi-mediated gene silencing (Siomi & Siomi 2009). The first step includes ribonuclease III breaking down long dsRNA into little dsRNA; the second stage involves unwinding these small RNAs to generate one guide strand, which is loaded into the RISC, while the other strand, referred to as the passenger strand, degrades. Ultimately, the RISC finds mRNAs with guide-complementary sequences, attaches to these sequences, and either destroys the mRNA or prevents its translation, all under the guidance of the guide strand (Winter et al. 2009).

2.3.2 RNAi for plant disease resistance

Pathogens pose a threat to extinction for entire plant species and can drastically reduce agricultural yields, which can have a severe negative economic impact. RNAi-induced gene silencing has been a useful tool for engineering plants resistant to pathogens in the past ten years (Duan CG et al. 2012). According to Jiang CJ et al. (2009), rice can employ RNAi to knockdown OsSSI2 (OsSSI2-kd), which is responsible for fatty acid desaturase activity and increased resistance against blast fungus (*Magnaporthe grisea*) and bacterial pathogens (*Xanthomonas oryzae* pv. *Oryzae*). Avra10, a host-induced gene that causes fungal disease in wheat (*Triticum aestivum*) and barley (*Hordeum vulgare*), can be used to silence the genes by causing temporary gene expression through RNA interference. This shows that RNAi-based plant protection against these infections results from the transfer of RNA from the host plant to the fungal pathogen *Blumeria graminis* (Escobar MA, et al. 2001). Viral-induced gene silencing is another natural antiviral defense mechanism that RNA silencing uses to create resistance to viral infections (Ding SW et al. 2010). By RNA interference (RNAi), plants may also regulate viral infections and exhibit resistance provided they possess appropriate hairpin or anti-sense RNAi constructions (Sudarshana MR, et al. 2007).

2.3.3 RNAi for resistance to pests and plant insects

A strong and more intensive method for combating a variety of harmful insects and pests that result in large financial losses is provided by RNAi. It is known that insects have two different types of RNAi pathways: non-cell-autonomous and cell-autonomous. Only the cells

that the supplied or administered have cell-autonomous RNAi. Environmental and systemic RNAi are the two classes into which non-cell-autonomous RNAi may be divided, depending on how the cell obtains the dsRNA. Environmental RNAi refers to the uptake of dsRNA by a cell from its surrounding background. The reaction does not always propagate throughout the body as a result of environmental RNAi. Environmental RNAi is the term for dsRNA that has to be absorbed by gut cells from the gut lumen to effectively elicit RNAi. If the target gene transcripts are widely expressed in organs other than the intestine, systemic RNA interference (RNAi) is required for the silencing signal to propagate. Delivering dsRNA to the trypsin-like serine protease gene *NItry* of *Nilaparvata lugens*, the carboxypeptidase gene *NIcar*, and the hexose transporter gene *NIHT1* allowed for the development of transgenic rice. The study found that the insects that consumed these transgenic rice plants had lower transcript levels of these three targeted genes. Insect lethality, however, was not mentioned (Zha et al., 2011).

2.4 GWAS (Genome-wide association mapping)

The substantial correlation between a marker locus and phenotypic trait is necessary for genome-wide association mapping (GWAS). This method takes thousands of polymorphisms into consideration when assessing the impact of QTLs, or quantitative trait loci. By using high resolution to identify single nucleotide polymorphisms (SNPs) inside genes that cause phenotypic change, the GWAS circumvents several limitations associated with traditional QTL/gene mapping techniques (Soto-cerda and Cloutier 2012). In maize, the idea of association analysis was used both on a genome-wide level (Beló et al. 2007) and as a candidate gene-based association research (Thornsberry et al. 2001). Since its creation, GWAS has been enhanced to increase the validity of marker-trait connections by utilizing a variety of statistical procedures and target population configurations. These days, GWAS mapping is frequently used to analyze the genetic makeup of many complex plant characteristics, including cereals. Apart from the traditional/wide GWAS, various methods were created using association principles to identify the relationships between markers and traits. These methods include nested association mapping (NAM), multi-parent advanced generation intercross (MAGIC), and other techniques related to population structure like genomic control (GC) (Soto-cerda and Cloutier 2012) and structured association (SA) (Pritchard et al. 2000).

To get around the drawbacks of biparental populations, geneticists have recently developed multi-parent populations (MPPs). The MPPs have been produced and used with success in a

variety of crops, including cereals, for gene mapping and breeding (Scott et al. 2020). With the establishment of the NAM population in maize, high-resolution mapping of the genomic areas linked to leaf architecture and quantitative resistance to leaf blight was achieved (Kump et al. 2011).

2.4.1 Nested Association Mapping (NAM) The benefits of association mapping and linkage mapping are combined in NAM, an integrated technique involving several parents. Fixed lines (RILs, NILs, and DHs) that were created by a mixture of multiple unique and common founding parents make up NAM. The collective RIL/NIL/DH populations derived from every cross of the donor-common founder parents make up the NAM population. Using the first NAM population created in maize, at least a dozen research has been published (Gireesh et al. 2021).

The RILs produced by a sophisticated crossover operation incorporating multiple paternal lines make up the MAGIC population. These populations are essentially a continuation of highly developed inbred lines through intercrossing. The benefits of large germplasm collections and biparental populations are combined in the MAGIC populations. Using GWAS and MPP-based mapping techniques, important QTLs and genes for different biotic and abiotic stress tolerances in cereals have mainly been identified. In terms of disease resilience, GWAS searches revealed a novel allele *Pikx* at the *Pik* locus for blast resistance and two LRR-containing loci (Os01g0601625; Os01g0601675) linked to *Bakanae* resistance (Li et al. 2019a). Furthermore, genomic regions associated with resistance to brown spot disease, submergence tolerance, and the brown planthopper (*Nilaparvata lugens*), a major rice insect pest, have been identified through the utilization of MAGIC panels (Satturu et al., 2020). Using multiple genome-wide association mapping in a 391-line MAGIC panel, thirteen putative genes linked to BPH resistance were found. According to Satturu et al. (2020), these genes included *WRKY70*, NHL repeat-containing protein, NB-ARC domain-containing protein, and LRR-containing protein.

Because of wheat's complex genome and a higher percentage of repetitive sequences than other important cereal crops like rice, typical GWAS applications are extremely difficult to implement in this crop (Pang et al. 2020). However, four pleiotropic QTLs for leaf and yellow rust diseases have been identified by recent GWAS using 90K SNP-chip genotyping: *Lr46/Yr29*, *QLr-2AL.1/QYr-2AL.1*, *QLr-2AL.2/QYr-2AL.2*, and *QLr-5BL/QYr-5BL.1* (Zhang et al. 2021). Additionally, possible QTLs for much additional biotic stress tolerance in wheat, such as stem rust (Megerssa et al. 2020), tan spot (Galagedara et al. 2020), wheat

blast (Juliana et al. 2020), and spot blotch (Tomar et al. 2021) have also been found by recent GWAS research.

Maize is an ideal crop for GWAS studies owing to quick LD decay, but barely any GWAS studies have been carried out on examining the genetic basis of stress tolerance-associated traits. Many general/classical GWAS investigations were reported for different stress tolerance phenotypes in maize, however only a small number of studies were able to uncover key genes, QTLs or alleles linked to stress tolerance. F-box protein (ZmFBL41) for banded leaf and sheath blight (BLSB) (Li et al. 2019b) and caffeoyl-CoA O-methyltransferase (ZmCCoAOMT2) for both southern leaf blight (SLB) and gray leaf spot (GLS) illnesses (Yang et al. 2017) were identified as the products of GWAS research related to biotic stress tolerance. In contrast to other cereals, MPPs were created and applied extensively for trait mapping in maize.

2.5 GENOME EDITING (GE)

It takes a lot of time, effort, and money to develop disease resistance into elite cultivars using the traditional strategy (Romero and Gatica-Arias 2019). But with the dawn of the genomics age, genome editing has become a viable way to deal with the problems associated with agricultural output. The enhancement of disease resistance in various crops has been made possible by the ongoing advancements in genome-editing tools such as transcription activator-like effector nucleases (TALENs), zinc-finger nucleases (ZFNs), site-specific mutagenesis (SSM), meganucleases (MNs), and the CRISPR/Cas system (Mishra R, et al. 2018; Zafar K, et al. 2020). When compared to SSM, MNs, and ZFNs, TALENs and the CRISPR/Cas system stand out among these technologies due to their variety, speed, and relative efficiency.

a) CRISPR

The CRISPR gene family comprises repeated DNA sequences that are present in the genomes of bacteria (45%) and archaea (84%). It was initially discovered in *Escherichia coli* downstream of the alkaline phosphatase isozyme gene (Ishino et al. 1987). Previously referred to as short, regularly spaced repeats (SRSRs), it aids in the identification and elimination of the virus's DNA. Small guide RNAs (gRNAs) are used by the CRISPR system to interfere with invasive nucleic acids in a sequence-specific manner. A collection of brief repeating sequences, or repeats, spaced apart by distinct sequences, is known as CRISPR. The CRISPR/Cas mechanism can be broadly divided into three stages: (1) spacer acquisition or adaptation, which involves inserting unique sequences into the CRISPR locus; (2) transcription of the CRISPR locus and processing of gRNA, which involves expression or

gRNA biogenesis; and (3) target interference, which involves the detection and degradation of nucleic acids by gRNA and Cas proteins (Liu et al. 2017). Two classes (Classes I and II) comprise the CRISPR/Cas system (Makarova et al. 2020). Although the genomes of both classes of CRISPR systems might be edited, the class II system is preferred for genome editing because of its far more straightforward technique. Three hallmark proteins—Cas1, 2, and 9—which comprise three subtypes (II-A, II-B, and II-C)—classify the class II CRISPR/Cas systems. The most used CRISPR system for editing genomes in a variety of species among the three proteins is Cas9 (Fig 4).

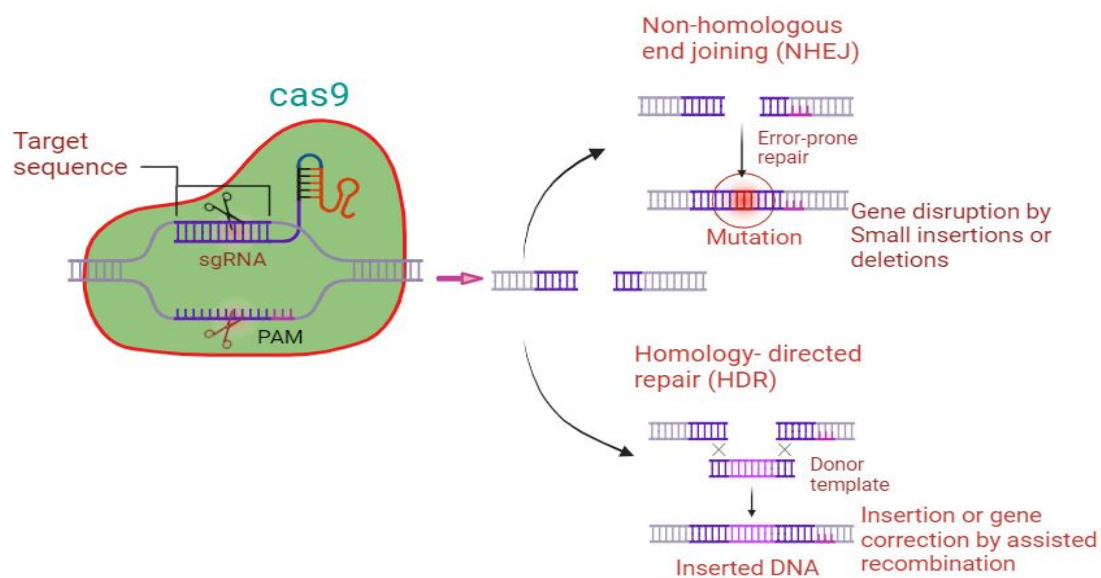


Fig 4 CRISPR cas9 mediated genome editing.

2.4.1 Improving biotic stress tolerance in cereals by CRISPR/Cas system

Various pesticides, herbicides, and fungicides are used to manage diseases of cereal crops but they all contaminate the environment and lead to risks to the health of human and animal. Therefore, plants become resistant to diseases including bacteria, viruses, fungi, and insects. CRISPR/Cas variants that have been used to target certain biotic stress-responsive genes in cereal are presented below.

2.4.2 Bacterial disease tolerance

Numerous diseases in which bacteria infect grains such as Bacterial blight is a serious rice disease in West Africa and South Asia. According to some studies, rice plants afflicted with bacterial blight disease exhibit higher growth due to the presence of sucrose family (SWEET) transporters. Rice growth against bacterial blight disease was enhanced by OsSWEET13 gene knockout using CRISPR/Cas9 (Zhou et al. 2015). In another research, the CRISPR/Cas9 system altered three SWEET family genes (SWEET11, 13, and 14) to improve rice plant height and panicle length while lowering bacterial blight infection (Oliva et al. 2019). Only one family transporter has yet to be targeted by the CRISPR/Cas system. Numerous genes belonging to the resistance (R) and bacterial blights (BB) families were found and given functional descriptions in cereals. CRISPR/Cas variants that target the BB and R family genes improve grain development in the presence of bacterial illness.

2.4.3 Fungal disease tolerance

Chemical fungicides are used in agriculture to inhibit fungal infections from causing losses. To create plants resistant against powdery mildew wheat, (Wang et al., 2014) used the CRISPR/Cas9 technology to modify the mildew resistance locus (MLO) genes (TaMLO-A1, B1, and D1). The ethylene-responsive factor 22 (OsERF922) gene in rice was knocked out using the CRISPR/Cas9 technology allowing the generation of a disease-resistant rice variety without compromising the rice's normal growth (Wang et al, 2016). The CRISPR/Cas9 system's disruption of the rice component exocyst complex 3A (OsSEC3A) gene improved rice plant development resistance to blast disease (Ma et al. 2018). With the use of the CRISPR/Cas9 system, (Zhang et al., 2017) produced powdery mildew-resistant wheat by utilizing the enhanced disease resistance 1 (EDR1) gene. Therefore, using the CRISPR/Cas system to target the genes that confer resistance to fungal illnesses may reduce the virulence of infections, aiding in the management of fungal diseases throughout plant growth.

2.4.4 Insects or pest tolerance

Insects are the main carriers of viral infections in cereals, so a lot of pesticides are needed to stop the infection from spreading. The tungro bacilliform virus and the tungro spherical virus work together to cause tungro disease, which is a serious obstacle to rice farming throughout tropical Asia. The function of the translation initiation factor 4 gamma (eIF4G) gene in controlling tungro spherical viruses in rice has been demonstrated in earlier research (Lee et al. 2010). Rice lines resistant to the tungro spherical virus were successfully created by researchers (Macovei et al. 2018) by introducing mutations into the eIF4G gene using a CRISPR/Cas9 system. With the use of a base editor, plant genome can be modified or added which develop point mutations, assisting in the development of herbicide-resistant plants.

When the acetolactate synthase (OsALS) gene was modified using a base editor, a herbicide-resistant rice plant was developed (Kuang et al. 2020). Additionally, rice growth was increased against five herbicides (nicosulfuron, imazapic, pyroxsulam, flucarbazone, and bispyribac) when the same OsALS gene was targeted by CBE (editing efficiency 37.5–61.5%) (Zhang et al. 2020). They have specifically targeted the OsALS and ideal plant architecture 1 (OsIPA1) genes in rice using prime editing. Among them, rice growth was boosted by the OsALS gene (editing efficiency: 26%) against the herbicide Bispyribac sodium. The function of several weeds and insect stress-responsive genes in wheat has been described using functional genomics techniques. Nevertheless, the existing CRISPR/Cas system has not yet been able to pinpoint the precise function of weed and insect genes in any cereals.

2.5 Microarray technique in biotic stress development

Microarray analysis is a cutting-edge method for determining how hundreds of genes express themselves in response to biotic stressors in cereal crops, like pathogenic infection. They activate a cascade of molecular responses to defend themselves. This technique involves attaching DNA fragments or probes derived from certain genes to a solid surface, like a glass slide or microchips. An RNA sample or a DNA sample labeled with fluorescent, or radiolabels makes up the label. Biological samples are subjected to gene expression pattern analysis using microarray technology. Breezing eight pathogenic connections has been transformed by this microarray research. Microarray study has yielded several insights, such as the expression patterns altered during the interaction, the way pathogen-synthesized enzymes corrupt the gene protector in cereals, and how changes are induced in plants as a counterattack. (da Silva JA et al. 2008)

2.5.2 Microarray studies in biotic stress in cereals

Plant transcriptomes have been extensively studied using DNA microarrays to address a range of biological concerns about tolerance against biotic illnesses or abiotic stressors, toxicity or shortage etc. In cereals, biotic stress resistance is a complex trait regulated by multiple genes and pathways. Microarray analysis is used to identify key genes that are upregulated and downregulated during a stressful environment. For example, genes involved in pathogen recognition, such as receptor-like kinases (RLKs) and pathogenesis-related (PR) proteins are often induced upon pathogen attack. Moreover, microarray analysis can allow the

identification of candidate genes for breeding programs aimed at developing stress-resistant cereals. (da Silva JA et al. 2008)

IET8585 (Ajaya) an indica rice cultivar exhibited resistance against both bacterial leaf blight (blb) and various strains of the *X. oryzae* disease. The microarray analysis showed variations in the expression of several genes resistant to the blb-infected IET8585 cultivar compared to susceptible IR24. The resistant cultivar showed hypersensitive cell death in response to bacterial infection may be caused by increased expression of the EREBP TF gene and decreased expression of the genes that scavenge ROS and alcohol dehydrogenase. Additionally, it was proposed that upregulating defense genes during infection and inducing glutathione-mediated detoxification and flavonoid biosynthesis pathways would inhibit pathogen dissemination in host tissues (Kottapalli et al. 2007). Moreover, Wheat's Lr34/Yr18 gene contributes to resistance against yellow rust, leaf rust, and several other diseases. The flag leaves of two pairs of wheat near-isogenic lines for Lr34/Yr18 was subjected to microarray analysis after being mock- and rust-inoculated (Hulbert et al. 2007). Mock-inoculated leaf tips of resistant plants showed upregulation of 57 genes linked to seed development, osmotic stress, cold stress, and/or ABA inducible stress. Plants having false infection did not exhibit up-regulation of PR proteins in their resistant flag leaves. On the other hand, they were up-regulated in the flag leaves of rust-inoculated plants, both resistant and vulnerable. However, increased PR gene expression in resistant plants indicated that Lr34/Yr18 might play an important role in defense reactions.

3. Conclusion and Future Prospects

Traditional breeding methods have significantly contributed to cereal crops against biotic stress. These methods have less precision with more labor and time, thus instead of that method advanced approaches such as CRISPR-Cas9 gene editing, RNA interference, mutant breeding, Marker-Assisted Backcrossing, RNA interference, and genome-wide association studies have been intensively used in addressing biotic stress challenges. These methods allow accurate and rapid change to the plant genome enabling breeders to respond faster with agility to introduce the desired traits. MABC has greater importance in the development of resistance cultivars against oligogene disease resistance. This technique has an efficiency to transfer desirable genes from donor cultivars or wild relatives to elite crop varieties. To combat a wide range of pests and diseases, RNA interference has arisen as a powerful tool for

suppressing pathogen gene expression or bolstering plant defense systems. Advancements in breeding programs have been simplified with the identification of genomic regions associated with resistance to biotic stress through GWAS. The use of CRISPR-Cas9 technology has transformed precision breeding tool by permitting for precise modification of genes that deliver resistance to biotic stress through targeted mutations in plant genetics. Additionally, microarray technologies have aided in the creation of new breeding strategies by revealing the complex molecular pathways involved in plant-pathogen relationships.

In future breeding, the production of cereal crops that can withstand various challenges by using genomics, biotechnology, and bioinformatics can speed up. These approaches not only safeguard food security and sustainability in changing environmental conditions but also help address new issues caused by evolving pests and diseases. In the coming years, the full potential of plant breeding technologies will require collaboration across different fields and increased investment in research and development. Efforts to enhance the adoption of genetically modified crops must also focus on addressing regulatory concerns and gaining public trust. By leveraging advanced scientific and technological advancements, plant breeders can play a key role in addressing biotic stressors affecting cereal crop productivity and creating a resilient and sustainable agricultural environment.

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