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Developing Disease-Resistant Wheat Varieties Through Genomic Approaches

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Abstract Wheat diseases, particularly those caused by fungi, bacteria, and viruses, are one of the major threats to global food production. Advances in genomics have provided new opportunities for developing disease-resistant wheat varieties. By identifying resistance genes, quantitative trait loci (QTL), and utilizing gene-editing tools, breeders can accelerate the development of resistant varieties. This study reviews the latest progress in developing disease-resistant wheat using genomic approaches, with a focus on the application of genomic selection, genome-wide association studies (GWAS), gene editing, and multi-omics integration. These methods are crucial for improving wheat's resistance to diseases. Research has shown that genomic selection and GWAS have been successfully applied in improving resistance to various wheat diseases, including leaf rust, stripe rust, and powdery mildew. Gene-editing technologies, such as CRISPR/Cas9, have enhanced wheat's disease resistance by targeting and editing resistance genes. The integration of multi-omics data provides new insights for precision breeding for disease resistance. Genomic approaches enable breeders to more accurately select disease-resistant wheat varieties, shorten the breeding cycle, and increase the durability of resistance genes. The application of genomic tools also helps to better understand wheat's response mechanisms to pathogens, thereby promoting global food security.

Keywords Genomic selection; Genome-wide association studies; Gene editing; Wheat disease resistance; Multi-omics integration

1 Introduction

Wheat is a staple crop grown worldwide, providing a significant source of dietary protein and calories for the global population. However, wheat production faces numerous challenges, particularly from diseases that can severely impact yield and quality. Among these, rust diseases (leaf rust, stem rust, and stripe rust) and Fusarium head blight (FHB) are particularly problematic, causing substantial economic losses and posing threats to food security (Singh et al., 2016; Babu et al., 2020; Ghimire et al., 2020). The continuous evolution of new pathogen races exacerbates these challenges, rendering many existing resistance genes ineffective (Babu et al., 2020; Mapuranga et al., 2022).

The importance of developing disease-resistant wheat varieties cannot be overstated. Genetic resistance is the most sustainable and eco-friendly approach to managing wheat diseases, reducing the reliance on chemical fungicides and minimizing environmental impact (Babu et al., 2020; Ghimire et al., 2020; Mapuranga et al., 2022). Traditional breeding methods have successfully introduced resistance genes into wheat cultivars, but these methods are often time-consuming and may not keep pace with the rapid evolution of pathogens (Mondal et al., 2016; Dracatos et al., 2023). Therefore, there is a pressing need for innovative breeding strategies that can expedite the development of disease-resistant varieties.

Genomic-based breeding approaches offer significant advantages over conventional methods. Advances in next-generation sequencing (NGS) and bioinformatics have revolutionized wheat genomics, enabling the identification and deployment of resistance genes with greater precision and efficiency (Babu et al., 2020; Dracatos et al., 2023). High-throughput genotyping platforms and genome-wide association studies (GWAS) facilitate the dissection of complex traits and the construction of high-density genetic maps, which are crucial for marker-assisted and genomic selection (Mondal et al., 2016; Babu et al., 2020). These technologies allow for the stacking of multiple resistance genes, potentially providing more durable and long-lasting resistance against a range of pathogens (Sucher et al., 2016; Dracatos et al., 2023).

This study highlights the challenges posed by diseases to global wheat production and emphasizes the importance of disease resistance in current wheat breeding programs. It also discusses the advantages and prospects of genomic-based breeding methods and provides a comprehensive overview of the latest research developments in developing disease-resistant wheat varieties. By synthesizing recent research findings, this study offers insights into the future directions of wheat breeding and explores the potential of genomic tools in enhancing disease resistance and ensuring global food security.

2 Genomic Basis of Wheat Diseases

2.1 Mapping and function of known disease resistance genes

The mapping and functional characterization of disease resistance genes in wheat have been significantly advanced through various genomic approaches. For instance, the identification of multiple disease resistance meta-QTLs (MDR-MQTLs) has been a crucial step in understanding the genetic basis of resistance to diseases such as leaf rust, stem rust, and yellow rust. A study identified 86 MQTLs, including 71 MDR-MQTLs, which were validated using marker-trait associations from genome-wide association studies (GWAS). These MQTLs were found to co-localize with known resistance (R) genes, providing a robust framework for breeding disease-resistant wheat varieties (Pal et al., 2022). Additionally, the candidate-gene approach has been employed to map QTLs for resistance to various diseases, revealing that many minor resistance QTLs may be attributed to defense response (DR) genes. This approach has identified several candidate genes, such as oxalate oxidase and chitinase, which are associated with significant resistance effects.

Moreover, the creation of a wheat resistance gene atlas has been proposed to facilitate the rapid deployment of *R* genes in breeding programs. This atlas would serve as an online directory, enabling breeders to identify and utilize sources of resistance against major wheat pathogens. The atlas aims to capture the interacting molecular components governing disease resistance through various genomic techniques, including biparental mapping and whole-genome association genetics (Hafeez et al., 2021). This initiative underscores the importance of a coordinated effort to enhance the functional characterization and application of R genes in wheat breeding.

2.2 Genomic regions and QTLs associated with disease resistance

The identification and characterization of genomic regions and QTLs associated with disease resistance in wheat have been extensively studied. A meta-analysis of QTLs for resistance to multiple diseases, including septoria tritici blotch, fusarium head blight, and karnal bunt, identified 63 meta-QTLs (MQTLs) from 493 initial QTLs. These MQTLs were anchored to the reference physical map of wheat, and 38 of them were verified using marker-trait associations from GWAS. This study also identified 194 differentially expressed genes (DEGs) associated with disease resistance, providing valuable insights for fine mapping and marker-assisted breeding (Saini et al., 2021).

In another study, a meta-QTL analysis of tan spot resistance in wheat identified 19 meta-QTLs from 104 initial QTLs. These meta-QTLs were clustered on an integrated linkage map, with three major QTLs located on chromosomes 2A, 3B, and 5A, showing large genetic effects and conferring resistance to multiple races of the pathogen. This analysis highlights the potential of integrating race-nonspecific QTLs to achieve high and stable resistance to tan spot in wheat (Liu et al., 2020). Additionally, a genome-wide association mapping study for pre-harvest sprouting resistance in European winter wheat identified novel QTLs on chromosomes 1A and 5B, with the latter showing pleiotropic effects on phenology and grain quality. This study underscores the complexity of resistance traits and the importance of considering pleiotropic effects in breeding programs (Dallinger et al., 2023).

2.3 Advances in wheat genomic resources: reference genome and diversity maps

The development of wheat genomic resources, including reference genomes and diversity maps, has significantly advanced our understanding of the genetic basis of disease resistance. The recent surge in sequencing technologies and bioinformatics has facilitated the creation of a comprehensive wheat resistance gene atlas. This atlas aims to capture the molecular components governing disease resistance and provide a dynamic, durable approach to R gene deployment. The integration of genomic data from hexaploid and tetraploid wheat, as well as their wild relatives, is expected to enhance the breeding and deployment of disease-resistant wheat varieties (Hafeez et al., 2021).

Furthermore, the application of genomics-assisted breeding techniques has accelerated the resistance breeding process. By utilizing large populations analyzed with high-density marker arrays and extensive phenotyping, genomic selection models can be trained to predict breeding values of untested genotypes. This approach has been successfully applied to various pathosystems, including fusarium head blight and septoria blotch, demonstrating the potential of integrating genomic data for the improvement of disease resistance in wheat (Miedaner et al., 2020). The availability of a wheat reference and pan-genome has also facilitated the identification of structural variations and novel resistance QTLs, providing a comprehensive understanding of the genetic architecture underlying disease resistance (Dallinger et al., 2023).

3 Genomic Selection and Disease Resistance

3.1 Application of genomic selection in wheat breeding

Genomic selection (GS) has revolutionized wheat breeding by enabling the rapid selection of superior genotypes and accelerating the breeding cycle. The advent of next-generation sequencing technologies has made genotyping cost-effective, thus making GS a feasible selection tool in plant breeding (Sun et al., 2020). GS uses a statistical model to estimate all marker effects for an individual simultaneously, determining a genome estimated breeding value (GEBV). This allows breeders to select for performance based on GEBVs in the absence of phenotypic data, which is particularly useful for complex traits such as disease resistance (Larkin et al., 2019). The implementation of GS in wheat breeding has shown significant potential in improving the rate of genetic gain, especially for complex quantitative traits, by accelerating breeding cycles compared to traditional approaches (Crossa et al., 2017; Sun et al., 2020).

The success of GS in wheat breeding is attributed to its ability to incorporate all marker information in the prediction model, thereby avoiding biased marker effect estimates and capturing more of the variation due to small-effect quantitative trait loci (QTL) (Varshney et al., 2017). This comprehensive approach allows for more accurate predictions and selection, potentially leading to more rapid and lower-cost gains from breeding (Jannink et al., 2010). Additionally, GS has been successfully implemented for a number of key traits in wheat, including grain yield, grain quality, and quantitative disease resistance, such as that for Fusarium head blight (Larkin et al., 2019). The integration of GS into wheat breeding programs is still being explored, with many studies showing its potential to change wheat breeding through achieving higher genetic gain (Merrick et al., 2022).

3.2 Accelerating the selection of disease-resistant traits through genomic prediction

Genomic prediction (GP) models play a crucial role in accelerating the selection of disease-resistant traits in wheat. By analyzing phenotypes and high-density marker scores, GP models predict the breeding values of lines in a population, thus facilitating the rapid selection of superior genotypes (Varshney et al., 2017). The accuracy of GP models is influenced by several factors, including the selection of prediction models, marker density, trait heritability, and the relationship between training and validation sets (Larkin et al., 2019). Recent advances in hyperspectral image technology combined with GS and pedigree-assisted breeding have further enhanced the accuracy of GP models (Crossa et al., 2017).

The use of GP models in wheat breeding has shown promising results in predicting quantitative disease resistance. For instance, studies have demonstrated that GS models can accurately predict disease resistance traits such as stripe rust, with higher accuracies than traditional marker-assisted selection methods. The inclusion of fixed effects in low prediction scenarios has been shown to increase accuracy, indicating that GS can effectively predict quantitative disease resistance in the presence of both major and minor genes (Merrick et al., 2021). Overall, the integration of GP models into wheat breeding programs has the potential to significantly accelerate the selection of disease-resistant traits, thereby improving the efficiency and effectiveness of breeding efforts (Wang et al., 2018).

3.3 Case studies: development of disease-resistant wheat varieties using genomic selection

Several case studies have demonstrated the successful development of disease-resistant wheat varieties using genomic selection. One notable example is the use of GS to improve resistance to Fusarium head blight, a major disease affecting wheat. By incorporating GS into the breeding program, researchers were able to select for resistance based on GEBVs, leading to the development of wheat varieties with enhanced resistance to this disease (Larkin et al., 2019). Another study focused on optimizing GS models for selecting both major and minor genes for resistance to stripe rust. The results showed that GS models had higher accuracies than traditional marker-assisted selection methods, reaching an accuracy of 0.72 for disease severity (Merrick et al., 2021).

In addition to these specific examples, the broader application of GS in wheat breeding has shown significant potential in improving disease resistance. For instance, the integration of GS into a two-part breeding strategy, differentiating between population improvement and product development, has been proposed to optimize the breeding pipeline and achieve higher genetic gain (Merrick et al., 2022). This approach allows for the rapid selection of disease-resistant traits within and across breeding cycles, ultimately leading to the development of superior wheat varieties with enhanced disease resistance. Overall, these case studies highlight the effectiveness of GS in developing disease-resistant wheat varieties and underscore the importance of integrating GS into wheat breeding programs (Larkin et al., 2019; Sun et al., 2020; Merrick et al., 2021).

4 Association Analysis and Disease Resistance Gene Discovery

4.1 Localization of disease resistance genes through genome-wide association studies (GWAS)

Genome-Wide Association Studies (GWAS) have been instrumental in identifying genomic regions associated with disease resistance in wheat (Wang and Li, 2024). High-resolution GWAS has facilitated the fine mapping of quantitative trait loci (QTL) and the identification of candidate genes. For instance, a study involving 768 wheat cultivars identified 153 QTLs for traits such as leaf rust, yellow rust, powdery mildew, and cold tolerance, with 81 QTLs delimited to ≤1.0 Mb intervals (Pang et al., 2021). Another study identified 395 QTLs for 12 traits, including disease resistance, across seven environments, with 273 QTLs delimited to ≤1.0 Mb intervals (Pang et al., 2020). These findings underscore the effectiveness of GWAS in pinpointing specific genomic regions linked to disease resistance, thereby providing a foundation for further genetic analysis and breeding efforts.

4.2 Dissecting disease resistance through candidate gene association studies (CGAS)

Candidate Gene Association Studies (CGAS) offer a focused approach to understanding the genetic basis of disease resistance by examining specific genes known to be involved in plant defense mechanisms. A study on wheat recombinant inbreds mapped over 50 loci representing various classes of defense response (DR) genes, such as oxalate oxidase, peroxidase, superoxide dismutase, chitinase, and thaumatin, to QTLs associated with resistance to diseases like tan spot, leaf rust, Karnal bunt, and stem rust (Faris et al., 1999). This approach revealed that many minor resistance QTLs might result from the action of DR genes, highlighting the efficiency of CGAS in identifying key genes involved in disease resistance.

4.3 Practical applications of association analysis in wheat disease resistance breeding

The practical applications of association analysis in wheat breeding are extensive, ranging from identifying disease-resistant parent genotypes to developing genome-based prediction models. For instance, a study using a multi-trait restrictive linear phenotypic selection index (RLPSI) identified 22 parent genotypes with potential resistance to multiple diseases such as leaf rust, stripe rust, leaf spot, and common bunt (Figure 1) (Iqbal et al., 2022). Figure 1 illustrates the resistance of different genotypes to multiple diseases, including stripe rust, leaf rust, leaf spot, and common bunt, along with the distribution of grain yield. The study results indicate that the selected genotypes performed well in terms of both disease resistance and yield, contributing to crop improvement and the selection of disease-resistant varieties. Additionally, genomic prediction models based on GWAS data have shown high accuracy in predicting resistance to various diseases, promoting the selection of resistant varieties

(Pang et al., 2021). Integrating the findings from GWAS and CGAS into breeding programs helps develop wheat varieties with enhanced disease resistance, contributing to sustainable agriculture and food security.

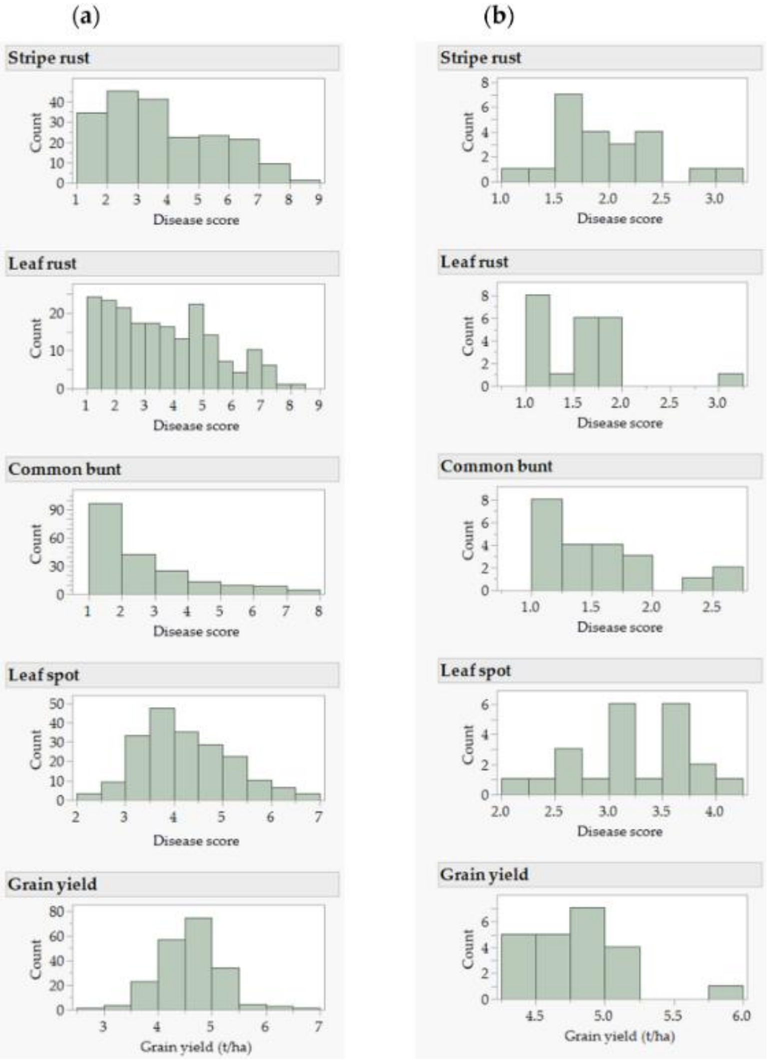

Figure 1 Frequency distribution of disease severity and yield among 196 genotypes and 22 selected genotypes (Adapted from Iqbal et al., 2022)

Image caption: (a): Frequency distribution of the best linear unbiased estimates (BLUEs) of disease severity and grain yield from 196 genotypes;(b): The same data for 22 selected genotypes; For disease severity, scores range from 1 to 9, representing resistant, moderately resistant, intermediate, moderately susceptible, and susceptible, respectively. Grain yield is expressed in tons per hectare (t/ha) (Adapted from Iqbal et al., 2022)

5 Application of Gene Editing Technologies in Wheat Disease Resistance Breeding

5.1 Advances in CRISPR-Cas9 system for wheat genome editing

The CRISPR-Cas9 system has revolutionized the field of genome editing, providing a robust and precise method for targeted modifications in plant genomes. This technology has surpassed other genome editing techniques such as TALENs and ZFNs due to its simplicity, efficiency, and lower cost (Borrelli et al., 2018; Mushtaq et al., 2019). Recent advancements in CRISPR-Cas9 have enabled the development of transgene-free disease-resistant crops, which is crucial for sustainable agricultural production (Ahmad et al., 2020; Erdoğan et al., 2023). The system's ability to introduce specific gene edits with high precision has made it a powerful tool for enhancing disease resistance in wheat and other crops (Chen et al., 2019; Wang et al., 2022). Additionally, innovations such as base-editing tools and DNA-free delivery methods have further expanded the potential applications of CRISPR-Cas9 in crop improvement (Chen et al., 2019).

5.2 Targeted editing of resistance genes to enhance disease resistance in wheat

CRISPR-Cas9 has been effectively utilized to target and modify specific resistance genes in wheat, thereby enhancing its resistance to various pathogens. One common approach involves the knockout of susceptibility genes, which are essential for pathogen colonization, thus rendering the plant resistant to the disease (Schenke and Cai, 2020). Another strategy includes the precise modification of resistance genes to improve their efficacy against pathogens (Mushtaq et al., 2019; Schenke and Cai, 2020). For instance, targeted mutations in genes responsible for viral, fungal, and bacterial disease resistance have been successfully implemented in model plants and crops, including wheat (Borrelli et al., 2018). These targeted edits not only improve disease resistance but also maintain the overall health and yield of the crop (Wang et al., 2022).

5.3 Success stories: Wheat varieties with improved disease resistance through gene editing

Several success stories highlight the potential of CRISPR-Cas9 in developing disease-resistant wheat varieties. For example, researchers have successfully edited wheat genes to confer resistance against powdery mildew, a common and devastating fungal disease (Borrelli et al., 2018; Mushtaq et al., 2019). By knocking out specific susceptibility genes, they were able to create wheat lines that showed significantly reduced disease symptoms and improved overall health (Schenke and Cai, 2020). Another notable achievement is the development of wheat varieties with enhanced resistance to rust diseases, which are caused by fungal pathogens and can lead to severe yield losses (Nascimento et al., 2023). These success stories demonstrate the practical applications of CRISPR-Cas9 in wheat breeding and its potential to address global food security challenges by developing robust, disease-resistant crops (Langner et al., 2018).

6 Whole-Genome Resequencing and Wheat Disease Resistance

6.1 Identifying resistance alleles using resequencing technology

Whole-genome resequencing (WGR) has become a pivotal tool in identifying resistance alleles in wheat. By comparing multiple wheat genomes, researchers have uncovered extensive structural rearrangements and introgressions from wild relatives, which are crucial for disease resistance (Walkowiak et al., 2020). The use of WGR has enabled the identification of single-nucleotide polymorphisms (SNPs) across different genomic regions, including those associated with disease resistance genes. For instance, a study identified 3.3 million SNPs in the wheat genome, which can be used to develop high-throughput genotyping arrays for breeding programs (Rimbert et al., 2018). Additionally, molecular approaches such as allele mining and ecotilling have been employed to characterize the genetic variability of resistance loci, allowing for the identification of new resistance alleles (Kaur et al., 2008).

6.2 The relationship between genomic diversity and disease resistance

Genomic diversity plays a crucial role in enhancing wheat disease resistance. Comparative genomic studies have shown that the genetic diversity among different wheat lines has been shaped by a complex breeding history aimed at improving resistance to various stresses, including diseases (Walkowiak et al., 2020). Studies on selective sweeps related to disease resistance genes highlight the impact of human selection on genomic diversity. Additionally, SNP-based diversity maps provide important insights into the geographic distribution of genetic diversity, which is essential for understanding the distribution of resistance alleles (Cavanagh et al., 2013). The creation of a wheat resistance gene atlas, which documents the sources of resistance, further underscores the importance of genomic diversity in breeding for durable disease resistance (Figure 2). Hafeez et al. (2021) emphasized the importance of dynamic diversity and rational stacking of R gene combinations in enhancing crop disease resistance. By integrating pathogen diversity information with gene-editing technologies, it is possible to effectively delay pathogen adaptation to resistance genes, contributing to the long-term management of crop disease resistance.

6.3 The role of resequencing in building the wheat disease resistance gene pool

Resequencing technology has significantly contributed to the expansion of the wheat disease resistance gene pool. By generating high-quality genome assemblies, researchers have been able to identify and characterize resistance genes, such as the nucleotide-binding leucine-rich repeat (NLR) proteins, which are involved in disease resistance

(Walkowiak et al., 2020). The integration of genomic data into breeding programs has facilitated the identification of multiple disease resistance (MDR) loci, which are crucial for developing cultivars with broad-spectrum resistance (Miedaner et al., 2019). Additionally, genome-wide association studies (GWAS) have mapped genomic regions associated with resistance to various diseases, providing valuable information for selecting parental combinations in breeding programs (Iqbal et al., 2022). The use of high-throughput genotyping platforms and next-generation sequencing (NGS) technologies has further accelerated the identification and deployment of resistance genes, enhancing the overall genetic diversity and resilience of wheat cultivars (Babu et al., 2020).

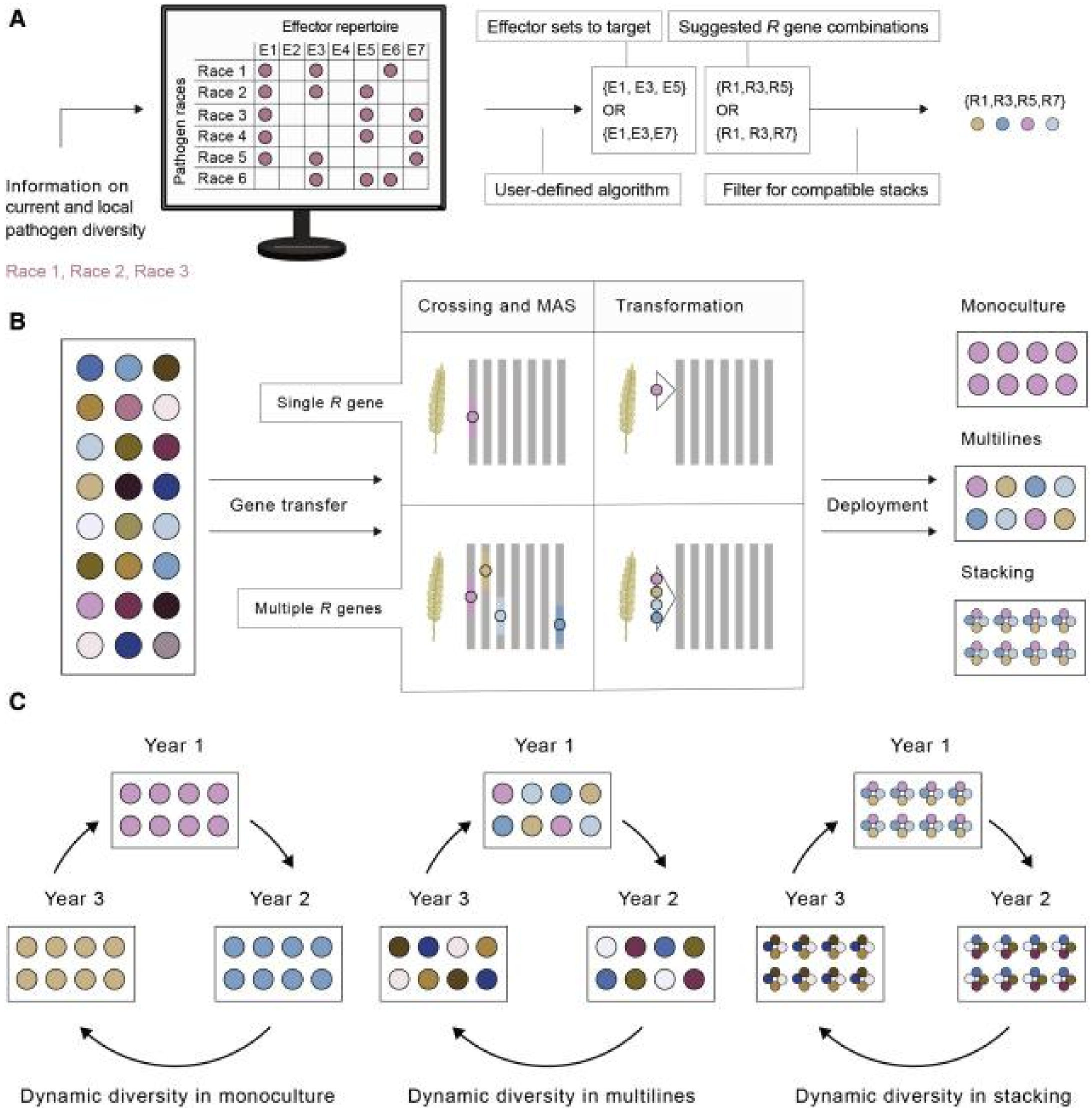

Figure 2 Utilizing the *R*-gene atlas and pathogen diversity information to determine appropriate gene combinations (Adapted from Hafeez et al., 2021)

Image caption: (A): By integrating pathogen effector and diversity information, optimal R-gene stacking strategies are calculated to maximize durable resistance; (B): The process of transferring single R genes or stacked R genes into cultivated varieties through traditional methods (crossbreeding and marker-assisted selection, MAS) or genetic transformation; (C): Dynamic diversity deployment strategies over different years, reducing the risk of pathogens developing resistance to these genes by rotating single or stacked R-gene varieties (Adapted from Hafeez et al., 2021)

7 Multi-Omics Integration Strategies

7.1 Transcriptomics in studying the regulation of resistance gene expression

Transcriptomics has been instrumental in understanding the regulation of resistance gene expression in wheat. By analyzing differentially expressed genes (DEGs) in response to pathogen attacks, researchers can identify key genes involved in disease resistance. For instance, a study identified 194 DEGs from five transcriptome studies, with 85 genes previously associated with disease resistance, providing valuable insights for marker-assisted breeding (Saini et al., 2021). Additionally, transcriptome analysis of wheat genotypes resistant and susceptible to wheat dwarf virus (WDV) revealed specific expression patterns of genes related to resistance, such as glycosyltransferase and MYB transcription factors, which are crucial for developing virus-resistant wheat varieties (Sharaf et al., 2023).

7.2 Applications of proteomics in understanding wheat disease resistance mechanisms

Proteomics offers a comprehensive view of the protein landscape in wheat, helping to elucidate the mechanisms underlying disease resistance. By profiling the proteome, researchers can identify proteins that play critical roles in the plant's defense response. For example, proteomic studies have highlighted the importance of proteins such as oxalate oxidase, peroxidase, and superoxide dismutase in resistance to various diseases, including leaf rust and stem rust. These findings underscore the potential of proteomics to uncover novel resistance mechanisms and inform breeding strategies aimed at enhancing disease resistance in wheat (Alotaibi et al., 2020; Sehgal et al., 2023).

7.3 Metabolomics revealing metabolic pathways involved in wheat disease resistance

Metabolomics provides insights into the metabolic pathways that contribute to disease resistance in wheat. By analyzing the metabolites produced in response to pathogen infection, researchers can identify key metabolic changes associated with resistance. For instance, metabolomic profiling has been used to study the response of wheat to biotic stress, revealing specific metabolites and pathways that are activated during pathogen attack (Kaur et al., 2021). This approach helps in understanding the biochemical basis of resistance and can guide the development of wheat varieties with enhanced metabolic resilience to diseases (Yang et al., 2021; Sen et al., 2023).

7.4 Integrating multi-omics for precision disease resistance breeding

The integration of multi-omics approaches, including genomics, transcriptomics, proteomics, and metabolomics, offers a powerful strategy for precision disease resistance breeding in wheat (Xu and Su, 2024). By combining data from different omics layers, researchers can construct comprehensive models of disease resistance mechanisms. For example, integrating transcriptomic and metabolomic data has provided deeper insights into herbicide resistance mechanisms in weeds, highlighting the potential of such approaches in crop science (Sen et al., 2023). Similarly, the integration of genomics with other omics has been shown to enhance the understanding of molecular regulator networks, facilitating the development of wheat varieties with improved resistance to multiple diseases (Miedaner et al., 2020; Yang et al., 2021). This holistic approach enables the identification of key genes, proteins, and metabolites involved in resistance, paving the way for the development of robust, disease-resistant wheat varieties (Alotaibi et al., 2020; Hafeez et al., 2020; Sehgal et al., 2023).

8 Challenges and Solutions in Genomic Breeding

8.1 Challenges of genomic complexity and polyploid genomes

The wheat genome is notably large and complex, which poses significant challenges for genomic breeding. The hexaploid nature of wheat, with its three sets of homologous chromosomes, complicates the assembly and analysis of its genome. This complexity is further exacerbated by extensive structural rearrangements and introgressions from wild relatives, which are common in wheat due to its complex breeding history aimed at improving various traits such as disease resistance and yield (Walkowiak et al., 2020). Additionally, the presence of multiple gene copies can obscure the identification of functional genes and their variants, making it difficult to pinpoint specific genes responsible for desirable traits (Babu et al., 2020).

8.2 Addressing the impact of the environment on genomic breeding strategies

Environmental factors significantly influence the effectiveness of genomic breeding strategies. The interaction between genotype and environment (GxE) can lead to variability in trait expression, complicating the selection process for disease-resistant varieties. For instance, traits that confer resistance in one environment may not be effective in another due to differences in pathogen populations and environmental conditions (Paux et al., 2022). To address this, extensive phenotyping across multiple locations and years is essential to train genomic models that can predict breeding values accurately under diverse environmental conditions (Miedaner et al., 2020). Additionally, integrating genomic data with environmental data can help in understanding GxE interactions and developing more robust breeding strategies (Thudi et al., 2020).

8.3 Overcoming technical costs and implementation barriers

The high costs associated with genomic technologies and the need for specialized infrastructure and expertise are significant barriers to the widespread implementation of genomic breeding. Next-generation sequencing (NGS) and high-throughput genotyping platforms, while revolutionary, require substantial financial investment and technical know-how (Babu et al., 2020). To mitigate these costs, collaborative efforts and shared resources, such as the proposed wheat resistance gene atlas, can provide breeders with access to essential genomic data and tools, thereby reducing individual costs and accelerating the breeding process (Hafeez et al., 2021). Additionally, advancements in bioinformatics and the development of cost-effective genotyping assays, such as KASP assays, have made it more feasible to implement genomic selection in breeding programs (Babu et al., 2020).

9 Future Perspectives

9.1 Future trends in genomic breeding technologies

The future of genomic breeding technologies in wheat is poised for significant advancements. The integration of high-throughput genomic tools, such as single nucleotide polymorphism (SNP) arrays and high-density molecular marker maps, will continue to enhance the precision and efficiency of breeding programs (Paux et al., 2022). The use of genome-wide association studies (GWAS) and quantitative trait loci (QTL) mapping will facilitate the identification of candidate genes associated with disease resistance and other agronomically important traits (Babu et al., 2020; Jabran et al., 2023). Additionally, the application of CRISPR/Cas-9 and other genome-editing technologies will enable precise modifications in the wheat genome, allowing for the development of varieties with enhanced resistance to diseases and environmental stresses (Li et al., 2021). The integration of machine learning and artificial intelligence in genomic prediction models is also expected to accelerate the breeding process by improving the accuracy of phenotype predictions from genotypic data (Thudi et al., 2020).

9.2 Accelerating disease resistance breeding through international collaboration and data sharing

International collaboration and data sharing are critical for accelerating disease resistance breeding in wheat. The generation of multiple wheat genome assemblies has revealed extensive genomic diversity, which can be leveraged through collaborative efforts to improve disease resistance (Walkowiak et al., 2020). Projects like BREEDWHEAT have demonstrated the importance of sharing genomic resources and tools with the global wheat community to enhance breeding programs (Paux et al., 2022). Collaborative efforts can also facilitate the large-scale phenotyping and genotyping required for effective genomic selection, as seen in the development of multi-disease resistance (MDR) strategies (Miedaner et al., 2020). By pooling resources and expertise, international collaborations can address the challenges posed by evolving pathogens and environmental changes, ultimately leading to the development of more resilient wheat varieties (Nelson et al., 2017; Paux et al., 2022).

9.3 Prospects of genomic breeding in contributing to global food security

Genomic breeding holds immense potential in contributing to global food security by developing wheat varieties that are more productive, resilient, and nutritionally enhanced. The application of genomics-assisted breeding has already shown promise in improving resistance to major diseases such as rusts, bunts, and smuts, which are significant threats to wheat production (Babu et al., 2020; Jabran et al., 2023). By incorporating diverse genetic resources and utilizing advanced breeding techniques, it is possible to develop wheat varieties that can withstand biotic and abiotic stresses, thereby ensuring stable yields under changing climatic conditions (Mondal et al., 2016; Thudi et al., 2020). Furthermore, the integration of genomic tools with conventional breeding methods can expedite the development of high-yielding, disease-resistant varieties, contributing to sustainable agriculture and global food security (Keller et al., 2018; Paux et al., 2022). The continued advancement and adoption of these technologies will be crucial in meeting the growing demand for wheat and addressing the challenges of food security in the coming decades.

10 Concluding Remarks

Genomic approaches have revolutionized the field of wheat disease resistance breeding by providing tools and methodologies that enhance the precision and efficiency of breeding programs. The integration of high-throughput sequencing technologies, molecular markers, and bioinformatics has enabled the identification and characterization of resistance genes at an unprecedented scale. These advancements have facilitated the development of wheat varieties with improved resistance to a wide range of pathogens, thereby contributing to global food security.

Current progress in genomic approaches for wheat disease resistance includes the generation of multiple wheat genome assemblies, which have revealed extensive genetic diversity and structural variations among different wheat lines. These assemblies serve as a foundation for functional gene discovery and the development of modern wheat cultivars. Genomics-assisted breeding has been successfully applied to identify quantitative trait loci (QTL) and marker-trait associations, which are crucial for breeding disease-resistant varieties. The use of next-generation sequencing (NGS) platforms and high-density molecular marker maps has further accelerated the breeding process by enabling genome-wide association studies (GWAS) and genomic selection.

Future research directions should focus on the creation of comprehensive resistance gene atlases and the exploration of untapped genetic diversity in wheat germplasm collections. The development of new breeding technologies, such as CRISPR/Cas-9 and advanced molecular markers, will be essential for achieving durable disease resistance. Additionally, integrating genomic data with phenotypic data and environmental factors will enhance the accuracy of genomic selection models, leading to the development of wheat varieties that are resilient to both biotic and abiotic stresses.

The potential of genomic breeding in improving wheat disease resistance is immense. By leveraging genomic tools, breeders can rapidly identify and deploy resistance genes from diverse sources, including wild relatives and landraces, into elite wheat lines. This approach not only enhances the durability of resistance but also reduces the likelihood of pathogen evolution and the emergence of new virulent strains. The judicious application of genomic resources, such as resistance gene atlases and high-throughput genotyping platforms, will enable the development of wheat varieties that can withstand multiple diseases, thereby ensuring stable and high yields. In conclusion, genomic approaches have significantly advanced wheat disease resistance breeding, providing a robust framework for future research and development. By continuing to harness the power of genomics, we can develop wheat varieties that are not only disease-resistant but also adaptable to changing environmental conditions, ultimately contributing to sustainable agriculture and global food security.

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Conflict of Interest Disclosure

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