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Letter to the Editor

The future of gene discovery and molecular marker development for rust resistance in wheat

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Wheat rust diseases, caused by the pathogens *Puccinia graminis* (stem rust), *Puccinia triticina* (leaf rust), and *Puccinia striiformis* (stripe rust), have been among the most devastating threats to wheat production worldwide. These diseases can cause significant yield losses, with global impacts on food security. The frequent emergence of new virulent strains of the rust pathogens, exacerbated by climate change and the expansion of monoculture wheat farming, makes the control of these diseases increasingly challenging. Traditional control methods, such as the use of chemical fungicides, are not only expensive but also environmentally unsustainable. Consequently, there has been a strong emphasis on developing wheat varieties with durable genetic resistance, and this is where gene discovery and molecular marker technologies play a pivotal role. The future of wheat breeding for rust resistance relies on expanding our understanding of the genetic mechanisms that underpin resistance to these pathogens, as well as the development and application of molecular markers that can accelerate breeding programs. In this context, gene discovery and marker-assisted selection (MAS) are essential tools that can revolutionize how wheat is bred for enhanced resistance to rust diseases.

Advances in gene discovery for rust resistance

The identification and functional characterization of rust resistance genes have been a key focus of wheat research for many decades. These genes, which confer resistance to wheat rusts, can be classified into two broad categories: race-specific (or qualitative) resistance genes and broad-spectrum (or quantitative) resistance genes. While race-specific resistance genes provide a high level of protection against particular rust races, they are often overcome by new pathogen variants. In contrast, quantitative resistance genes provide partial resistance that is more durable but typically confers lower levels of protection.

1. Advances in genomic tools for gene discovery

Recent advances in next-generation sequencing (NGS), transcriptomics, and CRISPR-based gene editing technologies have greatly enhanced the ability to identify and characterize genes involved in rust resistance. The sequencing of the wheat genome, which was completed in 2018, has provided researchers with a comprehensive map of wheat's genetic landscape, including regions linked to rust resistance. The use of high-throughput genome-wide association studies (GWAS) has accelerated the identification of candidate genes for resistance to wheat rust pathogens. These discoveries have revealed a wealth of previously uncharacterized genes, many of which can be targeted in breeding programs for the development of resistant varieties.

2. Genetic resources and allele mining

One promising avenue for gene discovery is the exploration of genetic diversity in wheat landraces and wild relatives, which may harbor untapped alleles that confer resistance to rust pathogens. These gene pools are often rich in beneficial alleles that have not been subjected to the selective pressures of modern breeding. In particular, the use of synthetic wheat and introgression from wild wheat species, such as *Aegilops* species, has led to the identification of novel resistance genes that can be incorporated into cultivated wheat varieties. These genes, particularly those that offer resistance to multiple rust diseases, represent critical genetic resources for developing wheat varieties with durable resistance.

The role of molecular markers in rust resistance breeding

Molecular markers are invaluable tools that allow breeders to track the inheritance of rust resistance genes with high precision, without the need for labor-intensive and time-consuming phenotyping. The development and application of molecular markers linked to rust resistance genes have greatly improved the efficiency of wheat breeding programs.

1. Marker-assisted selection (MAS)

MAS is a breeding strategy that uses molecular markers to select specific traits, such as rust resistance, at an early stage in the breeding cycle. By identifying markers linked to rust resistance genes, breeders can accelerate the incorporation of these genes into elite wheat lines. MAS reduces the reliance on phenotypic selection, which is often influenced by environmental factors, and allows for the development of rust-resistant varieties in a more efficient manner. MAS is particularly useful when dealing with race-specific resistance genes, which can be mapped to specific chromosomal regions, and for pyramiding multiple resistance genes to create wheat varieties with broad-spectrum, durable resistance.

2. Genomic selection (GS)

GS is an emerging breeding method that uses whole-genome data to predict the breeding value of an individual plant. Unlike MAS, which targets specific loci associated with resistance, GS takes into account the entire genome and allows for the simultaneous selection of multiple genes that contribute to rust resistance. This approach has the potential to significantly increase the speed and precision of wheat breeding, particularly when breeding for complex, quantitative traits such as broad-spectrum rust resistance. By integrating genomic selection with molecular markers, breeders can select for rust resistance in a more comprehensive and targeted manner, ultimately accelerating the development of resistant wheat varieties.

3. High-throughput phenotyping and marker integration

One of the challenges in wheat breeding for rust resistance is the accurate and rapid phenotyping of resistance traits. Traditional field-based phenotyping is time-consuming and subject to environmental variation, which can obscure the true genetic effects of resistance. However, advances in high-throughput phenotyping technologies, such as digital imaging, and controlled-environment screening, have enabled more precise evaluation of rust resistance. When combined with molecular markers, these phenotypic tools can greatly enhance the ability to identify and select resistant plants, further accelerating breeding cycles.

The future outlook: integrated approaches for durable rust resistance

The future of wheat breeding for rust resistance will rely on the integration of multiple approaches, including gene discovery, molecular marker development, and modern breeding technologies such as CRISPR gene editing and genomic selection. By leveraging these tools in tandem, researchers and breeders can develop wheat varieties that are not only resistant to current strains of rust pathogens but also capable of resisting future, evolving pathogen populations.

Moreover, the development of wheat varieties with multi-gene resistance, or pyramid resistance, will be essential for achieving long-term, durable protection against rust diseases. These varieties will be more resilient to the rapidly changing nature of rust pathogens, minimizing the risk of resistance breakdown. Collaboration between plant scientists, breeders, and farmers will be crucial in ensuring that these innovations are translated into practical solutions that can meet the challenges posed by wheat rust diseases on a global scale.

In addition, the continued exploration of the genetic diversity found in wheat’s wild relatives and landraces will provide a rich source of untapped resistance alleles. Integrating this genetic diversity into modern wheat breeding programs, using molecular markers and advanced genomics tools, will be key to achieving sustainable rust control in the long term.

Conclusion

The future of wheat breeding for rust resistance is bright, with promising advances in gene discovery, molecular marker development, and breeding technologies. By harnessing the power of genomics and molecular tools, breeders will be able to develop wheat varieties that are more resistant to rust diseases, improving global wheat productivity and food security. Through the integration of molecular markers, genomic selection, and innovative breeding strategies, the next generation of wheat cultivars will be better equipped to withstand the ongoing threat of rust diseases, ensuring a more sustainable and resilient food supply for future generations.