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Pangenome-Assisted Plant Breeding: Unlocking Hidden Genetic Diversity for Next-Generation Crop Improvement

Dr. Shivkumar. K[1*]., Dr. Praveenkumar. B[2] and Rajanna, B[3]

[1]Assistant Professor, AICRP on Groundnut, MARS, Raichur

[2]Scientist, AICRP on Pigeonpea, Zonal Agricultural Research Station, Kalaburagi

[3]Department of Genetics & Plant Breeding, University of Agricultural Sciences, Raichur

**Corresponding author - shivauasraichur@gmail.com*

Abstract

Plant breeding has traditionally relied on reference genomes and conventional genetic variation available within cultivated germplasm. However, a single reference genome often fails to represent the complete genetic diversity present within a crop species. Recent advances in DNA sequencing and computational genomics have led to the development of pangenomics, one of the most revolutionary approaches in plant genetics and breeding. A pangenome represents the complete collection of genes present across all individuals within a species, including both core genes shared by every genotype and dispensable genes found only in specific accessions. These unique genes frequently govern important agronomic traits such as disease resistance, drought tolerance, nutritional quality, stress adaptation, and yield potential. Pangenome-assisted breeding enables breeders to discover novel alleles that were previously undetectable using conventional reference genomes. When integrated with genome-wide association studies, genomic selection, CRISPR genome editing, speed breeding, and artificial intelligence, pangenomics provides an unprecedented opportunity to accelerate crop improvement. This article discusses the principles, applications, recent advances, challenges, and future prospects of pangenome-assisted breeding in modern agriculture.

Introduction

Plant breeding has contributed enormously to global food security by developing improved crop varieties with higher productivity, enhanced quality, and greater adaptability. For decades, breeders have relied on phenotypic selection, hybridization, and molecular markers to identify desirable traits. The publication of complete crop genome sequences further accelerated breeding by enabling scientists to identify genes responsible for important agricultural characteristics.

Despite these achievements, a major limitation of conventional genomics is the use of a single reference genome to represent an entire species. Every crop contains thousands of genetically distinct varieties, landraces, and wild relatives, each possessing unique genes that may not exist in the reference genome. Consequently, many beneficial genes remain undiscovered, limiting opportunities for crop improvement.

Pangenomics overcomes this limitation by analyzing multiple genomes simultaneously to capture the full spectrum of genetic diversity within a species. This technology is now transforming plant breeding by enabling breeders to utilize hidden genetic resources that were previously inaccessible.

What is a Plant Pangenome?

A plant pangenome is the complete collection of genes present across all individuals of a crop species. Unlike a conventional reference genome, which represents only one genotype, a pangenome incorporates genomic information from numerous cultivars, breeding lines, landraces, and wild relatives.

The pangenome consists of two major components. The first is the core genome, which contains genes present in every individual and generally controls fundamental biological functions essential for survival and growth. The second is the dispensable or accessory genome, which contains genes found only in certain genotypes. These accessory genes often contribute to adaptation, stress tolerance, disease resistance, nutrient efficiency, flowering behavior, and environmental resilience.

By identifying both shared and unique genes, pangenomes provide breeders with a much broader understanding of crop genetic diversity.

Importance in Modern Plant Breeding

Many valuable agronomic traits originate from rare alleles present in traditional varieties or wild relatives. Conventional breeding frequently overlooks these genes because they are absent from the reference genome.

Pangenome analysis enables researchers to discover novel resistance genes against fungal, bacterial, and viral pathogens. It also identifies genes associated with drought tolerance, heat tolerance, salinity resistance, nutrient-use efficiency, grain quality, oil composition, and yield stability.

This broader understanding of genetic diversity enables breeders to design more effective crossing strategies and accelerate the development of climate-resilient crop varieties.

Construction of a Crop Pangenome

Developing a pangenome begins with sequencing multiple genetically diverse accessions representing the crop's geographical and genetic diversity. Modern long-read sequencing technologies combined with high-quality genome assembly allow researchers to accurately reconstruct individual genomes.

Computational algorithms compare these genomes to identify shared and unique genes. The resulting pangenome provides a comprehensive catalogue of genetic variation across the species.

Continuous improvements in sequencing technology have significantly reduced costs, making pangenome development increasingly feasible for many economically important crops.

Applications in Crop Improvement

Pangenomes have already been developed for rice, wheat, maize, soybean, tomato, potato, cotton, chickpea, pigeonpea, mustard, sunflower, and several horticultural crops.

In rice, pangenome studies have identified genes responsible for flood tolerance, blast resistance, and grain quality. Wheat pangenomes have revealed hidden disease-resistance genes absent from traditional reference genomes. Maize pangenomes have uncovered structural variations associated with yield and environmental adaptation.

Similar advances are being reported in oilseed, pulse, and vegetable crops, providing breeders with valuable genetic resources for future variety development.

Integration with Modern Breeding Technologies

Pangenome-assisted breeding becomes even more powerful when integrated with marker-assisted selection, genomic selection, genome-wide association studies, and CRISPR genome editing.

Novel genes identified through pangenome analysis can be converted into molecular markers for rapid screening of breeding populations. Genome editing can then introduce beneficial alleles directly into elite cultivars, while speed breeding accelerates generation advancement.

Artificial intelligence further enhances breeding efficiency by analyzing large genomic datasets and predicting superior parental combinations.

Role in Climate-Resilient Agriculture

Climate change has intensified drought, heat waves, salinity, flooding, and emerging pest outbreaks. Many adaptive genes capable of improving crop resilience exist only in traditional landraces or wild relatives. Pangenome analysis allows breeders to identify these adaptive genes and incorporate them into modern cultivars. Future crop varieties developed using pangenomic information are expected to possess improved resilience while maintaining high productivity.

Advantages

Pangenome-assisted breeding provides several important advantages. It captures complete species-wide genetic diversity rather than relying on a single genome. It identifies rare beneficial alleles that would otherwise remain undiscovered. It improves the efficiency of marker development, genomic prediction, and genome editing while accelerating crop improvement. It also strengthens pre-breeding programs by facilitating the use of exotic germplasm and wild relatives.

Challenges

Although highly promising, pangenome research requires sophisticated sequencing platforms, advanced computational infrastructure, and specialized bioinformatics expertise. Managing enormous genomic datasets remains computationally demanding. Standardized analytical methods are still evolving, and integrating pangenome information into routine breeding programs requires additional research.

Future Prospects

Future plant breeding is expected to rely increasingly on species-wide pangenomes integrated with artificial intelligence, digital phenotyping, genome editing, and speed breeding. Researchers are moving toward graph-based pangenomes that more accurately represent complex structural variation than traditional linear genomes.

As sequencing costs continue to decline, pangenomes will become available for almost every major crop species. These comprehensive genomic resources will greatly accelerate the development of high-yielding, climate-resilient, nutritionally enhanced, and disease-resistant crop varieties.

Conclusion

Pangenome-assisted breeding represents one of the most significant recent breakthroughs in plant genetics. By capturing the complete genetic diversity within crop species, it enables breeders to discover previously hidden genes associated with economically important traits. Integration with genomic selection, CRISPR genome editing, speed breeding, and artificial intelligence is transforming plant breeding into a highly precise and efficient process. As agriculture faces increasing challenges from climate change and global food demand, pangenomics will play a central role in developing the next generation of resilient and productive crop varieties.

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