Reg. No.: COOP/2023/KOTA/201080/26/134

AGRICULTURE FORUM FOR TECHNICAL EDUCATION OF FARMING SOCIETY

Kota, Rajasthan

Pangenomics: A New Frontier in Plant Breeding

Authors

Santhosh B. L[1], Sonali Ambadas Aware[2], Mahiboobsa[3], Nandini Sarathi[4], Nimisha Joly Chennakadan[5]

[1]Agriculture Officer, Raitha Samparka Kendra, Singatagere, Office of Assistant Director of Agriculture Kadur, Department of Agriculture, Karnataka, India.
[2]Junior Research Assistant, Department of Genetics and Plant Breeding, VNMKV, Parbhani.
[3]Assistant Professor, Department of Genetics and Plant Breeding, College of Agricultural Sciences Iruvakki, KSNUAHS Shivamogga, Karnataka.
[4]Ph.D Scholar, Department of Vegetable Science, Mahatma Gandhi University of Horticulture and Forestry Sankra -Patan Durg (MGVUU).
[5]M. Sc Scholar, Department of Biotechnology and Bioinformatics, JSS Academy of Higher Education and Research, Mysore.

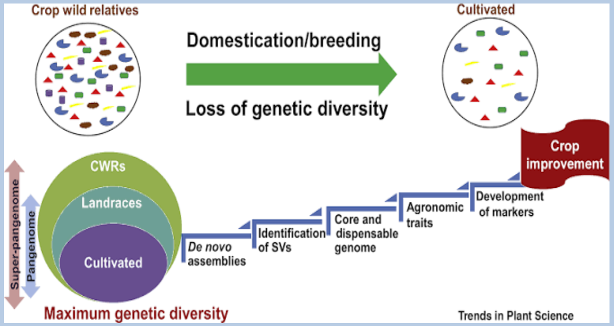
INTRODUCTION

What is Pangenomics

Pangenomics is a sophisticated technique of genomics that seeks to represent the entire genetic variation of a species through sequencing the genomes of multiple individuals as opposed to a single genome serving as the reference. It makes use of genomic data from various cultivars, breeding lines, landraces and wild-species to generate a species pangenome that captures all genes and SVs within the species. This method allows for a more accurate representation of the species genetic landscape and exposes polymorphisms that are not normally captured by single reference genome-based analyses. In contrast to traditional genomics, which views individuals through the lens of a single reference genome, pangenomics accepts that every genotype possesses unique genes and alleles that influence vital agronomic traits. Among the core (common) and accessory (variable) genes, new alleles can be discovered which are linked to yield, quality, disease resistance, and tolerance to biotic/abiotic stress. As a result, pangenomics has recently surfaced as a revolutionary tool in traditional plant breeding, harmonizing with innovative tools like genome editing, artificial intelligence (AI), genomic selection, and precision breeding to fast track the generation of superior, climate-smart cultivars.

Why is Pangenomics Needed

Conventional breeding and reference genome-based analyses are limited as a single reference genome fails to represent the entire genetic diversity of a crop. Crucial genes, structural variations, and rare alleles that originate from landraces and wild relatives may be lost. Pangenomics addresses these challenges and limitations by delivering a whole repertoire of genetic diversity for crop enhancement.



Evolution of Plant Genomics

Era	Major Advancement
Classical Genetics	Phenotype-based breeding
Molecular Genetics	DNA markers
Whole Genome Sequencing	Single reference genome
Genomics-Assisted Breeding	SNP discovery & GWAS
Pangenomics	Complete species-wide genome diversity

Major Crop Pangenome Projects

Pangenome initiatives have been developed for various staple crops such as rice, wheat, maize, soybean, tomato, Brassica, potato, cotton, chickpea, pigeonpea, mustard and barley. These resources are revolutionizing crop breeding by uncovering cryptic genetic diversity and enabling rapid precision breeding for high-yielding, climate-resilient, and disease-resistant varieties.

Types of Genetic Variation Captured

Pangenomics reveals various types of genetic variations, such as single nucleotide polymorphisms

(SNPs), insertions and deletions (InDels), presence-absence variations (PAVs), copy number variations (CNVs), structural variations, gene duplications, chromosomal rearrangements, and transposable element insertions. Such variation offers breeders a wider and more abundant source of genetic diversity than traditional genomics approaches to assist in finding useful genes and alleles for crop enhancement.

Advantages Over Single Reference Genome

Single Genome	Pangenome
Represents one genotype	Represents entire species
Misses many genes	Captures all genes
Limited diversity	Maximum diversity
Few structural variants	Comprehensive structural variation
Lower breeding efficiency	Higher breeding efficiency

Applications of Pangenomics in Plant Breeding

Discovery of Novel Genes

The most impactful use of pangenomics is the identification of novel genes and alleles with potential relevance for important agronomic traits in the economy. The analysis of the whole genetic diversity of a given organism within the species has led to the identification of genes related with resistance to diseases and pests, to heat, drought, salinity and flooding, to nutrient use efficiency, to yield potential, to grain and fruit quality and to a longer shelf-life. These novel genes are valuable genetic resource for the improvement of crop.

Precision Breeding

Pangenomics has been at the heart of precision breeding, facilitating more accurate identification and use of superior alleles by breeders. The development of trait-specific molecular markers, enhanced genomic prediction, increased selection efficiency and reduced breeding cycle enable to speed up development of superior cultivars and ultimately the delivery of improved cultivars.

Climate-Resilient Crop Development

The rich genetic diversity revealed by pangenomics enables the breeding of climate-resilient crops facing heat stress, drought, unpredictable rain, severe weather conditions, and other abiotic stresses. This is one major contributor for sustainable crop production in a changing climate.

Exploitation of Wild Relatives

Wild relatives and traditional landraces contain many useful genes that have been lost in the process of crop domestication. Pangenomics enables the discovery of disease resistance, abiotic stress tolerance, nutrient-use efficiency, and environmental adaptation-related genes that can be introgressed into elite cultivars to widen their genetic base and enhance resilience.

Improved Hybrid Breeding

Pangenomics facilitates the hybrid breeding systems by offering comprehensive information of genome-wide diversity and structural variations. It enables breeders to make more informed decisions on parental selection, heterotic group formation, hybrid performance prediction, and genetic diversity evaluation and narrows down the number of possible hybrid combinations for further evaluation, thereby increasing the effectiveness and efficiency of hybrid breeding.

Marker Development

The analysis of pangenomes provide highly informative molecular markers that makes current breeding efforts more accurate. These markers are widely applied in marker-assisted selection (MAS), genomic selection (GS), trait mapping and gene pyramiding that accelerate the selection of superior genotypes with higher efficiency and accuracy.

Functional Genomics

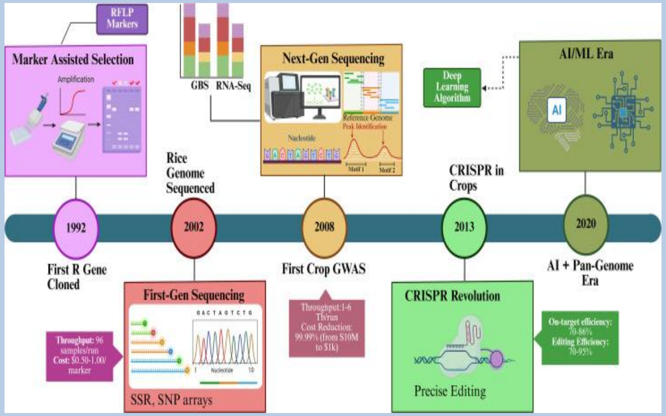
Pangenomics further promotes functional genomics by enabling gene annotation, gene function prediction, regulatory network analysis and gene expression analysis. These findings deepen our knowledge of gene function and molecular mechanisms in major agronomically relevant traits.

Major Traits Improved Using Pangenomics

The application of pangenomics to crop breeding has fast-forwarded the improvement of a number of important agronomic traits such as high yield, superior nutritional quality, disease and insect resistance, drought, heat and salinity tolerance, better water- and nitrogen-use-efficiencies, and longer shelf life. These advances result to the breeding of high yielding, climate resilient and sustainable crop varieties that can address the challenges of future agriculture.

Emerging Technologies Supporting Pangenomics

The effect of pangenomics is further amplified by its combination with next-generation technologies, including artificial intelligence (AI), machine learning, deep learning, bioinformatics, long-read sequencing, single-cell genomics, spatial transcriptomics, CRISPR/Cas genome editing, high-throughput phenotyping and digital breeding platforms. Collectively, these technologies have enhanced complex genomic data analysis, allowing faster identification of superior alleles and their subsequent deployment in contemporary breeding programs for the generation of high-yielding, climate-smart crop varieties.



Future Prospects

Pangenomics is set to be the foundation of the next generation of crop improvement, allowing breeders to tap into the entire genetic diversity of a crop species. Advances on the horizon are anticipated to include AI-based pangenome analytics, graph reference genomes, digital breeding platforms, multi-omics (genomics, transcriptomics, proteomics, metabolomics) integration, pangenome-based GS, precision genome editing, climate-smart breeding, de novo domestication of wild species and fast-track improvement of orphan crops. Collectively, these breakthroughs will increase breeding efficiency and the genetic diversity of crops, and enable farmers to access varieties with improved and stable yields under different climates and with improved nutritional value.

Challenges

Although it is no doubt full of potential, the broad application of pangenomes is facing the challenge of high sequencing cost for large populations, large computational and data storage demands, complicated bioinformatics pipelines, a lack of standardized analytical methods, integration to traditional breeding programmes, insufficient pangenome analysis expertise, and concerns of data sharing and interoperability. In the near future, ongoing improvements in sequencing technologies, cloud computing, and bioinformatics tools will surmount these challenges, enabling pangenome analysis for routine crop improvement.

Impact on Sustainable Agriculture

Pangenomics plays an important role in enhancing sustainable agriculture through sustainable crop production, ensuring food and nutrition security, climate resilience, and conservation of genetic resources. This also allows enhanced cultivars were developed faster with higher productivity, quality and tolerance to stresses, as well as with reduced need for chemicals by the inclusion of traits of natural resistances. In the end, these advances lead to better resource use, environmentally sustainable farm practices, and more productive and profitable farmers.

CONCLUSION

Pangenomics is a new era for plant breeding, as it moves away from relying on individual reference genomes for analyses, towards accounting for the entire genetic variability in the species. Revealing hidden genes, structural variations and useful alleles from the cultivated and wild germplasm, it creates unparalleled chances to boost the productivity, quality, nutritional values and resistance to biotic and abiotic stresses. With the decreasing cost of sequencing technologies and the advancement of bioinformatics tools, pangenomics will be a key element in future breeding programs not only for maximizing global food security and farm, but also for considering sustainable agriculture in the era of climate change.