



Agricultural Biotechnology as a Catalyst for Modern Crop Enhancement

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INTRODUCTION

In the era of climate change and day by day increase in disease incidence directly hampers crop yield and quality food supplied to the continuously increasing global populations are under risk. Therefore, rapid technological development to face the climatic cope and biotic stresses for sustainable crop production are essential. Recent advancement biotechnological inventions fulfil the requirement of sustainable crop production through crop improvement and development of new crop cultivars facing the global issues of climate change and disease incidence. Biotechnological strategies including marker-assisted breeding, genomic selection, genetic modifications have been employed in many staple food crops for the survival in the current scenario of crop production (Goold, et al., 2018). Now day's genome editing tools have been used by researchers for particular purpose of crop improvement.

Most of the cereal crops including rice, wheat, and maize have been targeted for improvement using biotechnological approaches. In context to varietal development for fungal, viral and bacterial disease resistance, molecular breeding and genetic modification have been successfully used to develop resistance in many crop cultivars. Crops other than cereals have been targeted for the development of resistance against various kinds of biotic stresses, salinity, drought and high temperature tolerance. Genes and QTLs have also been identified at various chromosomal locations of the crop genotypes and their wild relatives for introgression into popular crop cultivars for the development of tolerance over three decades (Riaz, et al., 2025). Genes associated with biological stresses have been identified and introgressed for developing improved crop cultivars. For example: genes conferring resistance against bacterial blight, blast, brown plant hopper, bakane, drought and salinity tolerance have been identified and incorporated for development of resistance (Lesk, et al., 2022).

Other than disease and abiotic stress tolerance, yield and quality attributing traits have been also targeted using biotechnological approaches to develop high yielding and fortified crop cultivars for fulfillment of global food demand and malnutrition (Yasmeen, et al., 2023). Horticultural and cash crops have been targeted for strategic improvement of yield, quality traits and stress management.

2. Molecular Breeding in Crop Improvement

Molecular breeding came into existence after discovery of DNA, restriction endonucleases

and polymerase chain reaction technique. Since 1990, molecular markers have been used by crop researchers for genetic diversity analysis, identification of genes associated with trait of interest and later have been used in marker-assisted selection (MAS) for genetic improvement of crop cultivars. Later in the early of 20th century, molecular mapping and tagging of genes and QTLs using DNA based markers have been used for identification of gene locus at chromosome of crop species (Genievskaya, et al., 2025).

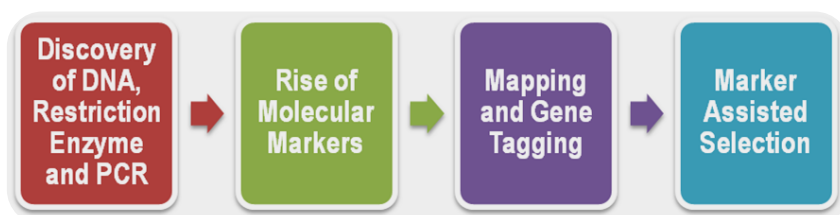


Figure-1: Molecular Breeding Discovery to Accelerated Crop Improvement.

Employing molecular breeding, major staple food crop cultivars have been targeted for genetic improvement for various oligogenic and polygenic traits with the help of DNA markers linked with gene of interest. Gene linked DNA markers have also been used for the screening of crop landraces, germplasm and wild crop relatives for identification of genes and their locus. For example: rice germplasm Tetep, C101A51, Nagina 22, have been identified for the major source of bacterial blight, blast genes and drought tolerant QTLs respectively. Later in other crops, genes and their donor lines have been identified and used

in marker-assisted breeding for introgression into commercially cultivated crop varieties.

Moreover, in the second decade of 20th century, genomic selections (GS) and genome-wide association studies (GWAS) accelerated molecular breeding. In genome-wide association studies, many traits have been targeted and introgressed into crop cultivars for strategic crop improvement. Now days, speed breeding approaches accelerates crop improvement strategy through incorporation of several genes and QTLs to achieve durable resistance for many traits.

Table 1: Historical progression of molecular breeding technologies.

Year	Milestone	Remarkable Achievement
1983	Invention of Polymerase Chain Reaction	Revolutionized DNA amplification and molecular analysis
1980-1990	Emergence of molecular markers (RFLP, RAPD, AFLP)	Indirect selection of desirable traits through DNA markers
Late 1990s	Widespread adoption of Marker-Assisted Selection (MAS)	Increased breeding precision and reduced breeding cycles
2005–2010	Development of Next-Generation Sequencing (NGS)	Enabled rapid, large-scale genome analysis at reduced cost
Late 2010	Expansion of Genomic Selection (GS)	Improved prediction of breeding values using genome-wide markers
2015–2020	High-throughput phenotyping and bioinformatics integration	Enhanced data-driven breeding decisions
2020s	AI-assisted breeding, multi-omics, and digital agriculture	Enabled predictive breeding and accelerated crop improvement.

3. Plant Genetic Engineering in Crop Improvement

Plant genetic engineering is the biotechnological approach used in genetic manipulation of plants through gene transfer from one to another organism. Most of the genetically modified and transgenic plants have been developed for targeting insect resistance, disease resistance and herbicide tolerance employing gene transfer techniques (Rozas, et al., 2022). In many crops' quality and shelf-life traits have also been targeted through various gene transfer methodology.

Golden rice, *Bt* cotton, herbicide tolerance maize is the popularly known transgenic crops. These *Bt* crops have been commercially cultivated across the world. Recently, *Bt* brinjal have been developed using genetic engineering approaches. In other crops, genes related to biotic and abiotic stress resilience have been identified and targeted for genetic transformation for development of genetically modified crops. Horticultural crops including fruits, vegetables, and ornamental plants have also been targeted for genetic improvement using genetic engineering approaches. The purpose of transgenic development in horticultural crops is to improve nutritional profile, fragrance, yield potential and resilience against stresses. Oil yielding crops for improving oil quality, yield and disease resistance have also been targeted using genetic engineering. Barnase – barstar system, low erucic acid in mustard have been targeted for transgenic development. Other oil yielding crops such as groundnut, canola,

safflower, sunflower needed to genetic improvement for production of quality oil and fulfillment of global oil demand.

Genetic engineering comes into existence after the discovery of restriction endonuclease, *Bacillus thuringiensis* (*BT*), plasmids and cloning vectors. Most of the restriction enzymes used to cleave DNA into small fragments have provided strength to the recombinant DNA (*r-DNA*) technology and gene cloning strategy. Restriction enzymes and cloning vectors are two most important tools used in the plant genetic engineering for development of transgenic/genetically modified organism. Brief description about restriction enzymes and cloning vectors are here under.

3.1. Restriction endonuclease: Most of the restriction enzymes used to cleave the DNA into small pieces are microbial in origin. On the basis of cleavage pattern, restriction enzymes are of three types but only restriction enzyme II is used in gene cloning and development of recombinant DNA.

3.2. Cloning vector: Cloning vectors are second most important tools used in genetic engineering. PUC, pBR series vectors are most popular and have been used in gene cloning for introgression of gene into plants for development of transgenics. Other than plasmid vectors, Lambda phase of bacteriophage, mini chromosome, yeast artificial chromosome (YAC), bacterial artificial chromosome (BAC) have importance to insert gene for strategically development of transgenic plants.

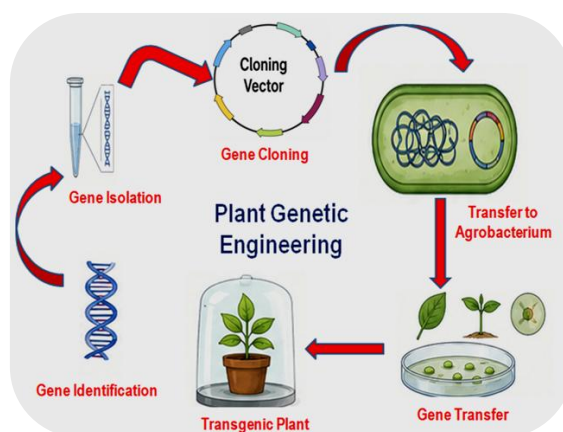
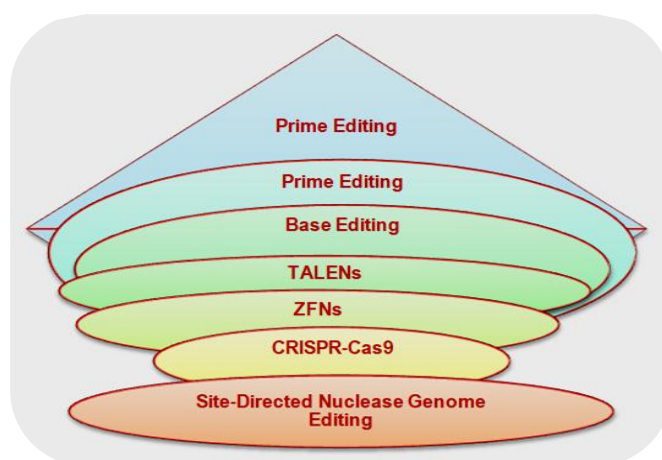


Figure-2: Procedure of transgenic plant development.

4. Genome Editing in Crop Improvement

Genome editing is the modern biotechnological tools that enable genetic modification of the plant DNA for useful purpose. Most the desirable plant traits like higher yield, improved stress tolerance and nutritional quality have been targeted by the genome editing tools *viz.* CRISPR, SFNs, TALENs (Wang, et al., 2017). Using these tools, genome editing allows targeted changes at specific location of the chromosome by addition, deletion or alteration of nucleotide sequences. Locus specific crop

genome editing accelerates crop improvement for insuring global food security by agricultural sustainability. Despite its potential, genome editing raises important concerns. Possible off-target mutations, ethical considerations, biosafety issues, and unequal access to technology require careful evaluation. Regulatory frameworks differ across countries, creating challenges for international trade and commercialization. Public acceptance also depends on transparent communication about the benefits and risks of genome-edited crops.



Figure–3: Genome editing approaches in crop improvement.

Among the genome editing tools, Cas-9 based CRISPR is widely used for genomic improvement of the plants due to its accuracy, cost-effectiveness and simplicity. In CRISPR Cas-9, guide RNA used to direct Cas-9 enzyme to specific DNA sequence, where it generates cuts. Such alteration repair naturally to modify genes for expression of targeted traits (Hmakov, et al., 2017).

In crop science, genome editing has numerous examples like development of rice cultivars with bacterial blight resistance, higher grain number in rice, fungal disease resistance in wheat, and longer shelf-life in tomatoes. Genome editing approaches (Pacesa, et al., 2024) has also accelerates biofortification to enhance nutritional status of plants like increasing vitamin content and enhanced quality of edible oils in oil yielding crop cultivars. Climate-ready crops that withstand environmental stresses like drought, salinity,

and heat tolerance have also been achieved in crop cultivars to achieve durable resistance in the era of climate change. Thus, the modern genome editing approaches represents transformative strategies of crop improvement to enhance agricultural productivity for fulfill the food demand of the continuously increasing global population. Precise genome-editing technologies, including base editing and base-pair editing, enable the rapid development of desirable traits, enhancing agricultural productivity by mitigating the impacts of biological and environmental stresses on staple crops.

5. Omic Approaches in Crop Improvement

Plant omics has emerged as robust tools for exploring complex biological systems in context to regulating plant growth, development and various stress response. Technologies like genomics, proteomics,

transcriptomics, metabolomics, and phenomics provide rapid platform for speed-up crop improvement strategy. These all technologies together facilitate consolidated understanding behind the cellular and molecular mechanism of various degree of plant response under variable environmental conditions (Xu, et al., 2022). Since last decades, these technologies have been employed by the researchers to explore the

drought, salinity and heat stress mechanism would helpful in the identification of traits and metabolic pathways related to tolerance mechanism (Li, et al., 2024). Additionally, disease cycle and degree of infection under diverse environmental conditions have been studied by the research to tackle the formulation of idea that accelerates crop improvement strategy (Derbyshire, et al., 2022).

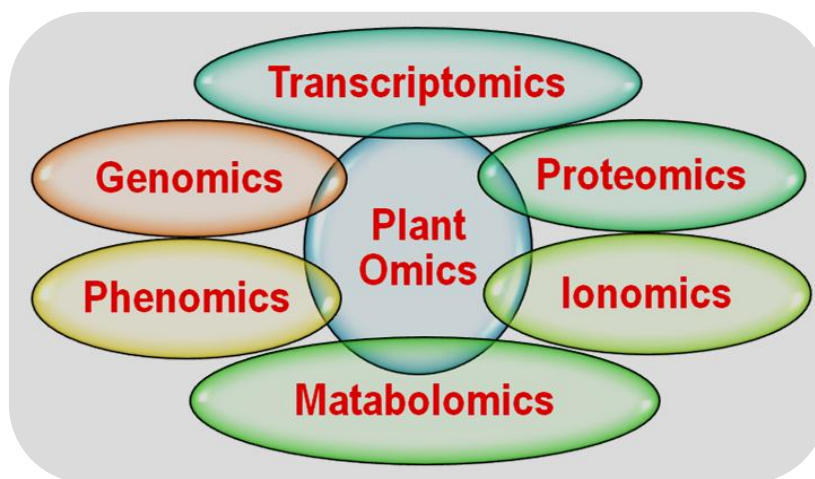


Figure-4: Omic approaches in crop improvement.

5.1. Genomics: Genomics focuses on the study about entire genome of the plants to identify the desirable genes location at the various chromosomal position and genetic variation among them to utilize in the genetic improvement program. Further, the whole genome sequencing of crops has enabled to quick and accurate identification of DNA markers linked with gene of interest may also accelerates genetic improvement of plants for various oligogenic and polygenic traits.

5.2. Transcriptomics: Transcriptomics is another type of omic approaches that play important role in examine gene expression pattern under environmental conditions. RNA transcript related studies may facilitate researchers to mine the genes suppressed or activated in diverse environmental conditions. Further information related to transcriptomics may targets genetic manipulation for enhancing tolerance for agricultural sustainability.

5.3. Proteomics: Any gene or DNA is not directly responsible for development of

resistance or tolerance for particular traits. The central dogma biology states that DNA or gene converted into mRNA through transcription and transcribed mRNA get converted into proteins through translation mechanism. If protein synthesized is governing tolerance for any traits, then said DNA nucleotides are considered as genes linked with particular traits. In proteomics, the synthesized proteins are studies to investigate the structure, function, and interactions are comes under the proteomics (Wuest, et al., 2021). Additionally, the deep and detail study about proteins significantly contributed to understand the process of plant response for stresses like heat, drought, salinity, pathogen attack would support the development of resilient crop cultivars under unfavourable climatic conditions.

5.4. Metabolomics: Metabolomics is one of promising discipline of omic science associated with naturally synthesized metabolites within the plants through sikhmic acid, malonic acid or

mevalonic acid pathways. These biosynthetic products are generally secondary metabolites responsible for defense mechanism. Further, plant secondary metabolites play crucial role in the development, defense, stress adaptation and nutritional quality of the plants. Development of biomarkers to identify the biochemical pathways associated with agronomic traits accelerates targeted genetic improvement of crop cultivars to increase tolerance under various environmental conditions.

5.5. Phenomics: Term phenomics is derived from word phenotype which encompasses among the observable morphological parameters including plant height, biomass, flowering duration, fruit/grain characteristics, leaf area, shoot and root architecture, photosynthetic efficiency, disease tolerance, and yield attributing traits. Plant phenomics is the proper and strategic study of the scaling of phenotypic data on broad spectrum using high-throughput and automated technology. The major objective of plant phenomics to quantify the plant traits under diverse range of climatic condition and development of relationship among the observation recorded with available genetic information (Hrzych, et al., 2025). Plant phenomics may further enables to comprehensive analysis of the major phenotypic traits at different plant growth stages under diverse range of environmental conditions.

CONCLUSION

Agricultural biotechnology plays vital role in genetic improvement of crop cultivars for addressing global challenges of food security in the era of climate change. Employing biotechnological tools and techniques like molecular breeding, genetic engineering, genome editing and omic approaches, several crops have been strategically improved and plays vital role in sustainable food production. These technologies have significantly contributed to the sustainable agricultural development by reducing dependency on chemical inputs, improving source-use

efficiency and enhanced crop adaptability under changing climatic conditions. Additionally, some biotechnological techniques accelerated the development of crop cultivars with enhanced nutritional quality, more resilience to biotic and abiotic threats.

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