



BIOFERTILIZERS IN SUSTAINABLE AGRICULTURE

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Dr. Mukesh Narwal

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Dr. Mukesh Narwal

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Carbon Sequestration Potential of **Agronomic Practices**

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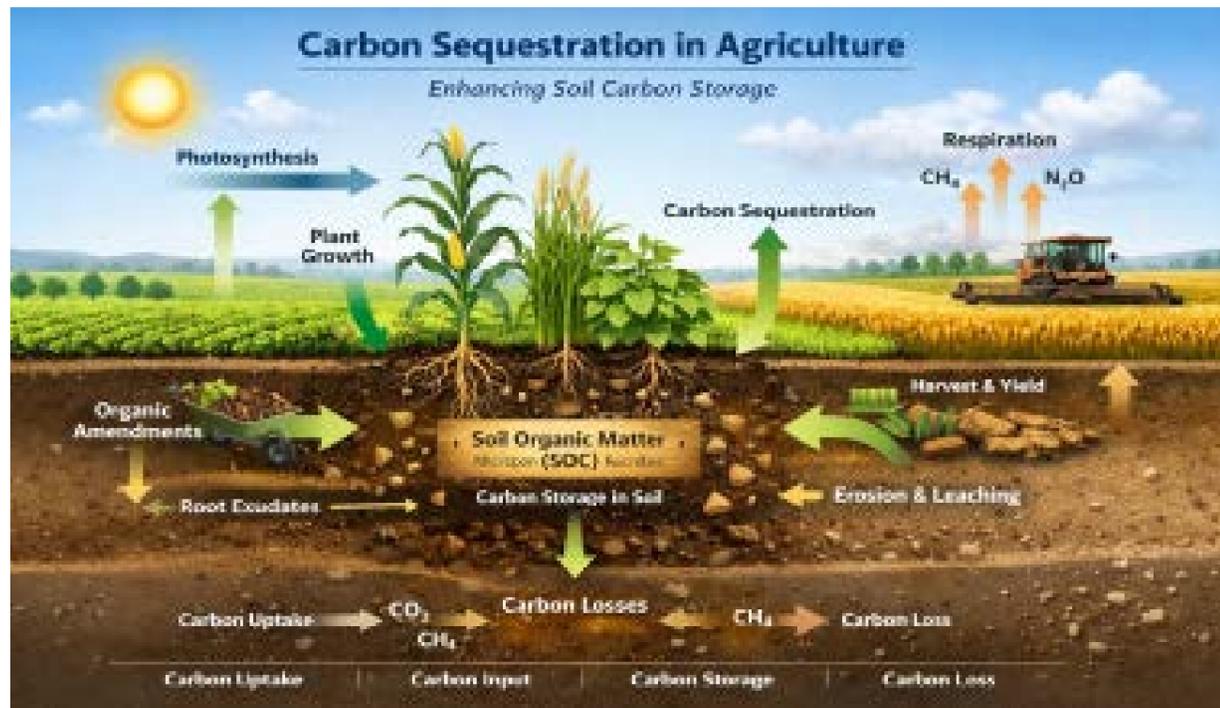
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Carbon Sequestration Potential of Agronomic Practices

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Abstract

Agricultural soils serve as a critical repository for terrestrial carbon, yet conventional farming methods including intensive tillage and monoculture have significantly depleted soil organic carbon and disrupted carbon cycle dynamics. Conventional farming practices such as intensive tillage and monocropping have contributed to SOC depletion and soil degradation. In contrast, improved agronomic practices offer significant potential for enhancing soil carbon sequestration while promoting sustainable agriculture. This article reviews the role of conservation tillage, no-till farming, cover cropping, crop rotation,



organic farming, agroforestry systems, and bio-char application in increasing SOC stocks. These practices enhance carbon inputs, reduce organic matter decomposition, and promote long term carbon stabilization in soils. Increasing SOC not only contribute to climate change mitigation but also improves soil fertility, nutrient availability, and crop productivity. The adoption of carbon-sequestering agronomic practices represents a cost cost-effective and environmentally sustainable strategy for achieving climate-resilient agricultural systems.

Keywords: Carbon sequestration, conservation agriculture, climate change mitigation and soil organic carbon.

Introduction

The increasing concentrations of greenhouse gases, particularly carbon dioxide, in the atmosphere have intensified the global interest in leveraging agricultural soils as carbon sinks (Rashid., 2024). Agricultural soils are a primary repository of terrestrial carbon, with soil organic carbon levels reflecting the balance between carbon inputs and losses. Conventional agricultural practices, such as extensive tillage, monoculture farming, and excessive synthetic fertilizer application, have often led to soil degradation and depletion of soil carbon thereby impacting the carbon cycle dynamics (Kumar et al., 2025). However, adopting specific agronomic practices offers a significant opportunity to sequester carbon in soils, mitigate climate change, and enhance agricultural sustainability.

The Role of Soil Organic Carbon

Soil organic carbon is crucial for soil health, fertility, and nutrient cycling. A decline in SOC adversely affects soil quality, depletes nutrient, and increase susceptibility to erosion (Kumar et al., 2025). Conversely, increasing SOC can lead to higher crop yields. For instance, an increase of 1 Mg/ha in soil organic carbon within the crop root zone can boost grain yields of wheat by 20-70 kg/ha, rice by 10-50 kg/ha, and maize by 30-300 kg/ha (Dass, 2023). Therefore, carbon sequestration in agricultural soils, which refers to the increase of soil carbon storage, is not only an environ



mental imperative but also an agricultural benefit (Tanveer et al., 2019).

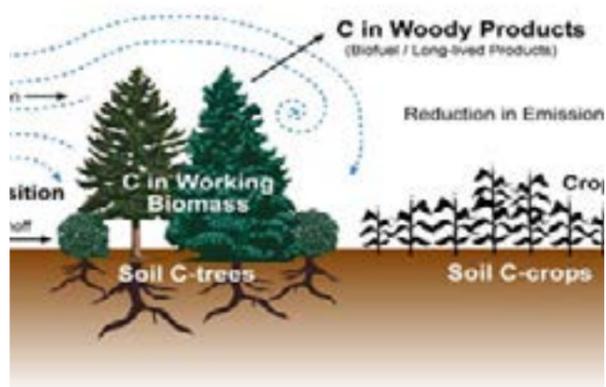
Key Agronomic Practices for Carbon Sequestration

Various agronomic management options can enhance soil carbon sequestration. These practices contribute to increasing carbon input in soils and reducing the decomposition potential of soil organic matter (Tanveer et al., 2019)

1. Conservation Tillage and No-Till Farming

Tillage practices significantly influence soil organic matter and carbon dynamics (Dass, 2023). Conventional tillage can often lead to the deprotection of organic matter, making it more vulnerable to decomposition. In contrast, conservation tillage approaches are considered highly effective and can be implemented relatively quickly compared to other atmospheric drawdown measures (Koushika et al., 2024).

No-Till Farming: The shift from conventional tillage to no-tillage is a widely adopted practice to reduce the decline rate of soil organic matter (Mehra et al., 2018). No-till farming helps maintain carbon storage by minimizing soil disturbance (Koushika et al., 2024). Studies have shown that an augmentation in soil carbon from reduced or conservation tillage to no-till can vary from 10-30% (Dass, 2023). No-till can prevent SOC losses from tilled soils, can be partially mitigated, thereby offsetting agricultural CO₂ emission from agriculture especially when associated with increased cropping intensity and the inclusion of legume cover crops (Nicolso & Rice, 2021).



2. Cover Cropping and crop Rotation



Cover crops and crop rotations are sustainable agricultural farming practices that enhance soil health and increase carbon storage (Koushika et al., 2024).

Cover Cropping: Cover crops, typically grown between main crop seasons, contribute to carbon storage by adding organic inputs in the form of root biomass and decomposing plant material. These inputs contribute directly to soil organic matter accumulation. In addition, root exudates released by cover crops stimulate soil microbial communities, promoting the transformation of complex organic substances into more stable forms of soil organic carbon (Koushika et al., 2024).

Crop Rotation: Varying plant residues, root architectures, and nutrient needs through crop rotation promotes microbial activity and organic matter absorption, thereby enhancing soil carbon storage (Koushika et al., 2024).

3. Organic Farming and Organic Amendments

Organic farming and the addition of organic manure contribute to increased carbon sequestration by providing conditions favourable for higher dry matter accumulation and fostering a more active and diverse microbial community (Mishra et al., 2024; Sagar & Singh, 2020). Organic farming has been shown to boost soil microbial health and exhibit higher soil organic carbon content compared to conventional farming (Koushika et al.,

2024; Mishra et al., 2024)

1. Agroforestry Systems

Agroforestry systems, which integrate trees and crops, boost organic carbon input and accelerate nutrient cycling due to symbiotic relationships between the trees and crops (Koushika et al., 2024).

2. Biochar Application

The addition of biochar is another approach to increase SOC content in agricultural soils (Weber et al., 2024). Biochar is a stable form of carbon that can persist in the soil for long periods, effectively sequestering carbon.

Global Potential and Economic Considerations

The global carbon sequestration potential of agricultural soils is estimated to range from 0.4 to 1.2 gigatons per year (Tanveer et al., 2019). Land use, land use change, and forestry activities, including sustainable agricultural practices, are considered cost-effective ways to offset emissions by increasing the removal of greenhouse gases from the atmosphere (Tanveer et al., 2019).

The adoption of these practices can vary depending on various factors, including economic incentives. For instance, policies valuing soil carbon in agricultural systems can strongly encourage the adoption of no-till and cover cropping (Weber et al., 2024). The relative soil carbon gain from practices like conservation tillage can represent a carbon credit, highlighting the economic viability of these sustainable practices (Lam et al., 2013).

Conclusion

Agronomic practices such as conservation tillage, no-till farming, cover cropping, crop rotation, organic farming, and biochar application play vital roles in increasing the soil organic carbon content sustainably. These practices not only contribute significantly to carbon sequestration and climate change mitigation but also offer co-benefits such as improved soil quality, increased nutrient

retention, reduced erosion, and sustainable agricultural strategies, the agricultural sector can move towards a more data-driven, efficient, and environmentally sustainable future, contributing significantly to global efforts in combating climate change.

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Role of Biofertilizers in Sustainable Agriculture



Volume 02 || Issue 01

Role of Biofertilizers in Sustainable Agriculture

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Abstract

Sustainable agriculture aims to balance productivity with environmental conservation, and biofertilizers have emerged as a key component in achieving this balance. Biofertilizers microbial inoculants containing beneficial microorganisms such as nitrogen fixing bacteria, phosphate solubilizing bacteria, mycorrhizal fungi, and cyanobacteria enhance nutrient availability, improve soil structure, and promote plant growth. Unlike synthetic fertilizers, they are eco-friendly and cost-effective, offering long-term soil fertility and reduced ecological harm. This article explores the role of biofertilizers in sustainable

agriculture, their benefits, limitations, technological advancements, and real-world case studies. It also highlights how biofertilizers contribute to food security, climate resilience, and environmentally responsible farming.

Introduction

Agriculture today faces multiple challenges: declining soil fertility, overuse of chemical fertilizers, pollution, loss of biodiversity, and rising production costs. While synthetic fertilizers played a major role in boosting agricultural productivity in the 20th century, their excessive use has contributed to soil degradation, water contamination, and greenhouse gas emissions. Sustainable agriculture, therefore, demands alternatives that maintain yield while minimizing ecological damage. Biofertilizers provide such an alternative. They are natural fertilizers containing living microorganisms that enhance nutrient availability through biological processes such as nitrogen fixation, phosphorus solubilization, potassium mobilization, and production of plant-growth promoting substances. By improving soil microbial activity and maintaining soil health, biofertilizers support long-term agricultural sustainability. Over the last decade, extensive research has demonstrated their effectiveness in improving crop productivity while reducing dependency on chemical inputs.

Benefits of Biofertilizers

1. Soil Fertility Improvement

Biofertilizers enhance soil fertility in several ways:

- Nitrogen fixation: Rhizobium, Azotobacter, and Azospirillum convert atmospheric nitrogen into plant-available forms.
- Phosphorus solubilization: Microbes like Pseudomonas and Bacillus release organic acids that convert insoluble phosphate into available phosphate.

- Organic matter improvement: Biofertilizers increase microbial biomass and activity, improving soil structure and nutrient cycling.
- Long-term application significantly improves soil organic carbon and microbial diversity, enhancing the soil's ability to support crops sustainably.

2. Enhanced Crop Yield and Growth

Biofertilizers promote root development and nutrient uptake, resulting in increased crop yield. They also produce phytohormones such as auxins, gibberellins, and cytokinins that stimulate plant growth. Research shows notable yield increases in cereals, legumes, vegetables, and horticultural crops when biofertilizers are used in combination with reduced chemical fertilizers (Keerthana and Singh, 2025).

3. Environmental Sustainability

Biofertilizers reduce:

- I. Chemical fertilizer use.
- II. Soil and water pollution.
- III. Greenhouse gas emissions from fertilizer manufacturing.
- IV. They also promote biodiversity by supporting beneficial soil microbial populations

4. Cost-Effectiveness

Biofertilizers are cheaper than chemical fertilizers and reduce the need for repeated application. Their long-term benefits improved soil health and reduced input costs make farming more economically sustainable for small and marginal farmers (Bhardwaj et al., 2014).

5. Stress Tolerance and Climate Resilience

Certain biofertilizers help crops tolerate drought, salinity, and disease by:

- a) Producing stress-relieving enzymes.
- b) Strengthening plant root systems.
- c) Enhancing water-use efficiency.
- d) This resilience is crucial under changing

climate conditions (Shahzad et al., 2025).

6. Compatibility with Organic Farming

Biofertilizers are essential inputs in organic farming systems where synthetic fertilizers are not allowed. They help maintain productivity while supporting ecological principles (Kumawat, 2022).

Challenges in the Use of Biofertilizers

1. Variable Performance in Field Condition

A major limitation is inconsistency in results due to:

- Soil pH
- Temperature
- Moisture levels
- Native microbial competition

Biofertilizers often perform excellently in laboratories but inconsistently in farmer's fields.

2. Poor Shelf Life

Because biofertilizers contain living microorganisms, they are sensitive to sunlight, heat, and storage conditions. Without proper packaging and carrier materials, their effectiveness declines.

3. Lack of Awareness

Many farmers lack knowledge about:

- How to use biofertilizers.
- Correct dosage and timing.
- Their long-term benefits.
- This limits widespread adoption.

4. Limited Quality Control

In some regions, the availability of low-quality or contaminated biofertilizer products reduces trust among farmers. Standardization and strict regulatory frameworks are needed.

5. Slow Mode of Action

Compared to chemical fertilizers, biofertilizers act slowly as they depend on microbial multiplication and soil interactions.

6. Need for Region-Specific Strains

Microbial strains effective in one region may not work well in another due to soil and climatic differences. More research is needed to develop location-specific formulations.

Case Studies

Rhizobium in Legume Cultivation (India)

In several Indian states, Rhizobium inoculation in pulses such as chickpea and lentil resulted in:

- 20–30% increased yield.
- Reduced nitrogen fertilizer requirement by up to 50%
- Improved soil nitrogen levels for next cropping seasons.
- This demonstrates the dual benefits of high yield and soil improvement.
- A critical analysis of Sri Lankan biofilm biofertilizers showed (Patel & Singh, 2023):
- Increased microbial activity and improved soil structure.
- Mixed yield outcomes depending on environmental conditions.

Conclusion

Biofertilizers offer a promising, eco-friendly, and cost-effective solution for achieving sustainable agriculture. They enhance soil fertility, crop productivity, and environmental health while reducing reliance on chemical fertilizers. As global agriculture faces challenges such as soil degradation, climate change, and rising input costs, biofertilizers represent a sustainable path forward. However, challenges related to field performance, shelf life, farmer awareness, and quality control must be addressed through scientific innovation, strong policy support, and capacity-building programs. With continuous advancements such as nano-biofertilizers, microbial consortia, and metagenomics biofertilizers are poised to play a central role in shaping the future of sustainable farming systems.

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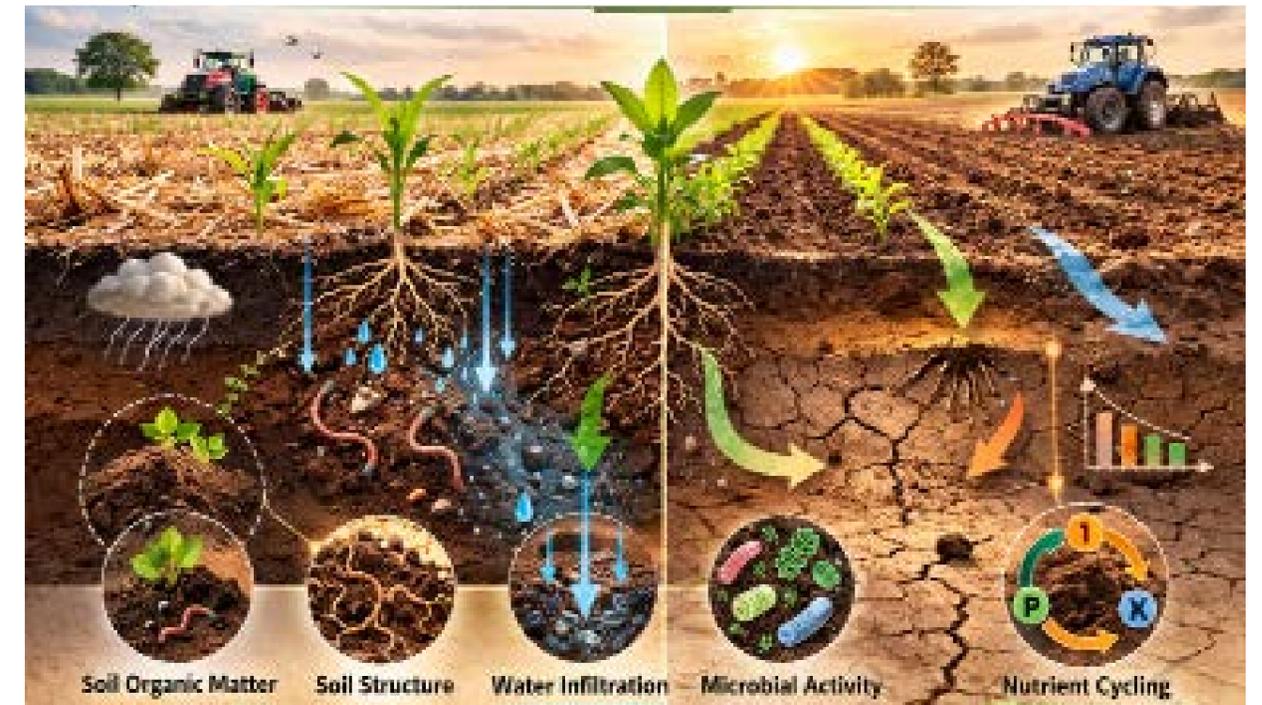
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Zero Tillage and Its Effect on Soil Properties



Volume 02 || Issue 01

Zero Tillage and Its Effect on Soil Properties

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Abstract

Zero tillage has emerged as a vital practice within conservation agriculture, especially in areas where intensive tillage has led to declining soil quality and reduced long-term productivity. Conventional ploughing disrupts natural soil aggregates, accelerates the breakdown of organic matter, and increases erosion, ultimately weakening soil fertility. Zero tillage is also known as no-till farming, minimizes soil disturbance by enabling direct seeding into undisturbed soil while crop residues remain on the surface. This approach significantly improves soil physical properties, including aggregation stability, water

infiltration, moisture retention and resistance to erosion. Chemical properties also benefit, as zero tillage enhances soil organic carbon, nutrient availability, cation exchange capacity and overall carbon sequestration. Biologically, it supports greater microbial biomass, earthworm activity, enzyme functions and biodiversity. Despite these advantages, zero tillage faces challenges such as increased weed pressure, potential pest harbouring in residues, and high initial equipment investment. Case study from the Indo-Gangetic plains highlighting its practical benefits, reporting higher wheat yield, reduced fuel consumption and substantial cost savings. Overall, zero tillage represents a sustainable and environmentally sound farming approach with strong potential to improve soil health and promote resilient agricultural systems.



Introduction

The continuous use of intensive tillage practices in modern agriculture has resulted in a significant decline in soil health and productivity. Excessive ploughing disturbs soil aggregates, accelerates organic matter decomposition, and increases erosion and nutrient losses. To overcome these problems, farmers and researchers have turned toward conservation agriculture (CA)- a sustainable system that includes zero tillage, crop residue management, and diverse crop rotations.

Among these, Zero Tillage (ZT), also known as No-Till Farming, is a revolutionary approach that aims to minimize soil disturbance. The crop is planted directly into undisturbed soil, often with

residues from the previous crop left on the surface. This technique conserves soil structure, maintains soil moisture, and supports long-term soil fertility-essential for ensuring sustainable food production and environmental conservation.

Definition and Concept of Zero Tillage

Zero tillage refers to the process of planting crops without prior soil tillage. Instead of ploughing and preparing a fine seedbed, seeds are placed into narrow slits opened by a zero-till seed drill or happy seeder, which simultaneously applies fertilizer. The basic idea is to disturb the soil as little as possible, allowing the natural biological and structural processes within the soil to remain intact. Over time, this builds a more resilient and fertile soil ecosystem.

Zero tillage is a key pillar of conservation agriculture, along with:

1. Minimal mechanical soil disturbance,
2. Permanent organic soil cover (crop residues), and
3. Crop rotation for biodiversity improvement.

Objectives of Zero Tillage

- To preserve natural soil structure and prevent erosion.
- To enhance soil organic matter and fertility.
- To reduce production costs and save energy.
- To improve water infiltration and retention in the soil.
- To promote beneficial microbial and faunal activity.
- To achieve sustainable crop productivity in the long term.

Implements Used in Zero Tillage

1. **Zero Till Seed Drill** – The most common implement that sow seeds directly into unploughed soil with fertilizer placement.
2. **Happy Seeder**– Allows direct seeding into standing rice residues, preventing residue burning.

1. **Turbo Seeder** – Suitable for multiple crops under residue conditions.
2. **Strip-Till Drill** – Disturbs only a narrow strip where seeds are sown, combining the advantages of both tilled and untilled systems.

Effects of Zero Tillage on Soil Properties

A. Soil Physical Properties

1. **Soil Structure and Aggregation:** In conventional ploughing, repeated tillage destroys soil aggregates and weakens soil structure. Zero tillage allows aggregates to stabilize, increasing soil porosity and improving aeration. Residue cover also protects the surface from raindrop impact, reducing crust formation and compaction.
2. **Bulk Density:** Initially, zero tillage soils may show slightly higher bulk density, but as root channels and biological activity increase, pore formation improves and bulk density decreases over time.
3. **Water Infiltration and Retention:** Mulch cover from crop residues enhances water infiltration and reduces evaporation losses. This increases soil water storage capacity-particularly beneficial for dryland farming and rainfed systems.
4. **Soil Erosion Control:** With residue cover and no mechanical disturbance, zero tillage minimizes soil erosion by both wind and water.
5. **Soil Temperature Regulation:** Crop residues act as a natural insulator, maintaining moderate soil temperature.

B. Soil Chemical Properties

1. **Organic Carbon and Matter:** Zero tillage increases the organic matter content due to reduced decomposition and residue incorporation.
2. **Nutrient Availability:** Surface residues release nutrients slowly through decomposition, reducing nutrient losses through leaching.

3. **pH and Soil Reaction:** Organic matter decomposition releases weak acids and basic cations, which help maintain a balanced soil pH.
4. **Cation Exchange Capacity (CEC):** Higher organic carbon in zero tillage soils improves nutrient retention and minimizes fertilizer losses.
5. **Carbon Sequestration:** Since the soil is not disturbed, more carbon remains trapped in stable organic forms.



C. Soil Biological Properties

1. **Microbial Activity and Biomass:** Zero tillage creates a stable and moist environment that promotes microbial growth.
2. **Earthworm Population:** The presence of mulch and undisturbed soil provides a perfect habitat for earthworms.

- 3. Enzyme Activities:** Enzymes like dehydrogenase, phosphatase, and urease show higher activity under zero tillage conditions.
- 4. Soil Fauna Diversity:** Zero tillage supports beneficial fauna such as nematodes, mites, and fungi.

Advantages of Zero Tillage

- Reduces fuel and labor costs by 25–40%.
- Enhances soil moisture conservation and reduces irrigation frequency.
- Encourages biological soil activity and biodiversity.
- Improves crop yields and long-term sustainability.
- Minimizes soil erosion and greenhouse gas emissions.
- Allows timely sowing of wheat after rice.
- Reduces residue burning and pollution.

Limitations of Zero Tillage

- Weed infestation can increase, requiring integrated weed management.
- Crop residues may harbor pests and diseases.
- Initial equipment cost is high for small-scale farmers.
- May not perform well in poorly drained or heavy clay soils.
- Requires farmer training and technical support.

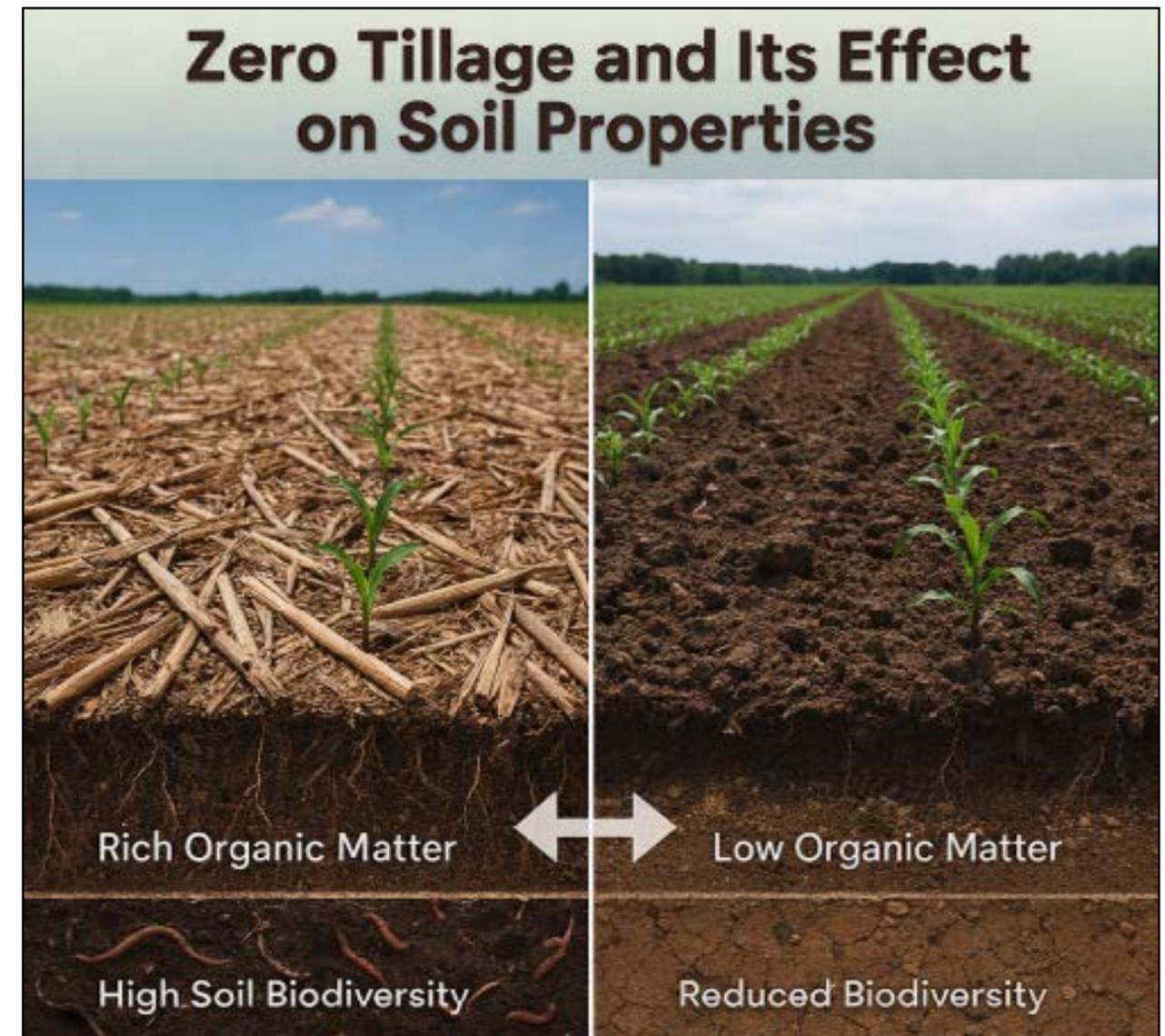


Case Study: Zero Tillage in India

In the Indo-Gangetic Plains, particularly in Haryana, Punjab, Uttar Pradesh, and parts of Himachal Pradesh, large-scale adoption of zero tillage has improved soil health and productivity. According to CIMMYT–ICAR research (2024): Zero tillage reduced fuel use by 60 liters per ha, increased wheat yield by 4–7%, and saved ₹4,000–₹5,000 per hectare in costs (Gathala et al., 2011).

Conclusion

Zero tillage represents a shift from traditional, energy-intensive agriculture to a soil-friendly and resource-efficient system. It positively affects all major soil properties like physical, chemical, and biological and builds a healthy, fertile soil base for sustainable agriculture. While challenges such as weed management and equipment cost exist, the overall benefits make zero tillage one of the most promising approaches for future farming.

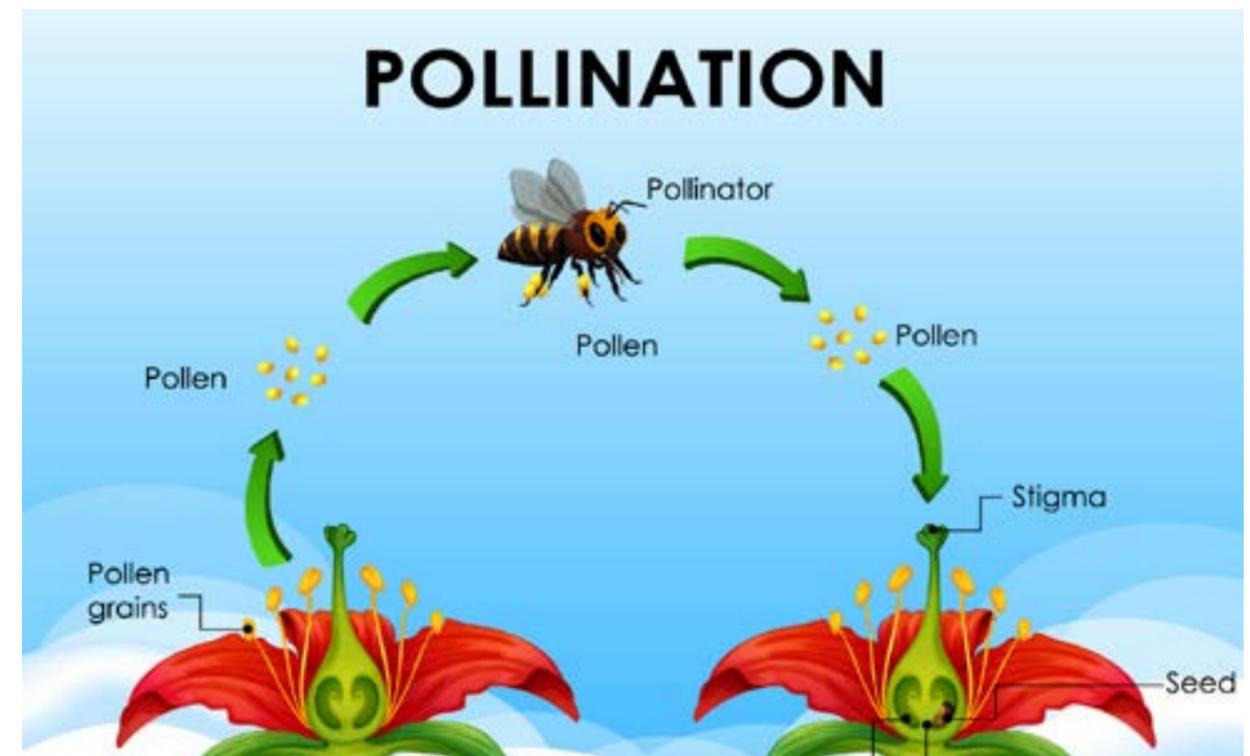


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Latest Trends in Cross-Pollinated Crop Breeding: Empirical and Molecular Approaches



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Latest Trends in Cross-Pollinated Crop Breeding: Empirical and Molecular Approaches

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Abstract

Cross-pollinated crops such as maize, pearl millet, sorghum, sunflower, rye, and forage grasses form the backbone of global food, feed, and industrial systems. Their genetic structure is characterized by high heterozygosity, strong inbreeding depression, and predominance of non-additive gene action, which historically shaped breeding strategies centered on population improvement and heterosis exploitation. With the advent of

molecular genetics, genomics, and digital technologies, breeding of cross-pollinated species has entered a new era in which empirical field-based selection is increasingly integrated with genome-assisted and data-driven approaches. This chapter provides a comprehensive review of the latest trends in cross-pollinated crop breeding, emphasizing the continuum from classical empirical methods—such as mass selection, family selection, recurrent selection, and hybrid breeding—to advanced molecular tools including marker-assisted selection, genomic selection, doubled haploids, transgenic technologies, and genome editing. The integration of high-throughput phenotyping, artificial intelligence, and systems biology has further transformed breeding into a predictive and precision-oriented science. Through conceptual frameworks and crop-specific case studies, the chapter highlights how the convergence of empirical and molecular approaches is accelerating genetic gain, enhancing stress resilience, and enabling the development of climate-smart, resource-efficient, and nutritionally superior cultivars suited to diverse agro-ecological conditions.

Keywords: Cross-pollinated crops; Heterosis; Recurrent selection; Marker-assisted selection; Genomic selection; Genome editing; Doubled haploids; Phenomics; AI-driven breeding; Climate-smart varieties.

Introduction

Cross-pollinated crops occupy a central position in global agriculture owing to their high productivity, wide adaptability, and versatility in end-use. Major cereals such as maize and rye, millets like pearl millet, oilseeds such as sunflower, and a wide array of forage grasses and vegetable crops belong to this category. The hallmark of these species is their predominantly allogamous mating system, which maintains a high level of heterozygosity and genetic variability within populations. Consequently, they exhibit pronounced inbreeding depression and substantial heterosis, attributes that have profoundly influenced their breeding methodology.

Traditional breeding of cross-pollinated crops relied heavily on empirical approaches based on

phenotypic selection and population improvement. Methods such as mass selection, family selection, and recurrent selection were developed to exploit additive genetic variance while preserving population diversity. The discovery and systematic utilization of heterosis led to the widespread adoption of hybrid breeding, transforming crops like maize and sunflower into some of the most productive agricultural species worldwide.

However, the challenges of the twenty-first century—climate change, resource scarcity, emerging pests and diseases, and the need for nutritional security—have necessitated a paradigm shift in breeding strategies. Empirical selection alone, though robust, is often slow and limited in its ability to dissect complex quantitative traits governed by many genes with small effects. The integration of molecular genetics and genomics has therefore become indispensable for accelerating genetic gain and improving selection precision.

The current trend in cross-pollinated crop breeding is towards a holistic, systems-based approach that combines:

- Classical population improvement and heterosis breeding,
- Genome-assisted selection and prediction,
- Biotechnological interventions such as doubled haploids and genome editing, and
- Digital tools including high-throughput phenotyping, envirotyping, and artificial intelligence.

This convergence marks the transition from phenotype-driven to genome-enabled and data-driven breeding, often referred to as Breeding 4.0. The present chapter aims to critically examine these developments, tracing the evolution from empirical foundations to cutting-edge molecular and computational methodologies, and to discuss their implications for sustainable crop improvement.

Genetic Architecture of Cross-Pollinated Crops

1.1 Mating System and Population Structure

Cross-pollinated crops are characterized by a predominantly outcrossing mating system facil



itated by mechanisms such as protandry or protogyny, self-incompatibility, or spatial separation of male and female organs. This promotes random mating and maintains high levels of heterozygosity within populations. As a result:

- Allelic diversity is extensive,
- Linkage disequilibrium decays rapidly, and
- Genetic variation is distributed both within and among populations.

Such populations are dynamic, with allele frequencies continuously reshaped by natural selection, genetic drift, migration, and artificial selection imposed by breeders.

1.2 Gene Action and Heterosis

The genetic control of most economically important traits in cross-pollinated crops is complex, involving both additive and non-additive components. While additive effects are responsible for the response to selection in populations, dominance and epistatic interactions underpin heterosis expressed in hybrids. The relative importance of these components varies with trait and environment:

Additive gene action predominates for traits like

plant height, flowering time, and some quality attributes.

Dominance and over-dominance play a major role in yield, biomass, and stress tolerance. Epistasis contributes to stability and adaptability across environments.

The exploitation of heterosis through hybrid breeding is therefore a direct consequence of the genetic architecture of cross-pollinated species, and understanding the underlying gene action is fundamental to designing efficient breeding strategies.

1.3 Genetic Variance Components in Populations

In a randomly mating population, the total genetic variance (VG) can be partitioned into:

Additive variance (VA),
Dominance variance (VD), and
Epistatic variance (VI).

Empirical breeding methods such as recurrent selection aim primarily at increasing VA, thereby improving the population mean. Conversely, hybrid breeding capitalizes on VD and VI by combining genetically divergent parents to maximize heterozygosity at key loci.

1.4 Heterotic Grouping and Genetic Divergence

The concept of heterotic groups—sets of genetically related lines that exhibit superior hybrid performance when crossed with members of another group—has become central to modern breeding of cross-pollinated crops. Traditionally, heterotic groups were identified through combining ability tests and pedigree information. Recent trends involve the use of molecular markers and genomic data to quantify genetic distance and population structure, enabling:

- More precise classification of germplasm,
- Prediction of heterosis, and
- Strategic broadening of the genetic base through introgression of exotic alleles.

1.5 Implications for Breeding Strategy

The genetic architecture of cross-pollinated crops necessitates a dual breeding approach:

Population Improvement:

Focused on accumulating favourable additive alleles through recurrent selection and maintaining broad genetic diversity.

Hybrid Development:

Exploiting non-additive gene action by crossing complementary inbred lines or populations to achieve high heterosis and yield stability.

The integration of molecular tools into this framework has enabled breeders to dissect the genetic basis of complex traits, track favourable alleles, and predict breeding values with unprecedented accuracy.

Empirical Breeding Approaches in Cross-Pollinated Crops

Empirical or conventional breeding approaches form the historical and conceptual foundation of improvement in cross-pollinated species. These methods rely on phenotypic evaluation and selection, guided by quantitative genetic principles, and are designed to manipulate gene frequencies in heterogeneous populations while maintaining sufficient genetic variability for long-term progress.

2.1 Mass Selection

Mass selection is the simplest and oldest method of population improvement. It involves selecting superior phenotypes from a heterogeneous population and bulking their seeds to constitute the next generation.

2.1.1 Principle

Selection is based on individual plant phenotype, assuming that superior phenotypes carry favourable alleles which, when intermated, will increase their frequency in the population

2.1.2 Types

Positive mass selection – selecting superior plants.

Negative mass selection (Roguing) – eliminating inferior or diseased plants.

Stratified mass selection – dividing the field into small blocks to reduce environmental variation and improve selection efficiency.

2.1.3 Genetic Basis

Primarily exploits additive genetic variance. Effective for traits with high heritability (e.g., maturity, plant stature, disease resistance).

2.1.4 Modern Refinements

- Use of selection indices combining multiple traits.
- Integration with molecular markers to avoid loss of favourable alleles.
- Participatory mass selection in farmer fields for local adaptation.

2.2 Family Selection

To overcome the low accuracy of individual plant selection for low-heritability traits, family-based selection methods were developed.

2.2.1 Half-Sib Family Selection

- Progeny from a common male or female parent are evaluated.
- Estimates general combining ability (GCA)

- and additive variance.
- Widely used in maize, forage grasses, and pearl millet.

2.2.2 Full-Sib Family Selection

Progeny derived from known male × female crosses.

Captures both additive and dominance variance. Higher accuracy than half-sib but more resource-intensive.

2.2.3 S1 and S2 Family Selection

Based on selfed progenies. Helps expose recessive deleterious alleles and improve inbred performance. Useful as a preliminary step toward inbred line development.

2.3 Recurrent Selection

Recurrent selection is the most powerful empirical method for systematic population improvement in cross-pollinated crops.

2.2.1 Concept

Repeated cycles of selection and recombination are carried out to progressively increase the frequency of favourable alleles in a population.

2.2.2 Types of Recurrent Selection

- Simple Recurrent Selection
- Based on phenotypic or progeny performance.
- Targets additive gene effects.
- Recurrent Selection for GCA
- Selection based on testcross performance with a broad-based tester.
- Improves population combining ability.
- Recurrent Selection for SCA
- Uses specific testers.
- Enhances non-additive gene action.
- Reciprocal Recurrent Selection (RRS)
- Simultaneous improvement of two populations.
- Maximizes heterosis between them.
- Foundation of modern heterotic group development in maize and pearl millet.

2.2.3 Genetic Gain

Genetic gain per cycle depends on:

- Selection intensity
- Heritability
- Genetic variance
- Cycle length
- Modern trend: shortening cycle length using doubled haploids and genomic selection.

2.4 Heterosis Breeding and Hybrid Development

Heterosis exploitation is the most successful application of quantitative genetics in cross-pollinated crops.

2.4.1 Types of Hybrids

- Single-cross ($A \times B$)
- Three-way cross ($A \times B$) × C
- Double-cross ($A \times B$) × (C × D)
- Top-cross (inbred × population)

2.4.2 Combining Ability

GCA reflects additive effects.

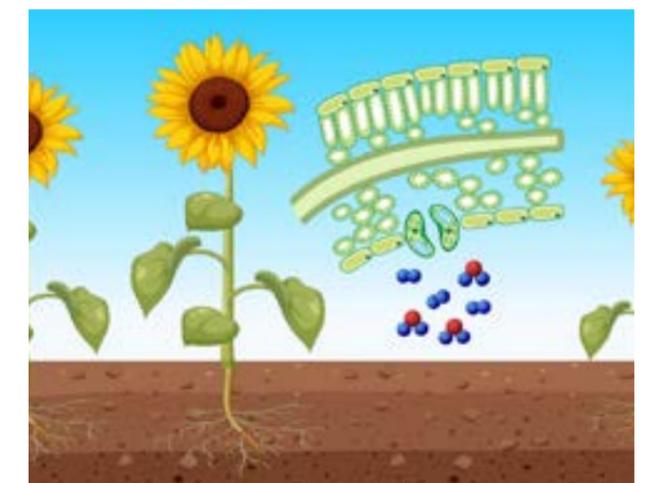
SCA reflects dominance and epistasis.

Line × Tester and Diallel analyses remain central empirical tools.

2.4.3 Cytoplasmic Male Sterility (CMS)

CMS, CGMS, and TGMS systems facilitate large-scale hybrid seed production.

Widely used in maize, pearl millet, sorghum, sunflower, and onion.



2.4.4 Heterotic Grouping

Traditionally based on pedigree and combining ability. Now increasingly refined using molecular diversity and genomic prediction.

2.5 Synthetics and Composite Varieties

2.5.1 Synthetic Varieties

Developed by intercrossing selected inbreds or clones with good GCA. Maintain heterozygosity and yield stability. Important in forage crops and maize in marginal environments.

2.5.2 Composite Varieties

Formed by mixing seeds of several superior populations or varieties. Broad genetic base and adaptation. Suitable for low-input and stress-prone regions.

2.6 Empirical Breeding under Abiotic and Biotic Stresses

Modern empirical breeding emphasizes managed stress screening:

- **Drought:** anthesis–silking interval, stay-green, root traits.
- **Heat:** pollen viability, silk receptivity.
- **Low N and P:** nutrient-use efficiency traits.
- **Diseases & insects:** host plant resistance, tolerance, and escape mechanisms.

Selection is increasingly conducted in multi-environment trials to capture $G \times E$ interactions and improve stability.

2.7 Limitations of Purely Empirical Approaches

Despite their robustness, empirical methods face constraints:

- Long breeding cycles
- Low precision for complex traits
- Difficulty in pyramiding multiple genes
- Inefficiency under strong $G \times E$ interaction

Molecular and Genomic Approaches in Cross-Pollinated Crop Breeding

The limitations of purely phenotypic selection in dealing with complex quantitative traits, strong genotype \times environment ($G \times E$) interactions, and long breeding cycles have led to the incorporation of molecular and genomic tools into breeding programs. These approaches enhance selection accuracy, accelerate genetic gain, and allow precise manipulation of the genetic architecture of cross-pollinated crops.



3.1 Molecular Markers and Genetic Mapping

3.1.1 Types of Molecular Markers

Modern breeding utilizes a wide array of DNA markers, including:

- RFLPs (Restriction Fragment Length Polymorphisms) – first generation markers, highly reliable but labor-intensive.
- SSRs (Simple Sequence Repeats / Microsatellites) – co-dominant, highly polymorphic, widely used in diversity and mapping studies.
- SNPs (Single Nucleotide Polymorphisms) – abundant, amenable to high-throughput genotyping platforms, now the marker of choice.
- InDels and functional markers – directly associated with gene sequences controlling traits.

3.1.2 Linkage Mapping and QTL Analysis



Development of bi-parental mapping populations (F_2 , RILs, DHs) to identify quantitative trait loci (QTLs) for yield, stress tolerance, and quality traits. In cross-pollinated crops, special populations such as testcross progenies and NAM (Nested Association Mapping) populations are used to capture broader allelic diversity. QTLs for drought tolerance in maize, downy mildew resistance in pearl millet, and oil content in sunflower are classical examples.

3.2 Genome-Wide Association Studies (GWAS)

GWAS exploits historical recombination in diverse germplasm panels to identify marker–trait associations at high resolution.

Key features:

- Utilization of natural populations, landraces, and elite lines.
- Detection of multiple small-effect loci underlying complex traits.
- Integration with population structure and kinship matrices to control false positives.
- GWAS has been widely applied in maize for:
- Yield components,
- Flowering time,
- Abiotic stress tolerance,
- Disease resistance, and
- Nutritional traits.

3.3 Marker-Assisted Selection (MAS)

MAS involves indirect selection of plants carrying desirable alleles using linked molecular markers.

3.3.1 Applications

Marker-assisted backcrossing (MABC) for introgression of major genes (e.g., disease resistance, quality traits). Gene pyramiding for combining multiple resistance genes into elite backgrounds. Early generation selection, reducing the need for extensive phenotyping.

3.3.2 Marker-Assisted Recurrent Selection (MARS)

Marker-assisted backcrossing (MABC) for introgression of major genes (e.g., disease resistance, quality traits). Gene pyramiding for combining multiple resistance genes into elite backgrounds. Early generation selection, reducing the need for extensive phenotyping.

3.4 Genomic Selection (GS)

Genomic selection represents a major paradigm shift in breeding of cross-pollinated crops.

3.4.1 Concept

Instead of identifying individual QTLs, GS uses genome-wide marker data to predict Genomic Estimated Breeding Values (GEBVs) through statistical and machine learning models.

3.4.2 Advantages

Captures both small and large effect loci.
Effective for low-heritability traits.
Enables selection at the seedling stage.
Significantly reduces breeding cycle time.

3.4.3 Integration with Recurrent Selection and Hybrid Breeding

Genomic recurrent selection accelerates population improvement.
Prediction of hybrid performance and heterosis using parental genomic profiles.
Refinement of heterotic group classification and tester choice.

3.5 Doubled Haploid (DH) Technology

DH technology allows the rapid development of completely homozygous lines from heterozygous populations in a single generation.



3.5.1 Methods

Anther and microspore culture (limited success in some crops).
In vivo haploid induction (highly efficient in maize).
Chromosome doubling using colchicine or spontaneous doubling.

3.5.2 Significance in Cross-Pollinated Crops

Drastically reduces time for inbred line development. Enhances accuracy of QTL mapping and genomic prediction. Facilitates rapid fixation of elite recombinants for hybrid breeding

3.6 Genome Editing Technologies

3.6.1 CRISPR/Cas Systems

Precise modification of target genes controlling yield, stress tolerance, and quality. Ability to knock-out, knock-in, or regulate gene expression.



3.6.2 Advanced Editing Platforms

Base editing for single nucleotide substitutions. Prime editing for precise insertions and replacements. Haploid-inducer mediated genome editing for rapid fixation of edits in breeding lines.

Applications include:

- Improvement of flowering synchrony,
- Enhanced nitrogen-use efficiency,
- Modification of oil and starch biosynthesis pathways,
- Development of disease-resistant genotypes.

3.7 Transgenic and RNA Interference (RNAi) Approaches

Bt hybrids for insect resistance in maize and cotton. Herbicide-tolerant crops for efficient weed management. RNAi-based resistance against insects and viruses through gene silencing. Trait

stacking to confer multiple stress tolerances in a single hybrid.

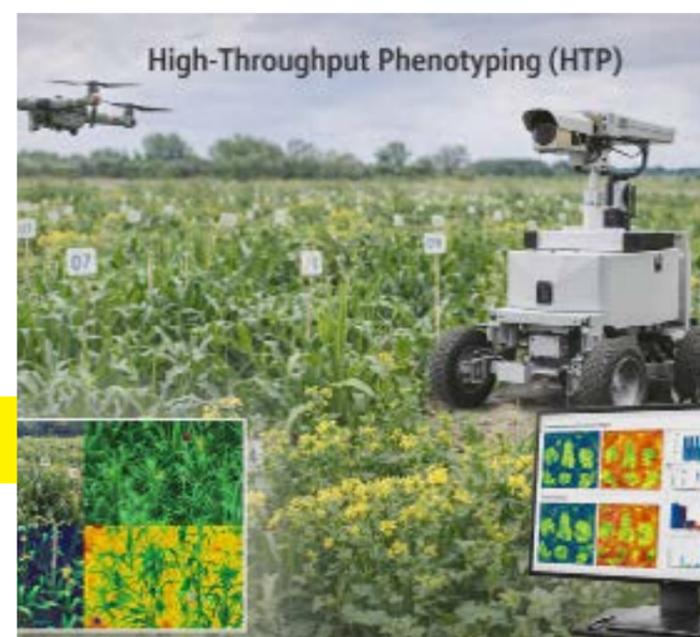
3.8 Integration of Molecular Tools with Empirical Breeding

The modern breeding pipeline in cross-pollinated crops involves:

Empirical Population Improvement
↓
Marker-Assisted and Genomic Selection
↓
Doubled Haploid Line Development
↓
Hybrid Evaluation and Heterosis Prediction
↓
Genome Editing for Trait Refinement

This integrated approach enhances:

- Selection accuracy,
- Speed of cultivar development,
- Exploitation of both additive and non-additive genetic variance.
- In Part 4, we will discuss:
- Phenomics, AI, and Digital Breeding in Cross-Pollinated Crops
- High-throughput phenotyping platforms
- Envirotyping and G×E modeling
- Machine learning and hybrid performance prediction
- Ideotype-based and systems breeding



Phenomics, Artificial Intelligence and Digital Breeding in Cross-Pollinated Crops

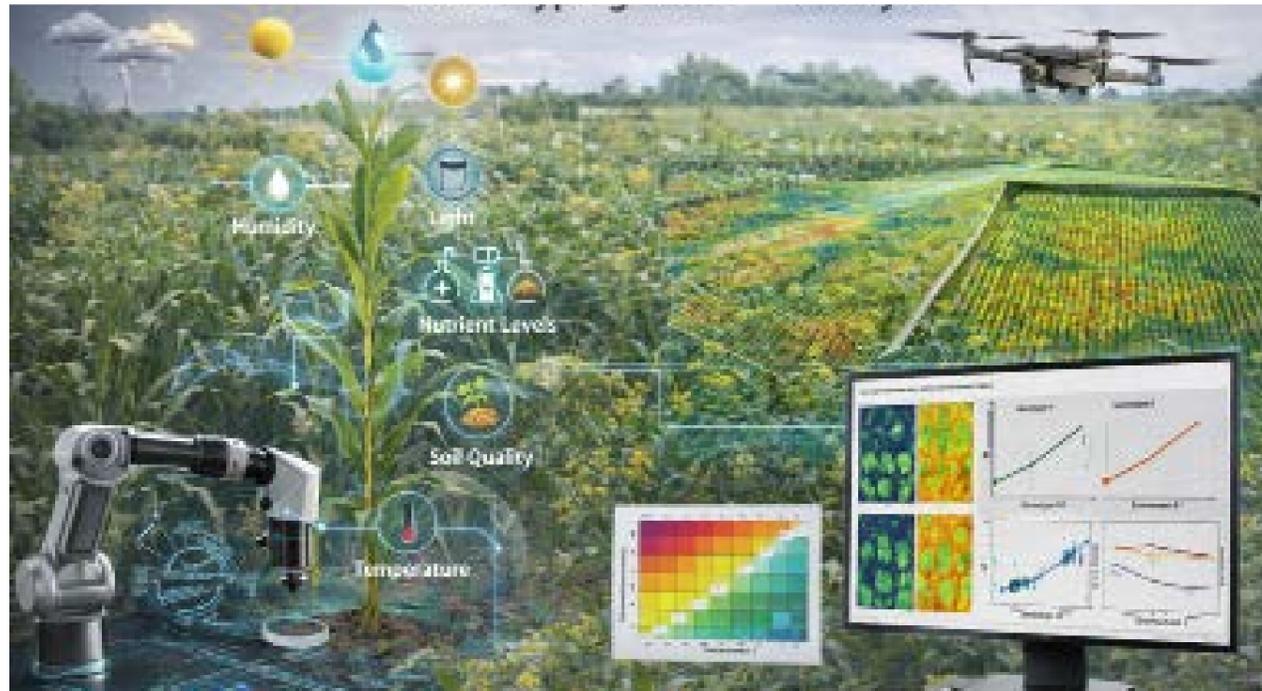
The rapid advances in genomics have created a bottleneck at the phenotyping level. To match the scale of genomic data, breeding has entered the era of phenomics and digital agriculture, where high-throughput, precise, and non-destructive measurement of plant traits is integrated with artificial intelligence (AI) and big data analytics. This transformation is particularly impactful in cross-pollinated crops, where large population sizes, strong G×E interaction, and complex quantitative traits demand robust and scalable evaluation systems.

4.1 High-Throughput Phenotyping (HTP)

4.1.1 Concept and Rationale

High-throughput phenotyping refers to rapid, automated, and repeated measurement of morphological, physiological, and biochemical traits in large breeding populations under field and controlled conditions.

It aims to:



Increase precision of trait measurement,
Reduce human bias,
Capture temporal dynamics of growth and stress responses, and
Enable selection for complex traits such as drought tolerance, nitrogen use efficiency, and canopy architecture.

4.1.2 Platforms and Sensors

Ground-based Platforms

Tractor-mounted or gantry systems.

RGB cameras, multispectral and hyperspectral sensors, thermal cameras, LiDAR.

Aerial Platforms (UAVs/Drones)

Rapid coverage of large breeding nurseries and multi-location trials.

Measurement of NDVI, canopy temperature, plant height, biomass, lodging, and disease severity.

Controlled Environment Phenomics

Automated growth chambers and glasshouses with imaging and root phenotyping systems (rhizotrons, X-ray CT, MRI).

4.1.3 Key Traits in Cross-Pollinated Crops

- Canopy temperature depression (drought and heat tolerance)
- Stay-green and senescence dynamics

- Root system architecture
- Flowering synchrony and anthesis-silking interval (ASI)
- Disease progression curves
- Biomass accumulation and radiation use efficiency

4.2 Envirotyping and G×E Analysis

4.2.1 Envirotyping

Envirotyping involves detailed characterization of environmental variables (soil, weather, management) that interact with genotype to determine phenotype.

It includes:

Soil moisture and nutrient profiling,
Microclimate monitoring,
Stress indices (drought, heat, flooding).

4.2.2 Integration with Breeding

Identification of mega-environments and adaptation zones. Dissection of G×E interaction using reaction norm models. Prediction of hybrid stability and specific adaptation.

4.3 Artificial Intelligence and Machine Learning

4.3.1 Role of AI in Modern Breeding

AI provides tools to handle and interpret massive datasets generated from genomics, phenomics, and envirotyping.

Applications include:

- Image-based trait extraction (ear traits, kernel number, disease lesions).
- Prediction of breeding values and hybrid performance.
- Optimization of crossing schemes and parent selection.
- Identification of complex non-linear G×E patterns.

4.3.2 Machine Learning Models

- Random Forests
- Support Vector Machines
- Deep Neural Networks
- Convolutional Neural Networks (for image analysis)
- These models outperform classical statistical methods in capturing non-additive genetic effects and environmental complexity.

4.4 Digital Breeding Platforms

- Integrated digital platforms now combine:
- Genotypic data (SNPs, haplotypes),
- Phenotypic data (HTP, field trials),
- Environmental data (weather, soil),
- Management data (agronomic practices).
- Such platforms enable:
- Real-time decision support,
- Virtual hybrid testing,
- In silico ideotype design,
- Optimization of multi-trait selection indices.

4.5 Ideotype-Based and Systems Breeding

The concept of ideotype breeding has been revitalized through digital tools.

4.5.1 Ideotype Design

In cross-pollinated crops, ideotypes are defined for: Optimal canopy architecture (erect leaves, light in-

terception),
Deep and efficient root systems,
Balanced source-sink relations,
Stress-adaptive phenology.

4.5.2 Systems Breeding

Systems breeding integrates:

- Quantitative genetics,
- Genomics,
- Physiology,
- Crop growth modeling,
- Agronomy and climate science.
- It aims to predict whole-plant and whole-system performance rather than individual traits, making it particularly relevant for climate-resilient hybrid development.

4.6 Impact on Breeding of Cross-Pollinated Crops

The combination of phenomics and AI has:

- Increased selection accuracy for complex



traits,

- Enabled early generation selection,
- Improved prediction of heterosis and stability,
- Accelerated breeding cycles,
- Facilitated climate-smart hybrid design.

Climate-Smart, Nutritional and Systems Breeding in Cross-Pollinated Crops

5.1 Climate-Smart Breeding

Climate change has imposed unprecedented selection pressures on cross-pollinated crops. Breeding objectives are shifting from yield maximization under optimal conditions to yield stability under stress.

5.1.1 Drought and Heat Tolerance

Key target traits:

- Deep and prolific root systems
- Reduced anthesis–silking interval (ASI)
- High pollen viability under heat
- Stay-green and delayed senescence
- Efficient stomatal regulation
- Integrated approaches:
- Empirical selection in managed stress environments
- QTL mapping and genomic selection for drought indices
- CRISPR-based editing of stress-responsive transcription factors
- AI-assisted prediction of stress resilience across environments

5.1.2 Flood and Salinity Tolerance

Selection for aerenchyma formation, anaerobic metabolism, Na⁺ exclusion

Introgression of tolerant alleles from wild relatives

Genome-wide association studies to identify adaptive haplotypes

5.2 Nutritional and Quality Improvement

Cross-pollinated crops play a central role in combating malnutrition.

5.2.1 Biofortification

Quality Protein Maize (QPM): opaque-2 modifiers for lysine and tryptophan

Pro-vitamin A maize: carotenoid pathway engineering

High-Zn and Fe pearl millet and sorghum

Tools used:

Marker-assisted backcrossing

Genomic selection for micronutrient density

Genome editing for metabolic pathway optimization

5.2.2 Industrial and Feed Quality

High-oil maize, waxy maize, specialty starch types

Modified fatty acid profiles in sunflower

Lignin reduction in forage grasses for digestibility

Case Studies in Major Cross-Pollinated Crops

6.1 Maize (*Zea mays* L.)

Heterotic grouping using SNP-based population structure

Genomic selection for drought and nitrogen-use efficiency

Doubled haploid-based rapid inbred development

CRISPR-edited flowering and ear architecture genes

AI-driven hybrid performance prediction

6.2 Pearl Millet (*Pennisetum glaucum*)

CMS-based hybrid breeding

Marker-assisted introgression of downy mildew resistance

Genomic recurrent selection for arid adaptation

Biofortification for Fe and Zn

6.3 Sorghum (*Sorghum bicolor*)

Stay-green QTLs for post-flowering drought tolerance

RRS for forage and grain ideotypes

Genome editing for tannin and digestibility traits

6.4 Sunflower (*Helianthus annuus*)

CMS-PET1 system for hybrid seed production

Molecular diversity-based heterotic grouping

Oil quality modification via gene editing

Phenomics for drought and heat screening

6.5 Forage Grasses

Synthetic variety development

Genomic selection for biomass and persistence

AI-assisted multi-environment stability analysis

Future Prospects

The future of cross-pollinated crop breeding lies in precision population breeding, characterized by:

- Genomics-Enabled Heterosis Engineering
- AI-Driven Hybrid Design and Prediction
- Genome Editing for Complex Trait Networks
- Speed Breeding with DH and Controlled Environments
- Climate-Resilient, Low-Input Ideotypes
- Systems Integration of Breeding, Agronomy and Climate Science.



Conclusion

Breeding of cross-pollinated crops has evolved from classical mass selection and recurrent selection to a highly sophisticated, data-intensive, and predictive science. While empirical approaches such as population improvement, heterosis exploitation, and hybrid breeding remain the backbone, their efficiency is now dramatically enhanced by molecular markers, genomic selection, doubled haploids, genome editing, phenomics, and artificial intelligence.

The integration of these empirical and molecular approaches enables:

- Faster genetic gain
- Precise manipulation of complex traits
- Stable performance under climate variability
- Sustainable intensification of agricultural systems

This convergence marks the transition from phenotype-based breeding to systems-level precision breeding, ensuring that cross-pollinated crops continue to meet global food, feed, nutritional, and industrial demands in a changing world.

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