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Biotechnology-An era in plant breeding

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Abstract

Biotechnology in plant breeding is transforming agricultural practices by integrating advanced molecular tools to enhance crop improvement. Biotechnology enhances these methods by providing tools to manipulate plant genomes, enabling the introduction of specific traits with greater speed and precision. Genetic engineering, Marker-Assisted Selection (MAS), and gene editing technologies like CRISPR/Cas9 are crucial in modern plant breeding. Plants can be modified to express traits such as resistance to environmental stress, diseases and pests, and boosted nutritional content, through genetic engineering. Marker-assisted selection enables the recognition of desirable traits at the molecular level, allowing breeders to choose plants with the high genetic potential even before they are fully grown. Biotechnology is also a cornerstone in contributing to the enhancement of plants with greater adaptability to changing climate conditions. Implication of Biotechnological and computational tools in plant breeding also eases the breeding process. However, continuing research and regulatory frameworks remain to address these concerns, ensuring that biotechnological innovations are carefully integrated into agricultural practices.

Keywords: Biotechnology, MAS, CRISPR/Cas9, GMO, gene editing, speed breeding, genomics

Introduction

Biotechnology is an interdisciplinary field which integrates biology, technology and engineering to manipulate living organisms or their components for practical applications. One of the most assuring areas of biotechnology is in the field of plant breeding, which is necessary in enhancing crop productivity, quality and resilience (Chawla., 2011) ^[14]. Traditional plant breeding practices, such as hybridization and selective breeding are the primary components of agricultural development for centuries. Nevertheless, these methods are often slow and limited due to the genetic diversity available in natural plant populations. Biotechnology provides advanced tools to overcome these limitations, enabling the ability to enhance and enhance plant breeding with greater precision and efficiency (Liu *et al.*, 2013).

The application of biotechnology in plant breeding involves the use of molecular biology tools to manipulate and modify plant genomes (Kumar *et al.*, 2009) ^[39]. Genetic engineering, for instance, allows scientists to change, insert or modify genes within a plant's DNA to introduce desirable traits. These traits may include resistance to diseases, pests or environmental stress, and improved nutritional content and a higher yield (Christou *et al.*, 2013) ^[16]. With the advent of techniques like Marker-Assisted Selection (MAS) and genome editing technologies like CRISPR/Cas9, plant breeders can now choose plants having the desired genetic traits much rapidly and accurately than before.

Marker-assisted selection, a method that employs molecular markers to recognise and identify for specific genetic traits, is a significant advancement in plant breeding. This method allows breeders to detect beneficial genes in plants at a very early stage of development, decreasing the time needed for field trials and ensuring that only the best candidates are chosen for further development (Nadeem *et al.*, 2018). Moreover, genome editing technologies like CRISPR enable precise modifications at the DNA level, offering new possibilities for trait enhancement without the need to introduce foreign genetic material, as when compared with traditional genetic engineering (Kozovska *et al.*, 2021) ^[38].

The key benefits of biotechnology in plant breeding are vast, particularly in addressing the challenges posed by climate change, environmental degradation and global population growth. Biotechnology can help develop crops that are highly resistant to drought, pests and diseases, improving food security in regions that face harsh growing conditions. Additionally,

biotechnology can play a vital role in decreasing the environmental impact of agriculture, promoting the efficient use of pesticides, fertilizers and water (Chawla., 2011) ^[14].

Despite its promise, the use of biotechnology in plant breeding provokes ethical, safety, and environmental concerns, especially surrounding genetically modified organisms (GMOs). Regulatory frameworks and ongoing research are vital to ensuring that these innovations are safe for both consumers and the environment (Buttel *et al.*, 1987) ^[12]. Nonetheless, biotechnology continues to denote a frontier

in agricultural research, offering vast potential to address the growing need for food in an increasingly unpredictable world.

History of biotechnology

The history of biotechnology in plant breeding can be trailed back to the early 20th century, but significant advancements in the field have emerged more recently with the arrival of genetic engineering and molecular biology.

Table 1: Milestones in plant biotechnology

Year	Discoveries in biotechnology	References
1860	Genetic basis of heredity by Mendel	Poczai <i>et al.</i> , 2021 ^[60]
1944	DNA proven as genetic material	Dahm., 2008
1953	Double helical DNA structure by Watson and Crick	Watson <i>et al.</i> , 1953 ^[84]
1971	Discovery of restriction enzymes	Loenen <i>et al.</i> , 2014 ^[47]
1982	Field test of GM crops	Levidow <i>et al.</i> , 2007 ^[41]
1985	Discovery of PCR	Bartlett <i>et al.</i> , 2003 ^[9]
1994	Flavr Savr tomato	Vessey., 2002 ^[80]
2000	Genetically modified Maize	Kausch <i>et al.</i> , 2021 ^[34]
2003	Golden rice	Potrykus., 2001 ^[61]
2012-2016	Use of CRISPER technologies	Kozovska <i>et al.</i> , 2021 ^[38]
2018 to till date	GM crops which tolerate stresses	Paul <i>et al.</i> , 2018 ^[58]

Conventional plant breeding engages the crossing of selected plants with needed traits to develop improved varieties. This process depends on natural genetic variation and methods such as hybridization, selection and mutation breeding. It is typically slow and depends on the availability genetic diversity within the species (Acquaah., 2015) ^[11]. Through successive generations, breeder targets to combine beneficial traits like stress resistance, environmental adaptability and higher yield. While effective, conventional breeding has drawbacks in speed and precision compared to modern biotechnological approaches (Jauhar, 2006) ^[31].

In the contrary, Molecular plant breeding, which is a modern approach that combines traditional techniques with molecular biology tools to speed up the development of improved crop varieties (Moose *et al.*, 2008) ^[55]. It utilizes molecular markers - DNA sequences linked with desirable traits which helps to recognise and select plants with the most optimal genetic potential early in the breeding process. This technique, known as marker-assisted selection (MAS), helps breeders to locate specific genes responsible for characters like enhanced nutritional content, drought tolerance and disease resistance, significantly reducing the cost and time of breeding programs (Collard *et al.*, 2008) ^[17].

Additionally, molecular plant breeding integrates advanced techniques such as genetic transformation and genome editing like CRISPR/Cas9, enabling precise changes at the DNA level (Liu *et al.*, 2017). These innovations allow for the initiation of traits that may not necessarily occur within the species, providing more control over crop improvement. Overall, molecular plant breeding improves the efficiency, accuracy and speed of breeding plants with better quality, yield and resistance to stress in diverse environmental conditions (Hussain *et al.*, 2015) ^[29].

The combination of molecular breeding and conventional techniques creates a powerful, synergistic approach to plant improvement. While conventional breeding being foundation in developing crop varieties with desirable traits through selection, hybridization and mutation, it often counts on natural genetic variation and can be time-consuming (Jauhar,

2006) ^[31]. Furthermore, Molecular plant breeding utilizes advanced tools such as molecular markers, genetic transformation, and genome editing to enhance the precision and speed of the breeding process (Jauhar., 2006) ^[31].

By combining both approaches, breeders can effectively identify and select plants with desired characters early in the breeding cycle using marker-assisted selection (MAS). This reduces the need for widespread field trials and accelerates the development of improved varieties. Furthermore, genome editing and genetic engineering can introduce novel characteristics that may not exist in the crop's gene pool, addressing challenges such as pest resistance or climate adaptability (Akhtar *et al.*, 2023) ^[3].

Genomics-assisted breeding (GAB) is a developed approach that combines the application of technologies along with genomic tools into traditional plant breeding methods to accelerate the development of improved crop varieties (Varshney *et al.*, 2005) ^[79]. By providing detailed information about the plant genome, GAB allows breeders to identify genetic markers, comprehend the genetic basis of traits and make more informed and precise breeding decisions (Varshney *et al.*, 2021) ^[78]. This approach utilizes the power of molecular markers, high-throughput sequencing, gene editing techniques, and bioinformatics, allowing breeders to choose plants with required traits more efficiently and quickly (Kole *et al.*, 2015) ^[37].

One of the primary tools in genomics-assisted breeding is the application of molecular markers. Molecular markers are certain DNA sequences correlated with the traits of interest, like disease resistance, drought tolerance or improved nutritional content (Farooq *et al.*, 2002) ^[23]. These markers allow plant breeders to recognise and identify plants with the anticipated genetic makeup comparatively early in the breeding process, significantly decreasing the time and resources needed for field trials (Nadeem *et al.*, 2018). Marker-assisted selection (MAS) assists breeders to target regions of the genome or specific genes associated with these traits, speeding up the development of varieties with higher accuracy and precision (Collard *et al.*, 2008) ^[17].

Another important method in GAB is Genome-Wide Association Studies (GWAS). GWAS encompasses the scanning of entire genome of a population to identify genetic variations that are correlated with certain traits. By linking these genetic markers to phenotypic traits, breeders can determine the genetic factors responsible for traits like quality attributes, resistance to abiotic and biotic stresses, and yield (He *et al.*, 2017). GWAS helps in knowing the genetic architecture of intricate traits. It also guides breeders in selecting the best candidates for further breeding (Khan *et al.*, 2021) [35].

Genome editing technologies like CRISPR/Cas9, represent another breakthrough in genomics-assisted breeding. Genome editing allows precise, precise adjustments to a plant's DNA, enabling the addition, deletion, or alteration of specific genes (Liu *et al.*, 2017). This provides a more efficient and precise way to introduce favourable traits into crops without the need for traditional crossbreeding or transgenic methods. For instance, CRISPR has been used to enhance disease resistance, improve nutrient content, and increase stress tolerance in various crops (Ma *et al.*, 2016). Genomics-assisted breeding also aid from advances in bioinformatics and computational tools, which enable breeders to analyse and interpret vast amounts of genomic data. These tools can assist in identifying the most promising

genetic combinations and making decisions based on large-scale data, enhancing the accuracy of breeding programs (Aglawe *et al.*, 2021) [2].

Molecular Markers

Molecular markers are particular DNA sequences that can be used to pinpoint genes or regions of a plant genome associated with desirable trait. These markers are helpful tools in modern plant breeding, allowing for more accurate, faster and more efficient selection of plants with the desired genetic characteristics. Molecular markers are commonly used in various breeding applications, including genetic mapping, marker-assisted selection (MAS) and the selection of quantitative trait loci (QTLs), which are associated to valuable traits (Nadeem *et al.*, 2018). The molecular markers play some vital role in plant breeding includes,

Marker-Assisted Selection (MAS): Which helps breeders to identify plants with desirable characters, based on their DNA rather than relying on lengthy field trials or physical characteristics. For example, molecular markers that are linked to stress resistance genes can be used to identify resistant plants in a breeding population, even before symptoms of disease appear on the crop (Collard *et al.*, 2008) [17].

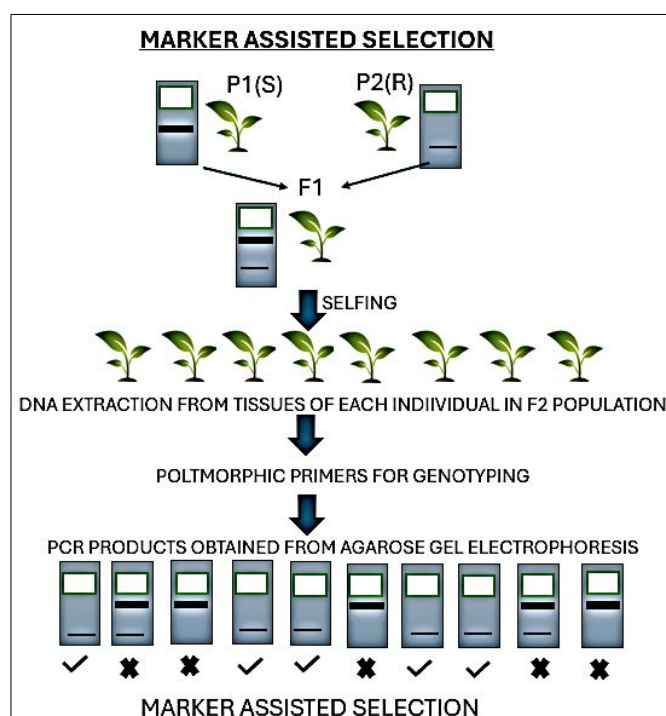


Fig 1: marker assisted selection

Genetic mapping, by identifying markers that segregate with specific traits in a population, breeders can develop genetic maps that locate the genes responsible for those characteristics. These maps assist in the establishment of improved varieties by providing breeders with the precise locations of important genes, assisting in efficient breeding decisions (Semagn *et al.*, 2006) [66].

QTL (Quantitative Trait Loci) are regions of the genome allied with complex traits that are controlled by various genes, like drought tolerance, disease resistance and yield (Miurra *et al.*, 2011). Molecular markers can help identify and locate these QTLs, allowing breeders to integrate

multiple beneficial traits into new varieties (Amanullah *et al.*, 2021) [6].

Molecular markers are essential in reducing disease resistance in plants by enabling early identification and selection of plants with desirable resistance traits (Farooq *et al.*, 2002) [23]. Traditionally, disease resistance was evaluated through field trials, which could be costly and time consuming. However, molecular markers offer a more efficient, precise and faster way to select plants that carry genes related with disease resistance, even before they are exposed to the pathogen (Jonah *et al.*, 2011) [33].

Markers have been successful in incorporating resistance to rice blast disease, which is caused by the fungus

Magnaporthe oryzae, into breeding lines (Liu *et al.*, 2007). The Pi series of resistance genes was identified using molecular markers and has now been mostly used in rice breeding program (Peng *et al.*, 2021) ^[59]. Wheat breeding programs use molecular markers which are linked to resistance against wheat rust diseases (e.g., stem rust, leaf rust) and Fusarium head blight. Markers linked to resistance genes like Lr34 for leaf rust and Sr31 for stem rust are widely used in MAS for wheat improvement (Savin *et al.*, 2024) ^[65]. In case of Tomato, Molecular markers are used to introduce resistance against bacterial speck and blight in tomato varieties by selecting for the Cf gene, which provides resistance to *Cladosporium fulvum* (Thomas *et al.*, 1998) ^[74]. Nutritional enhancement in crops is a key target of modern plant breeding, aiming to improve the composition of essential minerals, vitamins and other nutrients to address

global challenges. Molecular markers are crucial in accelerating the development of nutritionally enhanced crops by enabling precise and efficient selection for desired traits related to nutrition (Thangadurai *et al.*, 2020) ^[73]. By integrating molecular markers into breeding programs, breeders can recognise and select plants with higher levels of specific nutrients, such as provitamin A (β -carotene), zinc, iron, and essential amino acids, without the need for time-consuming phenotypic evaluation or extensive field trials (Tucker, 2003) ^[76]. Golden Rice is another notable example of using molecular markers for nutritional enhancement. By incorporating genes for β -carotene biosynthesis, this genetically modified rice provides a substantial source of provitamin A (beta-carotene), an essential nutrient for preventing blindness due to vitamin A deficiency mostly in evolving countries (Moghissi *et al.*, 2016) ^[54].

Crop	Nutritional enhancement	Molecular Marker Application	Example Outcome	Reference
Rice	Iron and Zinc fortification	Marker-assisted selection (MAS) for high iron and zinc content	Biofortified rice varieties (e.g., Iron-rich rice)	Sperotto <i>et al.</i> , 2012 ^[69]
Maize	Provitamin A (Beta-carotene) enhancement	MAS for increased provitamin A content	Golden maize (higher beta-carotene content)	Muzhingi <i>et al.</i> , 2011 ^[56]
Wheat	Increased zinc quality and quantity	MAS for high zinc and essential amino acid	High-zinc wheat varieties	Chattha <i>et al.</i> , 2017 ^[13]
Cassava	Increased pro-vitamin A (beta-carotene)	MAS for carotenoid biosynthesis genes	Biofortified cassava with enhanced carotenoids	Esuma <i>et al.</i> , 2016 ^[22]
Sweet Potato	Increased pro-vitamin A (beta-carotene)	MAS for beta-carotene biosynthesis genes	Orange-fleshed sweet potato (higher vitamin A content)	Van Jaarsveld <i>et al.</i> , 2005 ^[77]
Tomato	Increased lycopene and antioxidant levels	MAS for lycopene biosynthesis genes	Lycopene-rich tomatoes	Ashrafi <i>et al.</i> , 2012 ^[7]
Soybean	Increased protein content and oil composition	MAS for high protein and oil yield	High-protein, high-oil soybean varieties	Kumar <i>et al.</i> , 2021 ^[40]
Cowpea	Increased iron and zinc content	MAS for micronutrient fortification	Biofortified cowpea with higher iron and zinc content	Yadav <i>et al.</i> , 2024 ^[85]
Barley	Enhanced beta-glucan content for health benefits (cholesterol-lowering)	MAS for beta-glucan biosynthesis	Barley varieties with enhanced beta-glucan levels	Walling <i>et al.</i> , 2022 ^[81]
Pea	Increased protein quality, high levels of essential amino acids	MAS for high-protein content	High-protein pea varieties	Barac <i>et al.</i> , 2010 ^[8]
Chickpea	Increased zinc, iron, and protein content	MAS for micronutrient content enhancement	Biofortified chickpeas with higher zinc and iron content	Roorkiwal <i>et al.</i> , 2020

Genome-Wide Association Studies (GWAS) in Plant Breeding

Genome-Wide Association Studies (GWAS) is an operative tool in modern plant breeding that allows for the recognition of genetic variants associated with complex traits, like drought tolerance, disease resistance, quality characteristics and yield (Cortes *et al.*, 2021). GWAS examines the relationship between specific genetic variations (single nucleotide polymorphisms or SNPs) and phenotypic traits over a bulky population of plants. By linking these genetic variations to traits of interest, GWAS helps to reveal the genetic basis of complex polygenic characters, thereby

speeding up the breeding of improved crop varieties (He *et al.*, 2017).

GWAS works by genotyping a large population of plants (such as a breeding population or natural population) for a wide range of genetic markers (typically SNPs) that cover the whole genome. These markers demonstrate the differences in the DNA sequence between individuals. The phenotype of interest, such as resistance to a particular disease, drought tolerance or high yield is then assessed across the same population (He *et al.*, 2017). By statistically analysing the correlation between phenotypic traits and genetic markers, GWAS identifies which markers are associated with the expression of those traits (Hayes, 2013).



Fig 2: Key Steps in Conducting GWAS

Applications of GWAS in Plant Breeding

Gene Identification and Trait Dissection: GWAS is particularly helpful for dissecting polygenic traits which are complex, where multiple genes affect a single phenotype. It enables breeders to pinpoint the genes accountable for vital agronomic characters, such as nutritional content, disease resistance and yield. In addition, GWAS has been used to detect genes linked with drought tolerance in maize, providing a valuable source for breeding drought-resistant varieties (Thakur *et al.*, 2024) ^[72].

Marker Development for Quick Selection: The SNPs or other genetic markers identified through GWAS can be employed for marker-assisted selection (MAS) in breeding programs. Once significant markers are identified for specific traits, breeders can use these markers to choose individuals with desirable characters in the early stages, speeding up the development of more advanced varieties. This is especially useful in crops where phenotypic evaluation is time-consuming or difficult, such as resistance to soil-borne diseases (Perez-de-Castro *et al.*, 2012) ^[49].

Improvement of Complex Traits: GWAS has been applied to characters that are coordinated by multiple genes, such as grain quality, disease resistance and yield. For instance, in rice, it has been used to pinpoint genes associated with rice blast resistance, while in wheat breeding, GWAS has identified genetic loci linked to resistance to leaf rust (Cheng, 2024) ^[15].

Understanding Genotype-Environment Interactions: Since many traits are influenced by environmental factors, GWAS can help to evaluate how specific genetic variants interact with different environmental conditions. This can lead to the development of crops which are well-suited to a range of environmental conditions, such as drought, heat, or nutrient deficiency (Cui *et al.*, 2018) ^[20].

Accelerating Breeding Programs: GWAS allows for the detection of genetic variants linked with traits of interest early in the breeding cycle. This means that breeders can use molecular markers to choose plants with the required traits at an early stage, reducing the number of generations required to develop superior varieties and accelerating the overall breeding process (Kim *et al.*, 2020) ^[36].

Genome editing technologies

Genome editing technologies have transformed plant breeding by aiding accurate and targeted alterations to the DNA of plants. Unlike traditional breeding methods, which depend on selection and crossbreeding over many generations, genome editing allows for the direct modification of a crop genome to correct undesirable characteristics or introduce specific traits. The most widely used genome editing technologies in plant breeding are CRISPR/Cas9, Zinc Finger Nucleases (ZFNs) and TALENs (Transcription Activator-Like Effector Nucleases) (Shamshirgaran *et al.*, 2022) ^[67]. These technologies help breeders to make changes at the DNA level with exceptional accuracy and efficiency, opening new possibilities for crop improvement.

The CRISPR/Cas9 system has garnered substantial attention because of its simplicity, high precision and versatility. CRISPR (Clustered Regularly Interspaced Short Palindromic Repeats) relies on a bacterial defence mechanism that uses an RNA molecule to guide the Cas9 enzyme to a particular location in the genome (Liu *et al.*, 2017). This allows for targeted gene editing by cutting the DNA at the desired location, which could then be altered repaired by the plant's natural repair methods (Ma *et al.*, 2016). This system could be used to insert new genes, knock out genes or make small modifications to the genetic sequence. In plant breeding, CRISPR/Cas9 is used to improve characters like disease resistance, drought tolerance, nutritional content and yield (Belhaj *et al.*, 2015) ^[10].

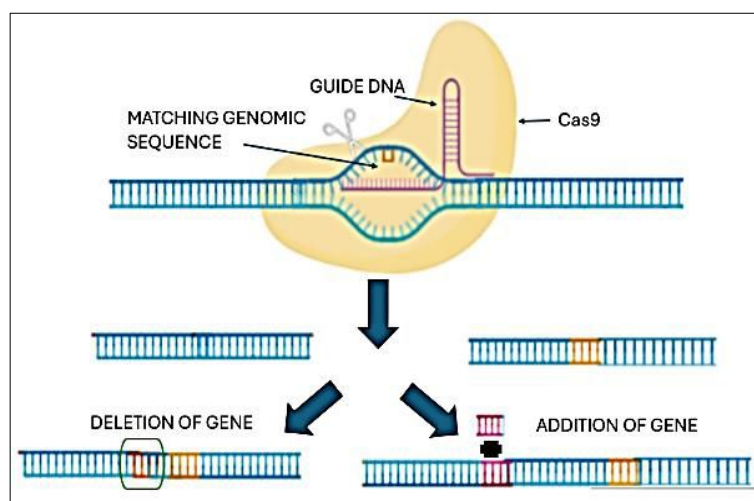


Fig 3: CRISPER Cas9

One of the major advantages of genome editing is its capability to make specific changes without introducing foreign DNA. This permits for the creation of genetically modified crops that do not carry transgenic material, which can be a significant advantage in regulatory environments where genetically modified organisms (GMOs) are constrained (Ma *et al.*, 2019). For example, CRISPR is used to edit genes in crops like wheat, rice, and tomatoes to enhance their

resistance to diseases like bacterial fungal and blight infections, improve nutrient content (such as increasing provitamin A in rice), or develop crops with better tolerance to stress (LeBlanc *et al.*, 2018).

In addition to CRISPR/Cas9, ZFNs and TALENs are also used in genome editing for plant breeding (Gupta *et al.*, 2014) ^[27]. Both technologies utilize engineered nucleases to create double strand cuts at certain locations in the genome. While

less widely used than CRISPR, they have been applied successfully to enhance character traits in crops like soybean and cotton (Gaj *et al.*, 2013) ^[24].

Bioinformatics and Computational Tools Used in GWAS

Genome-Wide Association Studies (GWAS) depend heavily on bioinformatics and computational tools to analyse, process and understand huge volumes of genomic and phenotypic data. These tools are necessary for identifying genetic changes associated with complex traits, ensuring the proficiency and accuracy of the analysis (Gumpinger *et al.*, 2018) ^[26]. The bioinformatics pipeline in GWAS involves several stages, including statistical analysis, data preparation, and result visualization (Aglawe *et al.*, 2021) ^[2]. These are some important bioinformatics and computational tools widely used in GWAS:

PLINK being one of the most used software tools for GWAS, a free, open-source tool designed for the analysis of genotype and phenotype data. PLINK offers a range of functions for data filtering, quality control and association testing. It is particularly useful for conducting basic GWAS analyses, such as performing association tests, calculating allele frequencies and generating summary statistics (Purcell *et al.*, 2007) ^[63]. PLINK also provides tools for handling large datasets, examining population structure and making it an essential tool in GWAS pipelines (Solo- Cerda *et al.*, 2012).

GEMMA (Genome-wide Efficient Mixed Model Association) is a powerful software used for conducting mixed model-based GWAS. Mixed models are particularly beneficial in GWAS because they are based on both fixed effects (such as SNP effects) and random effects (such as population structure and similarities between individuals) (Zhou *et al.*, 2012) ^[86]. GEMMA provides effective algorithm for association testing in large datasets and helps to control confounding factors, improving the accuracy of association results (Team *et al.*, 2024) ^[71].

Eigenstrat is a tool used for controlling population stratification in GWAS. Subgroups within the population have different allele frequencies, potentially leading to false associations (Alexander *et al.*, 2009) ^[5]. EIGENSTRAT uses principal component analysis (PCA) to adjust the population structure and ensure that the association results reflect true genetic effects relatively than artifacts caused by underlying population structure (Price *et al.*, 2006) ^[62].

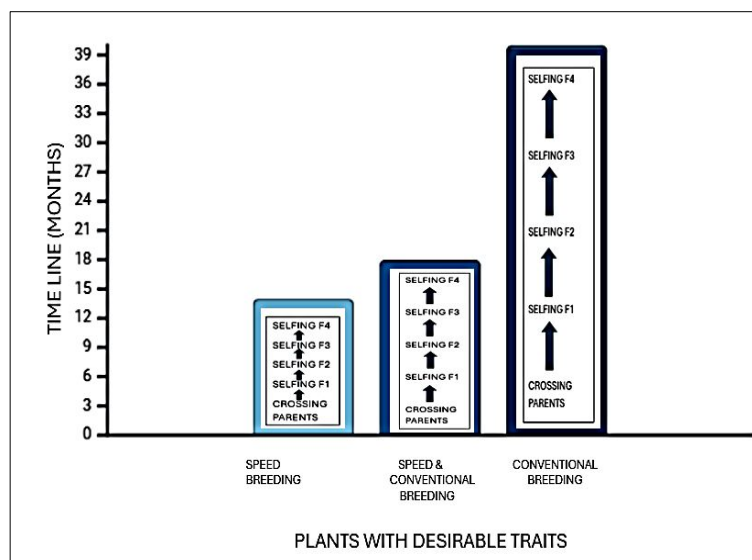
BOLT-LMM is a computational tool designed for large-scale GWAS. It is optimized for its capability of handling datasets and high-performance computing with millions of individuals and SNPs (Sullivan., 2015). BOLT-LMM utilizes mixed linear models to improve statistical power and control for confounding factors such as relatedness among individuals and population structure. Useful especially in large cohorts where computational efficiency is a concern (Jiang *et al.*, 2019) ^[32].

Fast SKAT: (Fast Sequence Kernel Association Test) is a software used for rare variant analysis in GWAS. It provides an effective way to test the association between complex traits and genetic variants (especially rare variants). Fast SKAT improves the ability to detect associations in regions of the genome where rare variants may have a significant impact, addressing the limitations of traditional GWAS methods that often focus on common variants (Lumley *et al.*, 2018) ^[18]. As genomic data continues to grow, the development and optimization of computational tools will be crucial in advancing GWAS applications and enhances our understanding of the genetic basis of traits in plants, animals, and humans (Conomos *et al.*, 2024) ^[18].

Genomic Selection and Speed Breeding in Plant Breeding

Genomic selection and speed breeding are two novel approaches that have significantly accelerated the development of enhanced varieties, addressing the increasing demand for agricultural sustainability and food security (Watson *et al.*, 2018) ^[82]. Genomic selection is a breeding method which uses genomic information, to calculate the genetic potential of plants for complex characters like yield, disease resistance and environmental adaptability (Jannink *et al.*, 2010) ^[30]. Unlike traditional breeding, which relies on phenotypic selection (observing physical traits), genomic selection comprises in creating prediction models based on genotypic data which allows breeders to choose plants with desirable traits early in the breeding cycle (Crossa *et al.*, 2017) ^[19]. Genomic selection refers to phenotypic traits measured on a group of plants in a reference population which are then genotyped (Goddard *et al.*, 2007) ^[25]. Then statistical models are developed using this data to link certain genomic regions, or markers, to the traits of interest. Once or models are established they can use genotype to calculate the performance of untested plants (Liu *et al.*, 2018). This method enables breeders to evaluate plants at the seedling or early vegetative stage without having the plants reach maturity. Integration of genomic selection into breeding programs allows breeders to make faster and more accurate decisions than currently possible practicing traditional phenotypic evaluations, and thereby eliminating time and cost spent in traditional phenotypic evaluations (Spindel *et al.*, 2015) ^[70].

In contrast to that, speed breeding refers to optimizing conditions under which plant grow to induce its life cycle and grow several generations within short period of time (Samantara *et al.*, 2022) ^[64]. It typically is a technique in which we manipulate environmental factors, like light exposure and temperature, to shorten the time taken for a plant to mature and to produce seeds (Watson *et al.*, 2018) ^[82]. Speed breeding is highly complementary to genomic selection because it enables breeders to cycle through numerous generations of plants very rapidly, so that they can assess whether selected genotypes affect crop performance. For instance, speed breeding can help breeders to complete up to six generations of barley, wheat or chickpeas per year, versus one or two generations (Alahmad *et al.*, 2018) ^[4].



Graph 1: Timeline comparison of the breeding techniques

Genomic selection and speed breeding are powerful tools that together improve plant breeding program efficiency and precision (Watson *et al.*, 2019) ^[83]. The integration of these approaches enabled breeders to speed up creation of new crop varieties with improved traits to address problems like climate variation, disease and food security (Pandey *et al.*, 2022) ^[57]. Together this integrated strategy holds potential to substantially decrease the amount of time necessary to get improved crop varieties to market, thereby enabling the development of sustainable agricultural systems (Samantara *et al.*, 2022) ^[64].

Conclusion

In summary, biotechnology has made great contributions towards plant breeding by providing new scientific tools that have improved breeding speed, precision and efficiency to produce improved crop varieties. Furthermore, genomic selection, molecular markers, and genome editing make it possible for breeders to address complex characters (e.g., drought tolerance, disease resistance, yield and nutritional enhancement) more accurately and more cheaply than through traditional breeding methods. The use of biotechnology in plant breeding not only enhance the development of crops to meet the needs of an ever-growing world population, but it also contributes to more sustainable agricultural practices by reducing the use of chemicals and promoting crops that are resilient and highly productive. With biotechnology advancing, enhances the capability to deal with issues of climate change, food security and malnutrition. Thereby making it a cornerstone of future sustainability and agricultural innovation.

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