“Genomics for Crop Improvement: From Genes to Fields"

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ABSTRACT

The exploration of genomics has become a transformational one, transforming many areas of research, including agriculture. The genetic potential of crops has been unlocked in the field of agricultural improvement via genomics, enabling the creation of more durable, nutrient-rich, and sustainable cultivars. This chapter gives a broad overview of the use of genomics in crop development, emphasizing major technologies, difficulties, and potential future uses. Although traditional crop breeding techniques have been effective at enhancing agricultural attributes, they are frequently limited by laborious phenotypic selection and scant access to genetic diversity. With the use of high-throughput genome sequencing technologies, crop genomes can now be easily analyzed by scientists, revealing the genetic underpinnings of a variety of desirable features. Specific genes linked to qualities like resistance to diseases, drought tolerance, and nutritional content can be found by techniques like genomic mapping and quantitative trait locus (QTL) analysis, facilitating Marker-Assisted Selection (MAS) for more effective and precise breeding. In addition, the development of genome editing tools like CRISPR-Cas9 has given scientists the ability to modify specific crop genomes to produce crops with desired features without introducing foreign DNA. Utilizing the genetic variety found in crops and their wild cousins has been made possible by omics technologies, including genomics, transcriptomics, proteomics, and metabolomics. A new era of crop improvement has arrived thanks to genomics, which has made it possible for researchers and breeders to make better use of the huge genetic resources available in agriculture. The future of crop improvement is bright, bringing solutions to global issues like food security and climate change. This is due to ongoing advances in genomics and its combination with conventional breeding techniques.

Keywords :- Genomics, Omics, CRISPR/Cas, MAS, DNA Sequencing, etc.

I. INTRODUCTION TO GENOMICS IN CROP IMPROVEMENT

A subfield of molecular biology called genomics focuses on understanding an organism's entire DNA sequence, including its genes and how they work. Genomic technologies have significantly impacted efforts to improve crops in a number of industries, including agriculture. In the following 30 years, food production will need to dramatically grow to feed the world. Food and nutritional security depend on sustainable food production. Studies show that 821 million people globally are at or below the minimal nutritional level, including 151 million stunted children under the age of five. Additionally, two billion individuals do not get enough micronutrients to sustain a healthy lifestyle. To meet these objectives, the manufacturing and supply chain must run efficiently. It has been estimated that by 2050, the industrial system will need to raise its output by 60% in order to address a number of climate change-related challenges. The price of food is predicted to rise by 1-29% by 2050, which is projected to make these problems even worse. We now have less access to agriculturally productive land as a result of increased urbanization brought on by rising population [1]. We will need to increase food production for a number of other reasons besides population growth. Rapidly developing nations experienced significant income development that gave rise to an emerging middle class, which sped up the dietary shift toward higher consumption of meat, eggs, and dairy products and increased the need to farm more grain to feed more cattle, pigs, and poultry [2]. Agriculture would have to generate between 60 and 100 percent more food and feed than it does currently by 2050 [3]. Scientists can now quickly study the complete genome of crops thanks to the development of high-throughput DNA sequencing technologies, enabling a greater understanding of their genetic make-up and potential. Using methods like genetic mapping and quantitative trait locus (QTL) analysis, researchers can now pinpoint individual genes linked to important features like drought tolerance, disease resistance, and nutritional content. The discovery of these genes makes Marker-Assisted Selection (MAS) easier and enables breeders to more quickly choose plants with desired features.

A. The Role of Genomic Selection in Crop Improvement:

By anticipating an individual's genetic worth based on its full genome, genomic selection advances the application of genomics in breeding. This makes it possible for breeders to make decisions early in a plant's development, even before particular features are completely manifested, leading to breeding cycles that are more precise and efficient. Recent advances in genome editing technologies, particularly CRISPR/Cas9, have opened up new avenues for quick and accurate genome modification, offering quick transfer of information from the lab to the field. In the target genome, genome editing enables the introduction of insertions, deletions, or a completely new sequence [4]. Genome editing enables the selective modification of known genes governing significant features, allowing for the alteration of phenotypes. Several genome-edited crop plants, such as waxy maize, drought- and salt-tolerant soybeans, and Camelina with more oil, have recently reached the end of the commercialization process in the United States of America [5].

B. Classification of genomics based on the techniques

The three basic classification of genomics have been listed below along with the techniques and databases used (Fig.1)

a. Structural Genomics:

The study of the arrangement and sequencing of DNA throughout an organism's whole genome is known as structural genomics. Additionally, each protein encoded by genes has its three-dimensional structure evaluated. The primary goal of structural genomics is to identify all potential protein structures of an organism because it is crucial to learn new information about an organism's biological processes. The following are the structural genomics methodologies:

1. Chromosomal maps
2. Cytogenetic map
3. Genetic map/Linkage map
4. Physical map
5. Transcriptome sequencing
6. Expressed sequence tags (ESTs) and cDNA clones
7. Full-length cDNA sequencing
8. Whole genome sequencing

Approaches of structural genomics

i. *de novo* method (experimental approach):

X-ray crystallography, NMR spectroscopy, or electron microscopy are common techniques for determining protein structure. The X-ray crystallography approach is the most accurate and is thought to have a higher degree of precision in determining the structure among all of these methods. For small- to medium-sized proteins, NMR spectroscopy can substitute X-ray crystallography. Heteronuclear Single Quantum Coherence, or HSQC, spectra are the primary tool in NMR spectroscopy for figuring out protein structures. The protein structure is first determined by electron microscopy at extremely low resolution, and it is then verified by the X-ray crystallography technique. New methods, such as transverse relaxation optimization spectroscopy, chilled probe technology, ultra-high field magnets, and isotope labeling methods, have been developed for quick determination.

ii. Modelling-based methods:

This method uses model building, threading, or profile-profile matching to compare proteins to the PDB (Protein Data Bank). Profile-profile matching is used in a PSI-Basic Local Alignment and Search Tool search to find closely related sequences of the query compound in the database. The most effective technique for protein projection is threading. By matching the new protein's main sequence to a related experimental structure in the PDB [6], it can determine the three-dimensional structure of the protein.

b. Functional Genomics:

The study of the activities of genes, gene products, and their interactions is known as functional genomics. It specifies the activities of an organism's entire genome before characterizing the genome in accordance with those functions. The primary goal of functional genomics is to investigate the connection between an organism's genome and phenotype. Techniques for functional genomics analysis include the following:

i. GTG banding (Giemsa banding) – GTG banding (Giemsa banding) - This technique is used to look at big chromosomal abnormalities (greater than 5 Mb) in karyotype.
ii. Microarray-Based Comparative Genomic Hybridization, or aCGH, is used to analyze the gain or loss of genomic regions. Compared to conventional karyotyping, it is more accurate in detecting DNA gains or losses. To detect genomic alignments and copy-number changes, cCGH is a precise, delicate, and quick approach [7].
iii. FISH (Fluorescence in situ Hybridization) – Using radiolabelled probes, this method is used to locate specific DNA sequences. The FISH technique was originally used to paint chromosomes [8].
iv. Sanger or Next-Generation Sequencing – These techniques are used to find known and unknown variations in an organism's genomic DNA. Both approaches are based on similar principles. The complementary integration of fluorescently labeled deoxyribonucleotide 5'-triphosphates (dNTPs) into the DNA template is catalyzed by DNA polymerase during the polymerase chain reaction (PCR), which consists of several cycles of successive DNA replication. The nucleotide sequences of a labeled DNA fragment are identified by the detector based on the color of the fragment for each cycle. The fundamental distinction between Sanger and Next Generation sequencing is that the latter uses massively parallel sequencing technology to analyze millions of DNA fragments rather of only one [9].
v. Mass spectrometry – It consists of three components: an ion generator for forming ions from the gas-phase sample, a mass analyzer for using electromagnetic fields to separate those ions, and detectors. That permits proteins and peptides to move into the gaseous phase without considerable degradation has proved crucial for mass spectrometry in large proteome studies. The two most often utilized ionization methods are matrix-assisted laser electrospray ionization and desorption ionization. The most advanced mass spectrometer at the moment is the Orbitrap, which has a large dynamic range, high mass accuracy, and outstanding resolution that make it suitable for many proteomics and metabolomics applications.

c. Comparative Genomics:

The genomic traits of several organisms are compared in the biological research discipline known as comparative genomics. The goal of comparative genomics is to discover the similarities between two organisms, which are frequently encoded in the DNA that is shared between species. The goal of comparative genomics is to analyze groups of genes that have a specific biological function in a given creature by differentiating gene counts, gene placements, and biological functions of genes in the genomes of various animals. We will be able to pinpoint the genes needed for essential processes in a wide range of species using comparative genomics. By comparing related species, it is crucial to study the evolutionary history of organisms. Because all living things have a common evolutionary ancestor, it is understandable that there are significant variances and overlaps within species as well as minute variations among individuals between species, which may affect disease susceptibility in some and resistance in others. It aids in establishing the connection between genotype and phenotype. On various databases, there are integrated resources for comparative genomics:

1. PlantGDB and GreenPhylDB – for all plants.
2. Gramene – for cereals.
3. RoBuST – for root and bulb crop families Apiaceae and Alliaceae
4. GRASSIUS – for grasses.

Aligning two genome sequences using a computational tool is the first step in doing a comparative genomics investigation. Recently developed tools include BLASTN and MEGABLAST, GLASS, MUMmer, PatternHunter, PipMaker, and VISTA for genome scale alignment and visualization.

Comparative analysis of genome structure - Examining global molecular structure, such as the nucleotide composition, syntenic linkages, or gene ordering, enables the understanding of similarities and differences between genomes. These comparisons shed light on the structure and evolution of a genome as well as its distinctive features. Three levels allow for comparisons between the structures of various genomes: a) Global nucleotide statistics b) DNA level genome structure c) gene level genome structure [10].

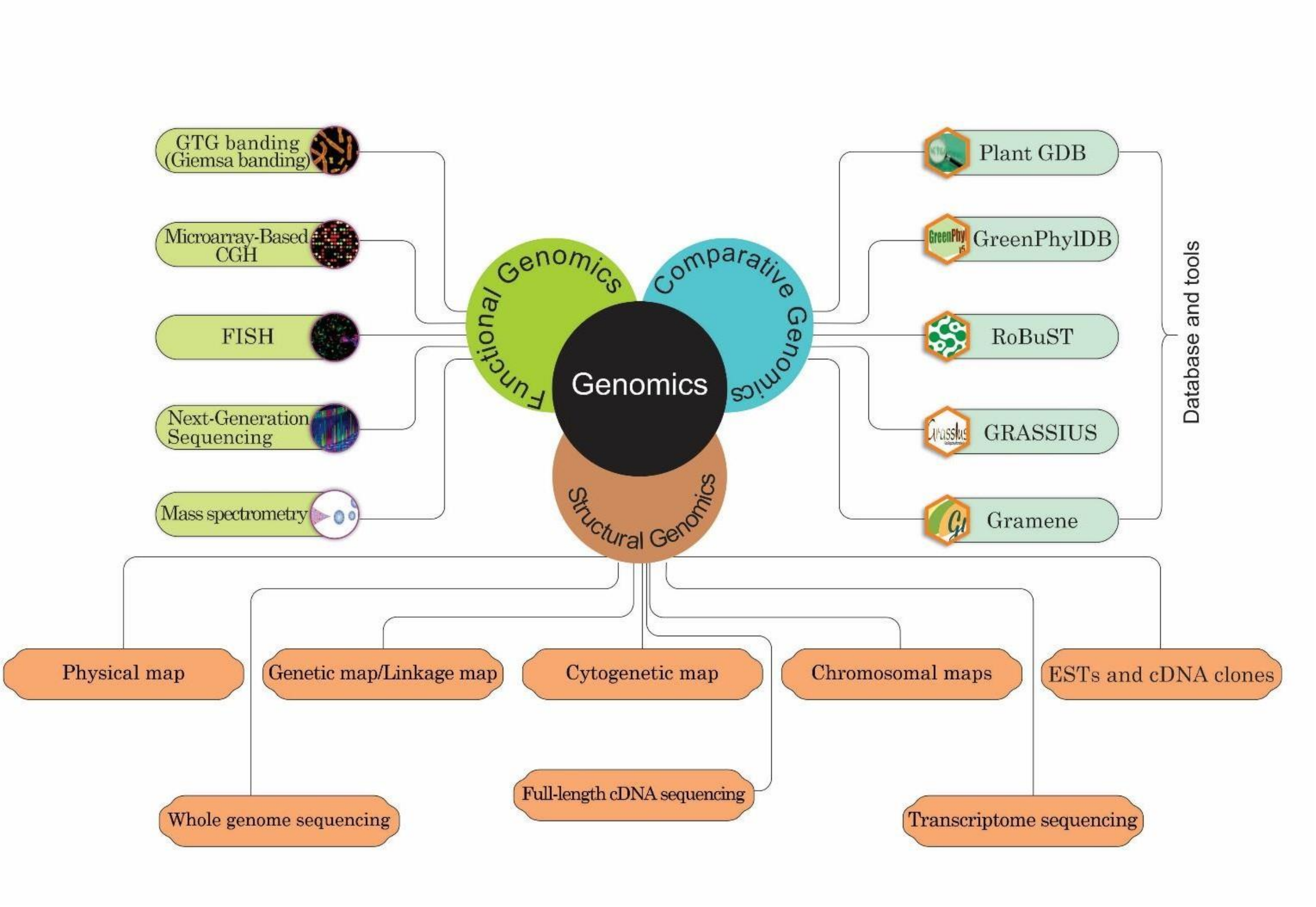

Fig. 1 Classification of genomics

C. Harnessing Genetic Diversity through Omics Technologies:

Crop development relies heavily on genetic variety because it offers a pool of genes that may be used to create crop types that are more tolerant and adaptive. Omics technologies, including genomics, transcriptomics, proteomics, and metabolomics, allow for the thorough analysis of crop variety, making it easier to find important genes and the regulatory networks that control them.

D. Challenges and Ethical Considerations:

There are challenges in integrating genomics into agricultural improvement. To ensure appropriate and sustainable use of genomic techniques in agriculture, issues like data management, intellectual property rights, and public acceptance of genetically modified crops need to be carefully considered and regulated.

II. Unraveling the Genetic Blueprint: Genome Sequencing and Analysis

Unprecedented opportunities to interpret organisms' genetic codes have been made possible by advances in genomics, offering priceless insights into their features, functions, and evolutionary past. The primary technology of genomics, genome sequencing, has changed a number of scientific disciplines, from medicine to agriculture. In this article, we explore the importance of genome sequencing and analysis, its uses, and the significant influence it has had on both theoretical knowledge and real-world applications. Identifying the sequence of nucleotides (A, T, C, and G) that make up an organism's whole DNA entails genome sequencing. By decoding the human genome, which took more than a decade and the combined efforts of experts from all around the world, the Human Genome Project, which was finished in 2003, marked a key milestone in genomics. Since then, technical developments have significantly lowered the time and expense of genome sequencing, making it available to researchers and institutions around the world. Genome sequencing in agriculture has paved the road for crop development as researchers find genes linked to desired qualities like disease resistance and enhanced yield. With the help of links between organisms and the discovery of crucial moments in their divergence, it has thrown light on the evolutionary histories of numerous species. Scientists can track the evolutionary pathways of various species and identify the genetic alterations that led to speciation and adaptation by comparing the genomes of different species. Genome sequencing creates enormous amounts of data, making its management, analysis, and interpretation computationally challenging. High-performance computing and bioinformatics technologies are necessary for processing massive data and deriving relevant insights from genomes.

A. Genome Sequencing

Genetics and genomics have undergone a major transformation thanks to the introduction of high-throughput sequencing tools. Whole genome sequencing (WGS) has become widely used for the first time, allowing detection of a full range of common and rare genetic variants of various types across almost the entire genome. This facilitates research and clinical applications for rare diseases and can enhance the discovery of common disease and annotation of the causal variants. We are at the beginning of a new age when WGS will be a dominating method for genetic analysis now that hundreds of thousands of genomes have been sequenced globally. In contrast to earlier decades of human genetic research, which relied on genetic markers that serve as indirect proxies of other genetic variations in the surrounding region, or sequencing data from the genome's exonic regions only. In order to understand how variations affect phenotypes, functional interpretation of WGS-discovered variants is a crucial part of human genetics investigations. Assays for genome-wide functional genomics now make it possible to identify, characterize, and forecast variations' molecular effects with increasing accuracy. But since these impacts reveal the whole complexity of genome function, which we still don't fully understand, there is still much to learn about different moleculareffects and how they could affect higher-level organismal phenotypes (Fig. 2).

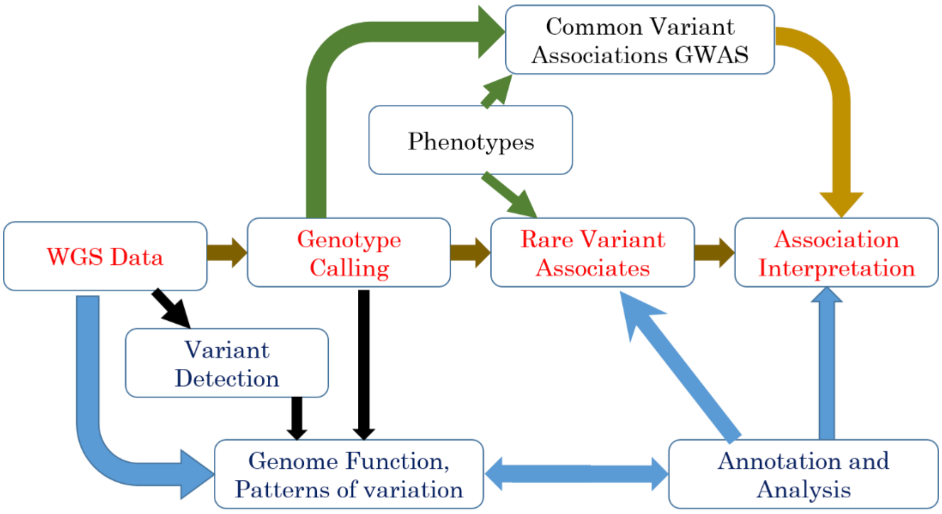

Figure 2 :- General frame of WGS

A typical WGS study's primary goal is to provide a precise map of the samples' genomic variation. Since inaccurately detected and genotyped variations won't be directly evaluated in trait-focused studies, this critical step establishes the groundwork for all subsequent analyses geared at genome interpretation and genetic discovery. The technology utilized for sequencing and the level of coverage attained have a significant impact on the methodologies employed to map genomic variation [11]. Currently, there are three main WGS techniques : There are three types of whole genome sequencing (WGS): (1) short-read WGS using Illumina technology, which currently produces paired-end reads of 150 bp or less with error rates in the range of 0.1-0.5%; (2) long-read WGS using single molecule technologies from Pacific Biosciences (PacBio) or Oxford Nanopore Technologies (ONT), which produces reads of 10–100 kb or even longer on occasion; (3) linked-read WGS using technology from 10X Genomics We concentrate largely on the analysis of this data format because the vast majority of human genetics research use short-read WGS employing the Illumina HiSeq or NovaSeq platform due to factors like as cost, usability, and accuracy. The required amount of coverage is a key factor in the design of WGS investigations. Each nucleotide in the genome must be sequenced several times from randomly selected DNA molecules in order to identify variations from mistakes.

B. Functional annotation and genetic variant impact forecasting consequences, both qualitative and quantitative

The simplest method for annotating genetic variations is based on the allele frequency and location of the variants in the genome's coding or noncoding regions. Diverse research communities have historically examined them. The majority of the attention in the rare and Mendelian illness community has been on exome-sequenced uncommon, strong-effect gene-disrupting coding mutations. The common illness community, on the other hand, has often concentrated on the investigation of non-coding variants with plausible regulatory implications driving GWAS relationships and common variants genotyped by SNP arrays. The basic coding/noncoding categorization, which frequently contains implicit assumptions that coding variants produce gene knockouts or affect protein structure, is challenged by a more nuanced knowledge of the functional impact of genetic variations. In truth, protein structure and dose may be affected in a variety of qualitative and quantitative ways by both coding and noncoding variations. In the end, annotation of variations according to their projected functional effects rather than their chromosomal location will have a stronger biological foundation and be more broadly applicable. For instance, loss-of-function effects from non-coding mutations that have a significant impact on gene expression should be comparable to those from coding variants that cause nonsense-mediated decay of the same gene.

The difficulties in predicting the impacts of variants are more complicated, and the plan and timetable are less distinct. There is general agreement, however, that a variety of techniques will be necessary and that they must be used on a variety of systems, including cellular, organoid, and animal models as well as human samples. Analysing ever-larger and more varied human populations as well as cell kinds is crucial [12]. To enable direct investigation of different impacts and more precise computational prediction techniques, we anticipate that advancements in experimental techniques, the generation of substantial and comprehensive data sets, and algorithm development will work hand in hand.

C. Genome sequenced Agriculturally important plants

Reduced hunger is the main goal of the current boom in plant genome sequencing. Most of the plant genomes that have been sequenced are those of food crops, which are crucial for tropical nations. Various grains, pulses, tuber crops, fruits, vegetables, and oil plants are among these crops. For several of these crops, functional markers have been created, and genes affecting crucial agronomic features have been found. For a thorough knowledge of the genetic mechanisms underlying each attribute and to discover allelic variants, re-sequencing and gene expression experiments are still being carried out. Numerous genome studies are active or in the planned stages in addition to the crops that have been sequenced. Below is the list of some agriculturally important plants which are sequenced (Table 1). Genetics has undergone a radical transformation as a result of the development of sequencing technology and the mass sequencing of genomes and transcriptomes. Using the most latest technology, many crop genomes have been sequenced. However, the research is still in its infancy. Several crop genome assemblies still exist in draft form. The density of repeats in many plant genomes makes it difficult to assemble the short reads from NGS systems. It would be promising to launch third-generation sequencing technologies like Pacific Biosciences in order to get longer reads for the assembly of whole chromosomes. Another effective way to extract the whole genome assembly is by the purification of individual chromosomes, which may then be used for shotgun sequencing or the creation of BAC libraries [13]. The focus of this decade should be on information acquisition, with the expected application of that knowledge in the form of enhanced crop varieties with higher yields and resistance to biotic and abiotic stress in the following decades [62].

III. Breeding for Resilience: Genomic Selection and Marker-Assisted Breeding

Breeding for resilience is a crucial strategy in modern agriculture and livestock management to enhance the ability of crops and animals to withstand various stressors and challenges. With the increasing impacts of climate change, emerging diseases, and changing environmental conditions, there is a growing need to develop resilient plant varieties and animal breeds that can thrive in these unpredictable circumstances. Two prominent techniques used in breeding for resilience are Genomic Selection (GS) and Marker-Assisted Breeding (MAB). These approaches leverage advancements in genomic technology to accelerate the breeding process, making it more efficient and targeted.

A. Genomic Selection (GS):

A cutting-edge breeding technique called genomic selection makes use of genomic information to forecast a person's genetic potential for particular traits. It entails scanning an organism's complete genome to find areas connected to features that are desirable, such drought tolerance, disease resistance, or yield potential. These genomic areas, sometimes referred to as markers, act as signs of the existence of advantageous genes linked to the desired attributes. The GS process involves the following steps:

a. Genotyping: The genome of a large population of plants or animals is analyzed using high-throughput genotyping technologies to detect markers associated with the desired traits.
b. Phenotyping: The same individuals are phenotyped to measure their actual performance for the target traits.
c. Training the model: A statistical model is developed to establish the relationship between the markers and the phenotypic data of the individuals in the population.
d. Selection: The model is then used to predict the breeding value of untested individuals, allowing breeders to select candidates with the highest potential for desired traits.

Genomic Selection significantly accelerates the breeding process by allowing breeders to identify superior candidates at an early stage without the need for lengthy and resource-intensive field trials. This results in more efficient and precise breeding programs that can rapidly introduce desirable traits into new varieties and breeds. Numerous studies have been conducted to determine how well genomic selection (GS) may be used to enhance crops since the theory and conceptual underpinning for GS were first developed. However, marker-assisted selection has demonstrated its potential for improving qualitative characteristics with huge impacts regulated by one to few genes. It has a minor impact on the enhancement of quantitative traits that are controlled by a variety of small-effect genes. Using genomic-estimated breeding values of individuals derived from genome-wide markers, GS, which chooses candidates for the following breeding cycle, is a useful technique for improving quantitative traits in this context. Over the past 20 years, GS has been widely adopted in animal breeding programs all over the world due to its capacity to maximize genetic gains, reduce phenotyping, shorten cycle times, and increase selection accuracy. Considering the positive preliminary findings of the GS evaluation for increasing production, biotic and abiotic stress tolerance, and quality in cereal crops like wheat, maize, and rice, prospects of integrating GS in breeding crops are also being examined. Improved statistical models that employ genetic data to increase prediction accuracy are essential for the success of GS-enabled breeding programs. The creation of production markers that can greatly speed up the generation of crop varieties. Improved statistical models that employ genetic data to increase prediction accuracy are essential for the success of GS-enabled breeding programs.

that are stress-resistant through GS is aided by research on genetic architecture under heat and drought stress. The figure below shows the major steps involved in genomic selection (Fig.4)

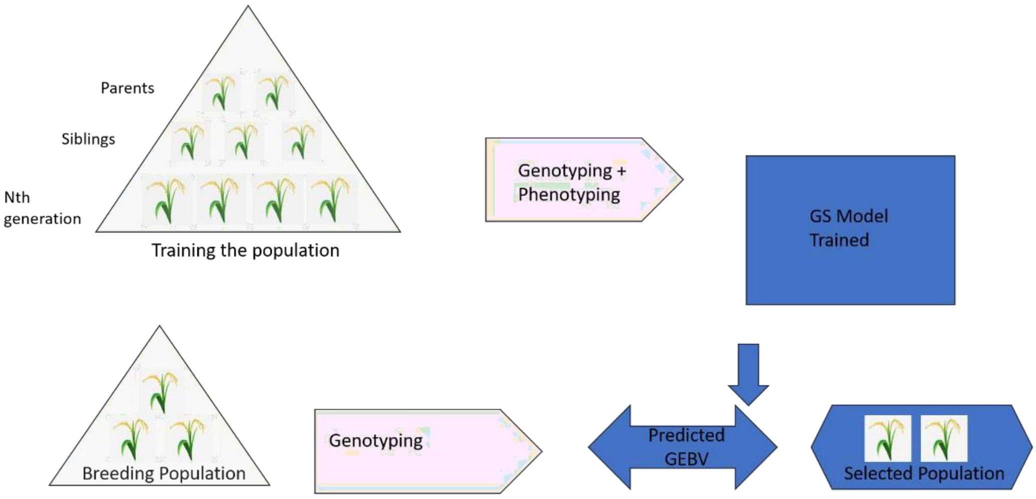

Figure 4:- General Steps of Genomic Selection

One of the advantages of GS, which predicts phenotype using data from genome-wide DNA markers, is a large cost decrease in repetitive phenotyping [63]. Breeding cycles can be shortened thanks to GS's excellent predictive accuracy in elite genetic materials, particularly in the early generations, and genomic estimated breeding values (GEBVs) [64]. The crop performance of hybrids may be accurately predicted using the GS models. Werner et al., for example, calculated general combining ability (GCA) and specific combining ability (SCA) based on RR-BLUP and Bayesian models to forecast hybrid performance in oilseed rape [65].

Model for Genomic Selection Using Statistics

A basic linear model, often known as least-squares regression or ordinary least-squares regression (OLS), is the first step in the GS process of choosing the appropriate candidates:

$$Y=1n\mu+X\beta+\varepsilon$$

Where, X = design matrix of order n×p (where each row represents the genotype/individuals/lines (n) and each column corresponds to the marker (p)), $Y=n\times1$ vectors of observations, is the mean, $\beta=p\times1$ vectors of marker effects, $\varepsilon=n\times1$ vectors of random residual effects, and $\varepsilon\sim N(0,\sigma2e)$.

The number of markers (p) surpasses the number of observations (n), i.e., genotype/individuals/lines, causing the problem of over-parameterization (big "p" and small "n" problem ($p >> n$)). This is the main issue with linear models utilizing thousands of genome-wide markers. The big "p" and small "n" problem can be solved alternatively by using a subset of significant markers. For GS, Meuwissen et al. modified the least-squares regression [63]. Each marker was subjected to a separate least-squares regression analysis using the following model:

$$Y=Xj\beta j+\varepsilon,$$

where Xj is the jth column of the marker design matrix and βj is the genetic impact of the jth marker. This model's log likelihood is used to choose markers with significant effects, and those markers are subsequently used to estimate breeding values. It must be understood, nonetheless, that selection based on the subset of markers may result in the loss of some important information [66].

Table 1 : List of genome sequenced agriculturally important plants

Scientific name	Common name	Economic importance	Haploid chromosome number	Estimated genomic size (Mb)	Size of Assembly (Mb)	Number of gene predictions	Repeat (%)	Reference
Azadirachta indica	Neem	Pesticides, medicine	12	364.00	–	20,000	13.03	[14]
Beta vulgaris	Sugar beet	Sugar production	9	714.00–758.00	567.00	27,421	63.00	[15]
Brassica napus	Rapeseed	Oil, animal feed, biodiesel	19	1130.00	892.70	1,01,040	34.80	[16]
Brassica oleracea var. capitata	Cabbage	Food (vegetable)	9	630.00	535.50	45,758	38.80	[17]
Brassica rapa	Chinese cabbage	Food (vegetable)	10	529.00	283.80	4l,174	39.50	[18]
Cajanus cajan	Pigeon pea	Food	11	833.07	605.78	48,680	51.67	[19]
Cametina sativa	Camelina	Oil, animal feed, biodiesel	20	785.00	641.45	89,418	28.00	[20]
Carica papaya	Papaya	Food (fruit, vegetable)	9	372.00	271.00	24,746	52.00	[21]
Cannabis sativa	Marijuana	Drug	10	~820.00	534.70	30,000	–	[22]
	Hemp	Fibre, oil			220.80	–	–	
Capsicum annum	Hot pepper	Spice	12	3,480.00	3,060.00	34,903	76.40	[23]
Cicer arietinum	Chickpea	Food	8	~738.00	532.29	28,269	49.41	[24]
Citrullus lanatus	Water melon	Food (fruit)	11	~425.00	353.50	23,440	45.20	[25]
Citrus clementina	Clementine mandarin	Food (fruit)	9	367.00	301.40	24,533	45.00	[26]
Citrus sinensis	Sweet orange	Food (fruit)	9	367.00	320.50	29,445	20.50	[27]
Coffea canephora	Robusta coffee	Food	11	710.00	568.60	25,574	50.00	[28]
Cucumis melo	Melon	Food (fruit)	12	450.00	375.00	27,427	19.70	[29]
Cucumis sativus	Cucumber	Food (vegetable)	7	367.00	243.50	26,682	24.00	[30]
Elaeis guineensis	Oil palm	Edible oil	16	1,800.00	1,535.00	34,802	57.00	[31]
Eragrostis tef	Tef	Food	20	772.00	672.00	–	14.00	[32]
Eucalyptus, grandis	Eucalyptus	Wood, biofuel, medicine	11	640.00	605.00	36,796	50.00	[33]
Fragaria vesca	Strawberry	Food (fruit)	7	240.00	209.8	34,809	16.00	[34]
Glycine max	Soybean	Food	20	1,115.00	950.00	46.430	57.00	[35]
Musa acuminata	Banana	Food (fruit)	11	523.00	472.20	36,542	43.72	[36]
Nicotiana tabacum	Tobacco	Smoking	12	4,500.00	3,700.00	90,000	72.00–78.00	[37]
Oryza sativa- spp indica	Rice	Food	12	430.00	466.00	46,022–55,615	42.20	[38]
Oryza sativa-spp japonica				420.00	389.80	37,544	35.00	[39]

Phaseolus vulgaris	Common bean	Food	11	587.00	473.00	27,197	45.37	[40]
Phoenix dactylifera	Date palm	Food (fruit)	18	671.00	605.40	41,660	21.99	[41, 42]
Phyllostachys heterocycla	Moso bamboo	Building material, furniture, paper	24	2,075.00	2,050.00	31,987	59.00	[43]
Populus trichocarpa	Poplar	Wood, paper	19	485.00	410.00	45.555	44.00	[44]
Prunus mume	Chinese plum/Mei	Food (fruit)	8	280.00	237.00	31,390	45.00	[45]
Pyruss bretschneideri	Pear	Food (fruit)	8	265.00	226.60	27,852	29.60	[46]
Pyruss bretschneideri	Pear	Food (fruit)	17	527.00	512.00	42,812	53.10	[47]
Ricinus communis	Castor bean	Oilseed	10	320.00	350.00	31,237	50.33	[48]
Setaria italica	Foxtail millet	Food. fodder, biofuel	9	490.00	423.00	38,801	46.00	[49, 50]
Solanum lycopersicum	Tomato	Food (vegetable)	12	900.00	760.00	34,727	63.28	[51]
Solanum melongena	Eggplant	Food (vegetable)	12	1126.00	833.10	85,446	70.40	[52]
Solanum tuberosum	Potato	Food	12	844.00	727.00	39,031	62.20	[53]
Sorghum bicolor	Sorghum	Food, beverage	10	~730.00	698.00	27,640	62.00	[54]
Theobroma cacao	Cocoa	Food	10	430.00	326.90	28,798	25.70	[55]
Triticum aestivum	Bread wheat	Food	21	17,000.00	3,800.33	94,000–90,000	80.00	[56]
Vaccinium macrocarpon	Cranberry	Food (fruit)	12	470.00	420.00	36,364	5.60	[57]
Vigna radiata	Mungbean	Food	11	579.00	431.00	22,427	43.00	[58]
Vitis vinifera	Grape	Food (fruit), beverage	19	475.00	487.00	30,434	41.40	[59]
Zea mays	Maize	Food	10	2,300.00	2,048.00	32,540	85.00	[60]
Ziziphus jujuba	Jujube	Dry fruit, medicine	12	444.00	437.65	32,808	49.49	[61]

B. Marker-Assisted Breeding (MAB):

Marker-Assisted Breeding is an earlier version of genomic selection that employs markers associated with specific traits but doesn't involve complex prediction models. Instead, it directly targets specific genes or genomic regions known to influence desirable traits. MAB is particularly useful for traits controlled by major genes, which have a significant impact on the phenotype. The process of Marker-Assisted Breeding involves the following steps:

a. Marker identification: Researchers identify markers that are closely linked to genes responsible for the target trait through genetic mapping and association studies.

b. Marker-assisted selection: Breeders use these markers as a tool to select individuals that carry the desired genes during the breeding process.

c. Phenotypic evaluation: The selected individuals are then subjected to rigorous phenotypic evaluation to validate their performance for the targeted trait.

While Marker-Assisted Breeding lacks the predictive power and efficiency of Genomic Selection, it remains a valuable technique for traits with known genetic markers. Additionally, it can be more cost-effective, especially in cases where genomic data for the entire genome is not necessary. In conclusion, both Genomic Selection and Marker-Assisted Breeding play crucial roles in breeding for resilience. They empower breeders with the knowledge of an organism's genetic makeup and aid in the selection of individuals with desired traits, ultimately leading to the development of more robust and resilient crops and animal breeds. As these technologies continue to advance, they will undoubtedly contribute significantly to food security and sustainable agriculture in the face of evolving challenges. The phenology of several agricultural species has been impacted by climate change, which has a negative impact on productivity and output. Stresses like heat, cold, drought, and flood are examples of how the climate is changing. Traditional breeding has been effective in achieving phenotypic selection-based genetic improvement of crops. However, recent advances in genomics have revealed a number of underlying genes and quantitative trait loci (QTLs) that confer tolerance to these particular environments and have been applied in marker-assisted selection (MAS). In an indirect selection procedure known as MAS, individuals are chosen based on the known markers associated with a certain characteristic of interest [67]. This technique has been successfully employed in the past to boost individual selection efficiency in plant breeding. When compared to the conventional phenotype-based selection approach, this strategy has been successfully employed in the past for the selection of individuals in plant breeding to boost selection accuracy [68].

C. Implications of Genomic Selection for crop improvement

i. GS in Cereals

Around 50% of the total dietary energy supply comes from cereals, making them an important part of our daily diet. Wheat, rice, maize, and barley are the main cereal crops grown on arable land globally. The production of these products is threatened by disasters brought on by climate change [69], and on top of that, it is made more challenging by the increased demand brought on by a growing population [70]. To overcome these challenges, the production system needs to be efficient, environmentally friendly, and sustainable. For such production systems to be able to meet the challenges, it is imperative to use crop kinds with high yields and minimal resource requirements. The creation of such varieties, however, is a laborious process because the majority of agricultural productivity attributes are governed by a complex genetic system (most genes have little or no influence), which is complicated by poor heritability and a high degree of epitasis [71]. Although traditional selection techniques have produced a lot of varieties, the genetic gain per unit of time is not as rewarding as GS, but they do offer a chance to speed up the selection cycle [72]. The ability of GS to rapidly select individuals with high breeding value from early-generation populations without the need for significant phenotyping can be used to evaluate the viability of the method. The first candidate crops where the efficiency of GS has been investigated are wheat, rice, maize, and barley.

a) Improvements in Grain Yield and Related Characteristics

The thousand grain weight, the number of tillers bearing panicles, the number of grains per panicle, the number of filled grains per panicle, etc. are essential features that either directly or indirectly affect grain yield. It has been evaluated how well these variables can be predicted by genomics utilizing different training populations and model types. Variations in the precision of genomic prediction have been connected to differences in the heritability of the trait, the training population, and the models used. The genomic prediction accuracy ranged from 0.28 to 0.78 for a very complex and physiological trait-like distribution of weight to each individual grain in the panicle in rice [73]. Grain yield for maize ranged from 0.28 to 0.78 [74].

b) Tolerance to Biotic Stress

As a result of shifting weather patterns, reports are being made on a global scale about the emergence/resurgence of novel disease races and insect biotypes [75]. Therefore, to produce cultivars that can endure biotic stress, it is required to identify resistance genes in the germplasm and incorporate them into the breeding program. While MAS has shown useful when breeding for qualitative resistance, it has not been as effective when breeding for quantitative resistance, which is regulated by more genes with modest effects. GS has shown its efficacy in raising biotic stressor tolerance in cereals that are quantitatively controlled, while only being applied in a very small number of cereals. Wheat has been the subject of the majority of studies on the use of GS for biotic stress tolerance. A wide range of diseases, including three different forms of rusts, Fusarium head blight, *Septoria tritici* blotch, powdery mildew, tan spot, and *Stagonospora nodorum* blotch, have been recorded from wheat. Blast-tolerant lines in rice have been found using GS [76]. In maize, GS has been effectively used to choose lines from biparental populations for superior production under significant infestation of Striga

[78] and from natural populations for tolerance to *Stenocarpella maydis*, which causes ear rot.

c) Tolerance to Abiotic Stress

The chance of drought, high-temperature stress during agricultural growth phases, flood, etc. has increased due to climate change, which causes significant crop losses [79]. Liu et al. anticipated that a 1°C rise in global temperature would result in a yield decline of up to 6.4% in wheat [80]. The sustainable and cheap options in such situations to make up for the losses are changing cropping patterns or developing cultivars that are resistant to abiotic stress. Abiotic stress breeding using conventional methods has accuracy and reproducibility problems. Despite the fact that Beyene et al.'s [81] study on eight biparental populations of maize under drought conditions showed a gain of 0.176 t/ha for grain yield after three cycles of selection using the rapid cycling GS strategy, molecular markers have been used to locate and transfer yield QTLs under abiotic stress conditions [82]. This led to an increase in genetic gain compared to the conventional breeding strategy, where phenotypic selection required a selection time that was three times higher.

d) Quality Improvement

The genetic architecture of different quality vary; some, like grain color, are oligogenically controlled, whilst others, like grain size and protein content, are polygenic in origin [83]. The multi-family populations demonstrated higher prediction accuracies for quality-related variables, such as milling and flour quality, when prediction accuracies in biparental and multi-family populations were compared [84]. It is well known that protein content and yield have a negative relationship because of physiological compensation [85]. Rice grain length and breadth are important quality indicators, and 110 Japanese rice cultivars were able to predict these attributes with accuracy ranging from 0.35 to 0.45 and 0.5 to 0.7, respectively, using several GS models [86].

ii. GS in oilseeds

Oilseeds are a primary source of income for small-scale farmers in developing countries in Asia and Africa. The yield potential can still be attained by closing the yield gap by enhancing quality and biotic and abiotic stressor resistance [87]. Due to the qualitative nature of the majority of the features connected to biotic and abiotic stressors, the report of GS is limited in such potential crops. Oil quality and yield parameters are influenced by the environment and GxE interactions[88]. Therefore, it is vital to use the appropriate GS models to take into consideration the GxE effects for accurate selection. In contrast to the protein content alleles, which came from the wild progenitor of the soybean (G. max X G. sojae), Beche et al.'s research showed that the yield-related alleles were linked to the cultivated elite line [89]. The diversity in the distribution of trait-contributing alleles in such crosses has a greater impact on their predictive capacity. Hu et al. obtained a satisfactory prediction accuracy (0.78) when using GS to predict the capacity of soybean embryogenesis [90].

iii. GS in Pulses

Haile et al. showed that in the instance of lentils, single-trait GS (STGS) is appropriate in the absence of large-effect QTLs, whereas multi-trait-based Bayes B is the best GS model if large-effect QTLs are present in the population [91]. Additionally, they asserted that GxE interactions and MTGS improve prediction for low heritable traits. Diaz et al. investigated GS using multiple populations (RIL, MAGIC, Andean, and Mesoamerican breeding lines) while taking into account quality qualities in Phaseolus, such as cooking time [92] in order to screen quick culinary genotypes. MAGIC population genomic prediction accuracy for cooking time was high and promising (0.55) compared to Mesoamerican genotypes' (0.22) accuracy, and the variable was substantially heritable (0.64-0.89).

iv. Horticultural Crops GS

In order to achieve nutritional security, fruit and vegetables are essential. However, the issue with their breeding, particularly with fruits, has its own drawbacks, namely a protracted juvenile phase and a highly heterozygous character. In an analysis of 537 genotypes of apples for fruit texture attributes using GS, Roth et al. reported an accuracy of up to 0.81 [93]. Using a factorial mating strategy, Kumar et al. demonstrated high prediction accuracy in apples for various quality parameters (0.70-0.90) [94].

D. Statistical Tools for Implementing Genomic Selection

Several tools and packages have been developed for the evaluation of genomic prediction and implementation of GS, some of which are listed in table 3

S.No.	Tool	Description	Based	Availability	Access Website
1.	GMStool	Genomic prediction tool (Genome-wide association study (GWAS)-based) using genome-wide marker data, identifies SNP markers	R-based	freely available	(http://cassavabase.org/solgs)

2.	solGS	Stores a largeamount of phenotypic, genotypic and experimental data.	Linux operating system based	open-source tool	https://github.com/austin-putz/GenSel.
3.	rrBLUP	For genome prediction in animal and plant breeding. Estimates the marker effects from trainingdatasets	R based	open-source tool	https://CRAN.R-project.org/package=rrBLUP.
4.	BWGS	For estimation of GEBV for selection candidates.	R based	freely available	https://CRAN.R-project.org/package=BWGS.
5.	BGLR	Extension of the BLR package	used to implement several Bayesian models and also provides flexibility in terms of prior density distribution	freely available	https://CRAN.R-project.org/package=BGLR.
6.	GenSel	Used for estimation of molecular marker–based breeding values of animals for the trait of interest	Uses the Bayesian approach in the background	freely available user-friendly tool	https://github.com/austin-putz/GenSel.
7.	GSelection	Estimating the GEBV and to select the important markers and	R-based package	freely available	https://CRAN.R-project.org/package=GSelection

8.	lme4GS	For fitting mixed models with covariance structures	R-based package	freely available	https://github.com/perpdgo/lme4GS
9.	STGS	For genomic predictions by estimatingmarker effects, used for calculation of genotypic merit of individuals, i.e., GEBV	Performs genomic selection only for a single trait, hence namedSTGS	freely available	https://CRAN.R-project.org/package=STGS.
10.	MTGS	Genomic selection using multi-trait information	R-based package, only for a multiple trait	freely available	https://CRAN.R-project.org/package=MTGS

E. Next Generation Sequencing (NGS): The Secret to GS's Success

The most comprehensive method for studying polymorphism in any crop is to sequence or resequence the full genome (or a portion of it) of a large number of accessions. This was not conceivable prior to the development of the NGS platform, which has fundamentally changed the way genomic approaches to biology are carried out. The platform has dramatically increased the speed at which DNA sequence can be collected while sharply lowering the costs by several orders of magnitude. According to many scientists, NGS technologies have been extensively used for transcriptome and epigenetic analysis, whole genome sequencing (WGS), whole genome resequencing (WGRS), de novo sequencing, and GBS.

Third generation sequencing (TGS) technologies were created in recent years and are now being used to enhance NGS tactics. In less time and for less money each instrument run, these technologies yield longer sequence reads. NGS has grown to be a potent tool for genomic-estimated breeding (GAB) because of its ability to quickly detect a large number of DNA sequence polymorphism-based markers. Using NGS platforms, several targeted marker finding methods have been created. In GWAS and GS investigations, RAD-seq (or its variations) and GBS were often employed. These NGS technologies have already been demonstrated to be successful for GAB (Table 2).

Table 2 :- Genomic selection (GS) initiatives for various traits in different crops

S.no.	Species	NGS marker platform	Trait	Population size	Total SNP markers	Prediction accuracy	Model	Software packages	Reference
1	Rice	GBS	Yield, flowering time	363	73,147	0.31–0.63	RR-BLUP	R package rrBLUP	[95]
2	Rice	DArTseq	Yield,plant height	343	8,336	0.54	G-BLUP, RR-BLUP	BGLR and ASReml R packages	[96]
3	Wheat	GBS	Stem rust resistance	365	4,040	0.61	G-BLUP B	R package GAPIT	[97]
4	Wheat	GBS	Yield,plant height, pre-harvest sprouting	365	38,412	0.54	BLUP	R package rrBLUP	[98]
5	Wheat	GBS	Grain yield	254	41,371	0.28–0.45	BLUP	ASReml 3.0	[99]
6	Wheat	GBS	Yield and yield related traits, protein content	1127	38,893	0.20–0.59	BLUP	rrBLUP version 4.2	[100]
7	Wheat	GBS	Fusarium head blight resistance	273	19,992	0.4–0.90	RR-BLUP	R package GAPIT	[101]
8	Wheat	GBS	Grain yield, protein	659	–	0.19–0.51	RR-BLUP	R package rrBLUP	[102]

			content and protein yield						
9	Wheat	GBS	Grain yield	1477	81,999	0.50	G-BLUP	R package rrBLUP	[103]
10	Wheat	DArTseq	Grain yield	803	–	0.27–0.36	G-BLUP	BGLR and ASReml R packages	[104]
11	Wheat	GBS	,Fusarium head blight resistance, yield softness equivalence and flour yield	470	4858	0.35–0.62	BLUP	BGLR R-package	[105]
12	Wheat	GBS	Heat and drought stress	10819	40000	0.18–0.65	G-BLUP	BGLR R-package	[106]
13	Maize	GBS	Drought stress	3273	58 731	0.40–0.50	G-BLUP	BGLR R-package	[107]
14	Maize	GBS	Grain yield, anthesis date, anthesis-silkimg interval	504	158,281	0.51–0.59	PGBLUP, PRKHS	R Software	[108]
15	Maize	GBS	Grain yield, anthesis date, anthesis-silkimg interval	296	235,265	0.62	PGBLUP, PRKHS	R software	[108]
16	Maize	DArTseq	Ear rot disease resistance	238	23.154 Dart-seq markers	0.25–0.59	RR-BLUP	R package rrBLUP	[77]
17	Soybean	GBS	Yield and other agronomic traits	301	52,349	0.43–0.64	G-BLUP	MissForest R package, TASSEL 5.0	[109]
18	Canola	DArTseq	Flowering time	182	18, 804	0.64	RR-BLUP	R package GAPIT	[110]
19	Alfalfa	GBS	Biomass yield	190	10,000	0.66	BLUP	R package, TAASEL software	[111]
20	Alfalfa	GBS	Biomass yield	278	10,000	0.50	SVR	R package rrBLUP, R package BGLR, R package 'RandomForest	[112]
21	Miscanthus	RADseq	Phenology, biomass, cell wall composition traits	138	20,000	0.57	BLUP	R package rrBLUP	[113]
22	Switchgrass	GBS	Biomass yield	540	16,669	0.52	BLUP	glmnet R package, R package rrBLUP	[114]
23	Grapevine	GBS	Yield and related traits	800	90,000	0.50	RR-BLUP	R package BLR, R package rrBLUP	[115]

24	Intermediate wheatgrass	GBS	Yield and other agronomic traits	1126	3883	0.67	RR-BLUP	R package rrBLUP, BGLR R-package	[116]
25	Perennial ryegrass	GBS	Plant herbage dry weight and days-to-heading	211	10,885	0.16–0.56	RR-BLUP	R software	[117]

IV. BIOTECHNOLOGICAL APPLICATIONS IN CROP IMPROVEMENT

The whole genomes of model species like human, yeast, Caenorhabditis elegans, Arabidopsis thaliana, and rice have all been sequenced over the past ten years. *Zea mays*, *Sorghum bicolor*, *Medicago sativa*, and *Musa* spp. are among the other plant species that will probably have their whole genomes sequenced. Systematic whole genome sequencing will transform our understanding of the structure and function of genes and genomes, allowing us to better manage the traits that result in high agricultural productivity [118]. It takes five to six generations of conventional breeding to transfer a trait from a species into high-yielding, locally adapted cultivars, and choosing the plants with the optimal combination of qualities necessitates planting a large number of children. The improved lines required to undergo a round of multi-location tests before the farmers could select a variety for production. It takes this process at least seven to ten years. Genetic transformation, which also provides access to genes from other species that can be utilized to make transgenic crops, enables the variation of the level of gene expression as well as the geographical and temporal pattern of gene expression. After the necessary genes are transferred into the target crops or cultivars, it takes five to six years for cultivars with stable gene expression to be developed (Figure 5).

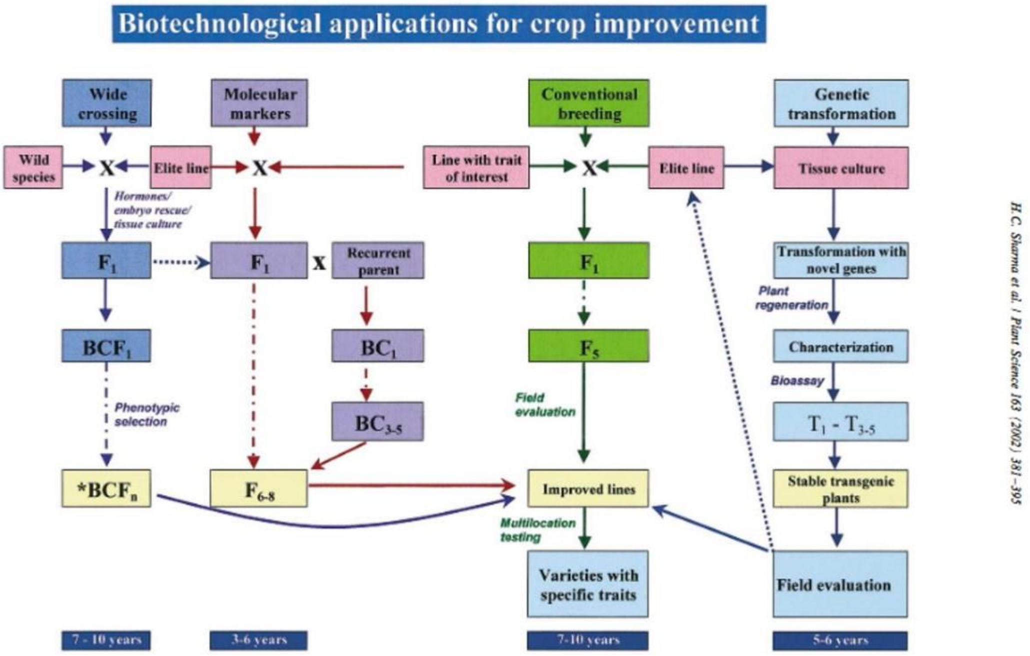

Figure 5 :- An illustration of biotechnology methods for crop development. Genetically altered lines can be issued as varieties or employed as donor parents in traditional breeding. To obtain homozygous and stable lines from wide-crossing lines, it may take several generations (BCFn), and such material may be employed as improved lines or as a donor parent in traditional breeding or marker-assisted selection.

Resistance against pests, diseases, and herbicides

The first transgenic plants with Bt (Bacillus thuringiensis) genes were developed in 1987. Although Bt d-endotoxin genes have been used to construct the bulk of insect-resistant transgenic plants, several experiments are currently being carried out to use non-Bt genes that interfere with the nutritional requirements of the insects. Lectins, chitinases, secondary plant metabolites, and protease inhibitor are a few of the genes in this group. There are currently a number of transgenic plants that can be grown in fields or for on-farm production. Cotton bollworms have been successfully managed with the use of transgenic cotton. To protect against lepidopterous pests, the Bt genes have also been successfully expressed in tomato, potato, brinjal, groundnut, and chickpea. Currently, sorghum, pigeonpea, and chickpea are being genetically modified with the Bt, trypsin inhibitor, and lectin genes to provide resistance to these insects. Transgenic sorghum and pigeonpea plants with Bt and trypsin inhibitor genes are now being tested in confinement glasshouse environments. Additionally, scientists are working to develop groundnut plants that are immune to viruses and fungus. The ecology will be greatly benefited by the use of transgenic plants along with integrated pest control (IPM) methods. Insecticide treatments will be decreased, natural enemies' activity will rise, and secondary pests will be managed through Integrated Pest Management (IPM) as a result of the development and usage of transgenic plants carrying insecticidal genes [118].

Abiotic stress tolerance

The creation of crops with the ability to endure abiotic stressors would aid in crop output stabilization and considerably improve food security in underdeveloped nations. Barley late embryogenesis (LEA) gene-transformed rice plants have reportedly shown improved performance [48]. Acid soil tolerance for aluminum is provided by plants with the capacity to create more citric acid in theirroots [49]. The introduction of a gene producing a plant farnesyltransferase [51] and inhibitors of this enzyme when produced in plants,boost drought tolerance, postpone senescence, and alter the growth habit, which together give tolerance to salinity [50].

Metabolism of starches and sugars

The enzyme known as sucrose phosphate synthase (SPS) is essential for regulating the metabolism of sucrose. To express the maize SPS, transgenic plants are controlled by a promoter from the tobacco small subunit. Rubisco has shown improved foliar sucrose/starch ratios in leaves and lower levels of foliar carbohydrates when cultivated with CO 2 enrichment. This has opened up intriguing possibilities for altering the chemical composition of dietary grains to meet specific demands.

Enhanced yield and photosynthetic effectiveness

An appealing experimental method for significantly raising crop productivity is to switch C3 plants like Arabidopsis [63] and potatoes [64] to the C4 type of photosynthesis. O 2 suppression of C3 photosynthesis results from the oxygenase reaction of ribulose 1, 5-biophosphate carboxylase/oxygenase (Rubisco) and the subsequent loss of CO 2 from photorespiration. An essential part of this system is the activity of phosphoenolpyruvate carboxylase (PEPC), an enzyme that fixes ambient CO2 in the cytoplasm of mesophyll cells. Agrobacterium-mediated transformation has recently been used to incorporate the whole maize PEPC into the C 3 plants. Oilseed rape that has experienced sublethal freezing during seed development can diminish the type I chlorophyll a/b binding protein of light harvesting complex II.

Vaccines and Pharmaceuticals

Plants can produce a variety of vaccinations. Bananas and potatoes have been used to generate vaccines against infectious disorders of the gastrointestinal system. Plants with a gene originating from human infections have been created via biotechnology.Anti-cancer antibodies found in wheat and rice may be helpful in the diagnosis and treatment of this condition. Through the use of transgenic technology, there is also a tremendous potential to boost the yield of medications generated from plants (such as salicylic acid).

Nutritional factor

Several quality traits can be targeted to improve the nutritional status of crop produce. These include carbohydrates, proteins, oils, It is possible to improve the nutritional value of crop products by focusing on a number of quality attributes. These consist of nutrients such as sugars, proteins, fats, vitamins, iron, and amino acids. The choice of target traits is impacted by the producers, the agro-based industry, and the final consumers. Utilizing genes that produce an iron-binding protein that makes iron more available in the human diet, transgenic rice with higher iron levels has been created. Reducing the number of oligosaccharides (such raffinose and stachyose), which cause flatulence during digestion, increases digestibility. Antinutritional factors can also be eliminated using transgenic technology [118].

V. FUTURE CHALLENGES

As we move into the future, the field of genomics holds immense promise for revolutionizing crop improvement and agricultural practices. Genomics, the study of an organism's complete set of DNA, offers valuable insights into the genetic makeup of crops, enabling scientists and researchers to understand the underlying genetic mechanisms responsible for specific traits. This knowledge opens up exciting possibilities for developing improved crop varieties with enhanced productivity, resilience, and nutritional content. Here are some of the future directions, innovations, and prospects in genomics for crop improvement:

Precision Breeding: Genomics allows for precise identification and selection of desirable genetic traits in crops. With advancements in genome sequencing technologies and data analytics, breeders can now identify specific genes or gene variants associated with traits such as drought resistance, disease tolerance, or increased yield. This targeted approach enables the development of crops tailored to specific environmental conditions and consumer demands.

Gene Editing Techniques: The emergence of gene editing techniques, particularly CRISPR-Cas9, has revolutionized crop improvement. CRISPR-Cas9 allows precise modifications of specific genes, enabling the development of crops with desired traits without introducing foreign DNA. This technology has the potential to accelerate the breeding process significantly and overcome some of the challenges associated with conventional breeding methods.

Omics Integration: Genomics is just one aspect of the larger "omics" family, which includes transcriptomics, proteomics, and metabolomics. Integrating these different layers of biological information provides a more comprehensive understanding of crop biology and how genes interact with various cellular processes. This integrated approach can uncover novel targets for crop improvement and reveal previously unknown relationships between genes and traits. The vast amounts of genomic data generated from various sources require sophisticated data analysis tools. Artificial intelligence (AI) and machine learning algorithms play a crucial role in analyzing these datasets efficiently. AI can identify patterns and correlations in genomic data, predict crop performance under different conditions, and optimize breeding strategies for faster and more effective crop improvement.

Resilience to Climate Change: Climate change poses significant challenges to global agriculture. Genomics can aid in the identification of genetic traits that confer resilience to extreme weather events, temperature fluctuations, and water scarcity.

Developing climate-resilient crop varieties is crucial for ensuring food security in the face of a changing climate. As genomics advances, it is vital to ensure its inclusive and ethical application in crop improvement. Balancing the benefits of genetic technologies with concerns related to biodiversity, intellectual property rights, and ethical considerations is essential to fostering public acceptance and sustainable agricultural practices.

VI. Conclusion

The implementation of biotechnology for long-term food security will depend heavily on access to knowledge and experience in undeveloped countries, where the need to increase food production is most urgent. The International Service for the Acquisition of Agrobiotech Applications (ISAAA), the International Service for National Agricultural Research (ISNAR), the Rockefeller Foundation, UNESCO, the International Cooperation Program of the European Union, and the International Service for National Agricultural Research (ISNAR) are a few of the organizations attempting to play a significant role in the technology transfer from public and private sector institutions in the developed world to the developing world. International assistance will be necessary for these initiatives, as well as the development of several others, in order to fulfill the needs of end-users in developing countries, notably in Africa.

The creation of appropriate regulations and a legalframework for the application of biotechnology in the production of sustainable food requires assistance and encouragement fromthe national governments. Crop production and food security will face significant challenges due to the projected increase in global population as well as the expected effects of climate change, especially in developing nations. Transgenic plants and marker-assisted selection combined with conventional breeding have the potential to significantly boost food production. However, understandingplant physiology and biochemistry will be crucial for creating new and more effective paradigms for plant breeding as well as for interpreting the data from molecular markers. Utilizing the massive and largely untapped pool of advantageous alleles found in crops' wild relatives will allow for the use of DNA marker technologies, opening up a vast new source of genetic variety that will power the subsequent stage of crop improvement. The transfer of genes crucial for crop quality and crop protection will yield the greatest benefits. However, a thorough understanding of how genes interact with their genomic context and the environment in which their given phenotype must interact will be necessary for the quick and cost-effective development and adoption of biotechnology-derived products.

In conclusion, the future of genomics in crop improvement is incredibly promising. As we gain a deeper understanding of crop genetics and harness the potential of gene editing and omics technologies, we can develop crops that are more resilient, nutritious, and sustainable. Leveraging big data and AI, along with advances in synthetic biology, will further accelerate progress in this field. Ultimately, the responsible and equitable application of genomics in agriculture will play a critical role in meeting the challenges of feeding a growing global population while safeguarding the environment**.**

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