“Genomics for Crop Improvement: From Genes to Fields"

Umesh Dnyaneshwar Shinde[1], Bhagyashree Gavande[1], Satish S Nichal[2], Raviprakash G Dani[3] and Torop Elena Alexandrovna[4]

Dr. Umesh Dnyaneshwar Shinde[1]
Biotechnology Centre, Department of Agricultural Botany, Dr. Panjabrao Deshmukh Krishi Vidyapeeth, Akola, Maharashtra State, India

Bhagyashree Gavande
Biotechnology Centre, Department of Agricultural Botany, Dr. Panjabrao Deshmukh Krishi Vidyapeeth, Akola, Maharashtra State, India

Dr. Satish S Nichal[2]
Regional Research Centre for Soybean, Dr. Panjabrao Deshmukh Krishi Vidyapeeth, Akola, Maharashtra State, India

Dr. Raviprakash G Dani[3]
3Gen Scan Inc. Global Consultancy, Houston, Texas, USA and Namangan Engineering and Technology Institute, Namangan, Uzbekistan

Dr. Torop Elena Alexandrovna[4]
Voronezh State Agrarian University, Voronezh, st. Michurina, 1, RUSSIA, 394087

Corresponding author email: umeshinde09@gmail.com

ABSTRACT

Genomics has emerged as a transformative discipline, revolutionizing various fields of science, and agriculture is no exception. In the realm of crop improvement, genomics has played a pivotal role in unlocking the genetic potential of crops, leading to the development of more resilient, nutritious, and sustainable varieties. This chapter provides an overview of the impact and applications of genomics in crop improvement, highlighting key technologies, challenges, and future prospects. Traditional crop breeding methods have been successful in improving crop traits, but they are often constrained by time-consuming phenotypic selection and limited access to genetic diversity. Genomics, with its high-throughput DNA sequencing technologies, has enabled scientists to analyze the entire genome of crops efficiently, providing insights into the genetic basis of various desirable traits. Through techniques such as genetic mapping and quantitative trait locus (QTL) analysis, specific genes associated with traits like disease resistance, drought tolerance, and nutritional content can be identified, facilitating Marker-Assisted Selection (MAS) for more efficient and precise breeding. Moreover, the emergence of genome editing technologies, such as CRISPR-Cas9, has empowered scientists to make targeted changes in crop genomes, enabling the creation of crops with desired traits without introducing foreign DNA. Omics technologies, including genomics, transcriptomics, proteomics, and metabolomics, have been instrumental in harnessing the genetic diversity present in crops and their wild relatives. Genomics has escorted in a new era of crop improvement, enabling scientists and breeders to leverage the vast genetic resources in agriculture more effectively. With continued advancements in genomics and its integration with traditional breeding methods, the future of crop improvement looks promising, offering solutions to global challenges such as food security and climate change.

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

I. INTRODUCTION TO GENOMICS IN CROP IMPROVEMENT

Genomics, a branch of molecular biology, deals with the study of an organism's complete set of DNA, including its genes and their functions. Genomic techniques have revolutionized various fields, including agriculture, and have had a significant impact on crop improvement efforts. The world will require a dramatic increase in food production in the next 30

years. The most important necessity for food and nutritional security is sustainable food production. According to studies, 151 million children under the age of five are stunted, and 821 million individuals worldwide are at or below the minimum nutritional level. Two billion people also lack the necessary amounts of micronutrients to maintain a healthy lifestyle. The manufacturing and supply chain must function properly to satisfy these needs. Various issues connected to the production system posed by climate change have been anticipated to need an increase in output of 60% by 2050. These challenges are further expected to aggravate by an increase in the price of food to the extent of 1-29% by 2050. The increase in population has led to an increase in urbanization, which is directly and indirectly, reducing our access to suitable land for agriculture [1]. Population growth is not the only reason we will need to increase food production. Significant income growth in rapidly developing economies gave rise to an emerging middle class, accelerating the dietary transition toward higher consumption of meat, eggs, and dairy products and boosting the need to grow more grain to feed more cattle, pigs, and poultry [2]. Agriculture in 2050 will need to produce almost 60–100% more food and feed than it is doing now [3]. With the advent of high-throughput DNA sequencing technologies, scientists can now efficiently analyze the entire genome of crops, enabling a deeper understanding of their genetic makeup and potential. Researchers can now identify specific genes associated with key traits, such as drought tolerance, disease resistance, and nutritional content, using techniques like genetic mapping and quantitative trait locus (QTL) analysis. The identification of these genes facilitates Marker-Assisted Selection (MAS), enabling breeders to select plants with desired traits more efficiently.

A. The Role of Genomic Selection in Crop Improvement:

Genomic selection takes the use of genomics in breeding a step further by predicting an individual's genetic value based on its entire genome. This enables breeders to make selections at the early stages of plant development, even before specific traits are fully expressed, resulting in more accurate and faster breeding cycles. Recently the development of genome editing technologies, especially CRISPR/Cas9, opened new routes of fast and precise genome modification promising rapid translation of knowledge from the lab to the field. Genome editing allows introduction of insertions/deletions or an entirely new sequence at a desired location in the target genome [4]. Known genes controlling important traits can be selectively modified using genome editing, allowing for manipulation of phenotypes. In recent years, several genome edited crop plants entered final stages of commercialization in the United States of America including drought and salt tolerant soybean, Camelina with increased oil content, and waxy corn [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:

Structural genomics is the study of configuration and sequence of DNA in the whole genome of an organism. It also includes the evaluation of three - dimensional structures of each protein encoded by genes. To determine all possible protein structures of an organism is the main aim of structural genomics because it is important to study something new about biological processes of an organism. Methodologies used in structural genomics are:

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):

It is conventional method of protein structure determination by using X-ray crystallography, NMR spectroscopy, or electron microscopy. Among all these techniques, X-ray crystallography technique is more precise and considered to have a better accuracy in determining the structure. NMR spectroscopy is replacement to X-ray crystallography for proteins of small-to-medium size. In NMR spectroscopy, HSQC (Heteronuclear Single Quantum Coherence) spectra are main factor which is used to determine protein structures. At very low resolution electron microscopy determine the protein structure and then it is confirmed by using X-ray crystallography technique. For fast determination, there are some new techniques are developed i.e., ultra-high field magnet, chilled probe technology, transverse relaxation optimization spectroscopy, and isotope labelling techniques.

ii. Modelling-based methods:

In this approach, compare with proteins of PDB (Protein Data Bank) are done through profile-profile matching, model building, or threading. To determine closely related sequences of query compound in database, a PSI-Basic Local Alignment and Search Tool search is done in profile-profile matching. Threading is the most successful method of protein projection. It determines the three-dimensional structure of new protein by aligning its primary sequence to similar experimental structure in PDB [6].

b. Functional Genomics:

Functional genomics is the study of functions of gene, gene products, and their interactions. It describes functions of whole genome of an organism and then characterization of genome done accordingly. Main aim of functional genomics is to study relationship between genome of an organism and its phenotype. Techniques used in functional genomics analysis-

i. GTG banding (Giemsa banding) – This method is used to examine large chromosomal aberrations (more than 5 Mb) in karyotype.
ii. aCGH (Microarray-Based Comparative genomic Hybridization) – It is used to analysis of gain or lost areas of the genome. It detects gain or losses of DNA more accurately than traditional karyotyping. cCGH is specific, delicate, and fast technique which detect genomic alignments and copy-number changes [7].
iii. FISH (Fluorescence in situ Hybridization) – This technique is used to detect the location of specific DNA sequences using radiolabelled probes. Chromosome painting was the first application of FISH technique [8].
iv. Sanger or Next-Generation Sequencing – These methods are used to identify known as well as undefined variants in organism's genomic DNA. Both methods have similar notion behind them. During polymerase chain reaction (PCR), which consist of several cycles of sequential DNA replication, DNA polymerase catalyses the complementary incorporation of fluorescently labeled deoxyribonucleotide 5'-triphosphates (dNTPs) into the DNA template. The detector records the colour of a labeld DNA fragment for each cycle, which determines its nucleotide sequences. The main difference between Sanger sequencing and Next Generation sequencing is the NGS is not limited to a single DNA fragment, but analyses millions of fragments in massively parallel sequencing technology [9].
v. Mass spectrometry – It is made up of three parts: an ion source used for converting the gas-phase sample into ions, a mass analyser to separate those ions by means of electromagnetic fields and detectors. For mass spectrometry in major proteomic studies, that allow proteins and peptides to migrate into the gaseous phase without significant degradation has been essential. Matrix-assisted laser electrospray ionization and desorption ionization are the most commonly used ionization techniques. The Orbitrap, which has excellent resolution, high mass accuracy and a wide dynamic range making it compatible with many applications in proteomics and metabolomics, is currently the most progressive mass spectrometer.

c. Comparative Genomics:

Comparative genomics is a field of biological research in which the genomic features of different organisms are compared. The principle of comparative genomics is to identify the common features of two organisms which are often encoded within the DNA that is conserved between the species. The role of comparative genomics is to differentiate gene numbers, gene locations, and biological functions of genes, in the genomes of distinct organisms, with an objective to examine groups of genes which has specific biological role in particular organism. Using comparative genomics we will be able to identify genes that are required for fundamental functions in a wide variety of species. It is important to study evolutionary history of organisms by comparing related species. Due to common evolutionary heritage of all living organisms, it can be understood that there are great differences and similarities among species as well as minute differences between individuals across species which could lead to disease susceptibility in one and resistance in other. It helps in determination of relationship between genotype and phenotype. Integrated resources for comparative genomics on some databases:

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.

Computational tool for genome sequence alignment - Alignment of two genome sequences is the first step of comparative genomics analysis. Recent tools used for genome scale alignment and visualization are BLASTN and MEGABLAST, GLASS, MUMmer, PatternHunter, PipMaker, VISTA etc.

Comparative analysis of genome structure – Understanding similarities and differences between genomes is made possible by analysing global molecular structure i.e. the composition of nucleotides, syntenic relationships or gene ordering. These comparisons give information on the organisation and development of a genome, as well as its unique characteristics. Structure of different genomes can be compared at three levels: a) overall nucleotide statistics b) genome structure at DNA level c) genome structure at gene level [10].

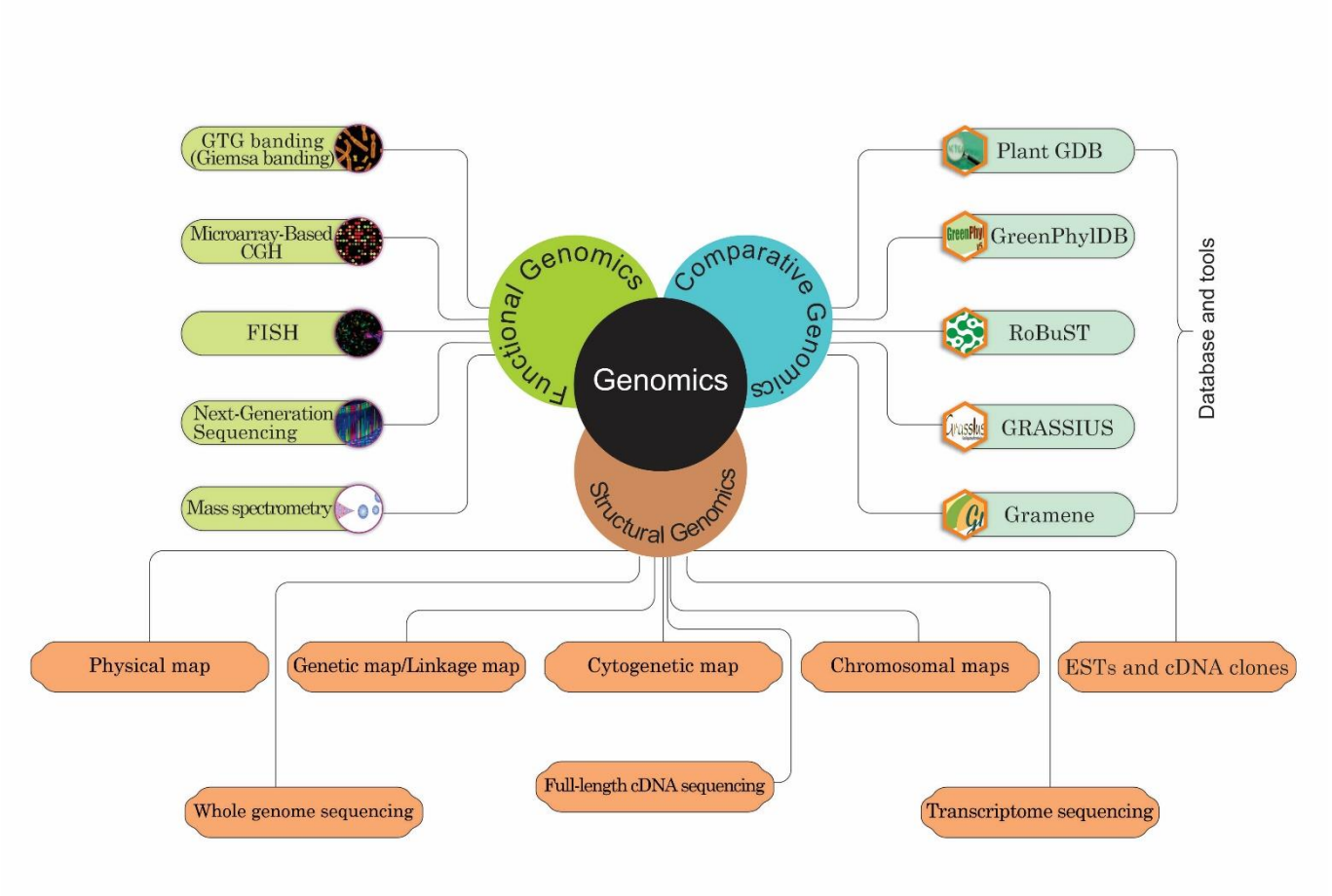

Fig. 1 Classification of genomics

C. Harnessing Genetic Diversity through Omics Technologies:

Genetic diversity is a vital resource for crop improvement, as it provides a reservoir of genes that can be tapped into for developing more resilient and adaptable crop varieties. Omics technologies, such as genomics, transcriptomics, proteomics, and metabolomics, enable the comprehensive study of crop diversity, facilitating the identification of valuable genes and their regulatory networks.

D. Challenges and Ethical Considerations:

The integration of genomics in crop improvement is not without challenges. Issues like data management, intellectual property rights, and public acceptance of genetically modified crops require careful consideration and regulation to ensure responsible and sustainable use of genomic tools in agriculture.

II. Unraveling the Genetic Blueprint: Genome Sequencing and Analysis

Advancements in genomics have opened up unprecedented opportunities to decipher the genetic blueprints of organisms, providing invaluable visions into their traits, functions, and evolutionary history. Genome sequencing, a fundamental tool in genomics, has revolutionized various fields of science, from medicine to agriculture. In this article, we delve into the significance of genome sequencing and analysis, its applications, and the profound impact it has had on scientific understanding and practical applications. Genome sequencing involves determining the order of nucleotides (A, T, C, and G) that constitute an organism's entire DNA sequence. The Human Genome Project, completed in 2003, marked a significant milestone in genomics by decoding the human genome—a feat that took over a decade and required the collaborative efforts of scientists worldwide. Since then, technological advancements have dramatically reduced the time and cost of genome sequencing, making it accessible to researchers and institutions globally. In agriculture, genome sequencing has paved the way for crop improvement, as scientists identify genes associated with desirable traits, such as disease resistance and increased yield. It has shed light on the evolutionary histories of various species, revealing relationships between organisms and uncovering key events in their divergence. By comparing the genomes of different species, scientists can trace their evolutionary paths and discover genetic changes that drove speciation and adaptation. Genome sequencing generates vast amounts of data, creating computational challenges in managing, analyzing, and interpreting the information. Bioinformatics tools and high-performance computing are essential in handling big data and extracting meaningful 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 only from the exonic regions of the genome. 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, characterise, 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 molecular effects and how they could affect higher-level organismal phenotypes (Fig. 2).

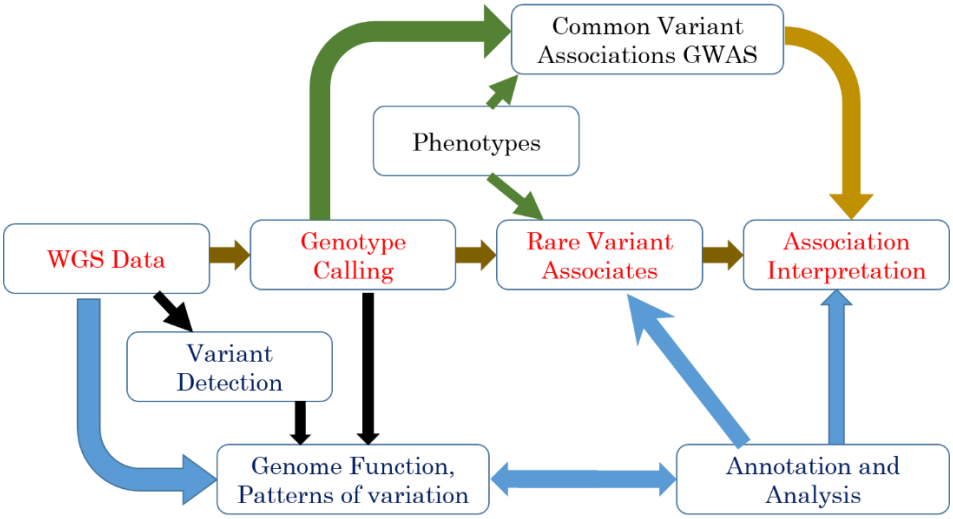

Figure 2 :- General frame of WGS

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 utilised 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). The bulk sequencing of genomes and transcriptomes has completely changed genetics thanks to the development of sequencing technologies. Many crop genomes have been sequenced by taking use of the most recent technology. The research is still in its early stages, though. Draught versions of several crop genome assemblies are still common. Assembling the short reads from the NGS platforms is challenging due to the abundance of repetitions in many plant genomes. 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):

Genomic Selection is a revolutionary breeding method that utilizes genomic data to predict an individual's genetic merit for specific traits. It involves scanning the entire genome of an organism to identify regions associated with desirable traits, such as drought resistance, disease resistance, or yield potential. These genomic regions, known as markers, serve as indicators of the presence of favorable genes related to the targeted traits. 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. Its contribution to the improvement of quantitative characteristics regulated by a number of small-effect genes is modest. In this context, GS, which selects candidates for the upcoming breeding cycle using genomic-estimated breeding values of individuals generated from genome-wide markers, is an effective method for enhancing quantitative characteristics. Because of its ability to maximise genetic gains, decrease phenotyping, shorten cycle times, and improve selection accuracy, GS has been enthusiastically embraced in animal breeding programmes across the world during the past 20 years. Prospects of integrating GS in breeding crops are also being investigated in light of the encouraging preliminary assessment results of GS for the enhancement of yield, biotic and abiotic stress tolerance, and quality in cereal crops including wheat, maize, and rice. The success of GS-enabled breeding programmes depends on improved statistical models that use genetic data to boost prediction accuracy. The creation of production markers that can greatly speed up the generation of crop varieties

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)

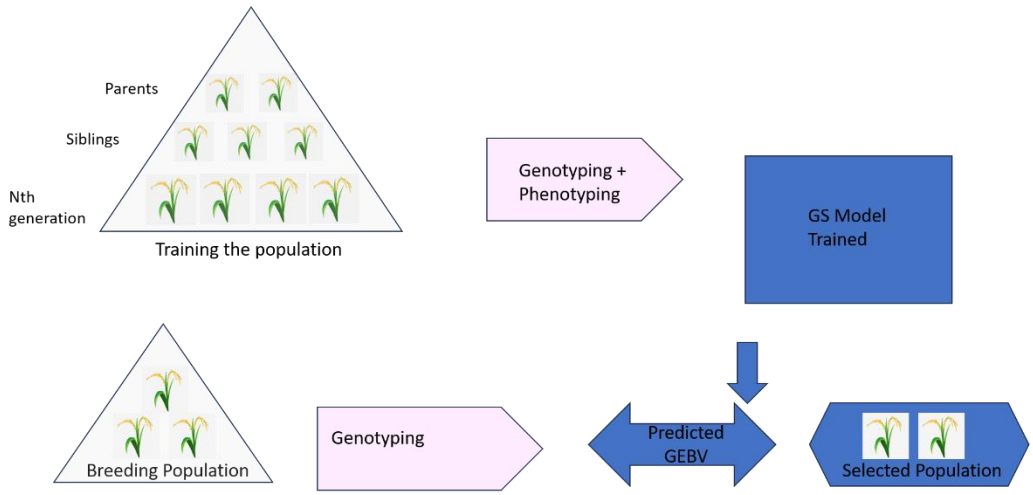

Figure 4:- General Steps of Genomic Selection

A significant cost reduction in repetitive phenotyping is one of the benefits of GS, which uses genome-wide DNA marker data to predict the phenotype [63]. Through genomic estimated breeding values (GEBVs), GS has a high predictive accuracy in elite genetic materials, especially in the first generations, and allows breeding cycles to be shortened [64]. The GS models are excellent for forecasting crop performance of hybrids. For instance, Werner et al. estimated general combining ability (GCA) and specific combining ability (SCA) based on RR-BLUP and Bayesian models to predict 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×1 vectors of observations, is the mean, β=p×1 vectors of marker effects,ε=n×1 vectors of random residual effects, and ε∼N(0,σ2e).

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. The log likelihood of this model is used to choose markers having substantial effects, and those are then utilized for estimation of breeding values. However, it has to be noted that some key information may be lost by selection based on the subset of markers [66].

Table 1 : List of genome sequenced agriculturally important plants

Scientific name	Common name	Economic importance	Haploid chromosome number	Estimated genome size (Mb)	Assembly size (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, pa per	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

Cereals make up around 50% of the overall dietary energy supply, making them a significant component of our daily diet. The principal cereal crops farmed on arable land worldwide are wheat, rice, maize, and barley. Disasters brought on by a change in the climate pose a threat to the production of these crops [69], and on top of that, it is made more difficult by the rising demand brought on by an expanding population [70]. The production system must be effective, sustainable, and put less strain on the environment in order to fulfill the difficulties. Crop types with high yields and low resource requirements are essential to such production systems that can handle the difficulties. 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

An important attribute that is directly or indirectly influenced by other traits such as thousand grain weight, the number of tillers bearing panicles, the number of grains per panicle, the number of filled grains per panicle, etc. is grain yield. The effectiveness of genomic prediction for these variables using various training populations and model types has been assessed. The heritability of the trait, training population, and models employed have all been linked to variances in the accuracy of genomic prediction. For a very intricate and physiological trait-like distribution of weight to each individual grain in the panicle in rice [73], the genomic prediction accuracy ranged from 0.28 to 0.78. For grain yield in maize [74], it ranged from 0.28 to 0.78.

b) Tolerance to Biotic Stress

Global reports of the emergence/resurgence of novel disease races and insect biotypes are being made as a result of changing weather patterns [75]. Therefore, finding resistance genes in the germplasm and incorporating them into the breeding program are necessary to create cultivars that can withstand biotic stress. While MAS has shown to be beneficial when breeding for qualitative resistance, it has not been as successful when breeding for quantitative resistance, which is controlled by multiple genes with smaller effects. Even though it has only been used in a very small number of cereals, GS has demonstrated its value in increasing tolerance to biotic stressors in cereals that are quantitatively controlled. Most of the studies on the utility of GS for biotic stress tolerance have been

reported from wheat, for a wide array of diseases including three types of rusts, Fusarium head blight, *Septoria tritici* blotch, powdery mildew, tan spot, and *Stagonospora nodorum* blotch. In rice, GS has been utilized to identify blast-tolerant lines [76]. In maize, GS has been successfully utilized to select lines from natural populations for tolerance to *Stenocarpella maydis* causing ear rot [77] and from biparental populations for superior yield under heavy infestation of Striga [78].

c) Tolerance to Abiotic Stress

Climate change has increased the likelihood of drought, high-temperature stress during agricultural growth phases, flood, etc., which results in large crop losses [79]. According to Liu et al., a yield drop of up to 6.4% in wheat has been predicted with a 1°C increase in global temperature [80]. Changing cropping patterns or creating varieties that are resistant to abiotic stress are the sustainable and affordable choices in such circumstances to make up for the losses. Traditional breeding techniques for abiotic stressors have accuracy and repeatability issues. Although Beyene et al. [81] reported a gain of 0.176 t/ha for grain yield after three cycles of selection using the rapid cycling GS strategy in eight biparental populations of maize under drought conditions, molecular markers have been used to identify and transfer yield QTLs under abiotic stress conditions [82]. In comparison to the usual breeding plan, where phenotypic selection needed a selection time that was three times higher, this resulted in an increase in genetic gain.

d) Quality Improvement

Quality attributes have different genetic structures, some of which are oligogenically controlled, such grain color, while others, like grain size and protein content, are polygenic in nature [83]. When prediction accuracies in biparental and multi-family populations were compared, it was found that the multi-family populations had higher prediction accuracies for quality-related traits, such as milling and flour quality [84]. Due to physiological compensation, protein content is known to be adversely linked with yield [85]. Grain length and breadth are crucial quality indicators for rice, and 110 Japanese rice cultivars using different GS models were able to predict these traits with an accuracy of 0.35 to 0.45 and 0.5 to 0.7, respectively [86].

ii. GS in oilseeds

Small-scale farmers in developing nations in Asia and Africa rely on oilseeds as a source of income. By bridging the yield gap through increasing resistance to biotic and abiotic stressors and improving quality, the yield potential can still be reached [87]. The report of GS is limited in such potential crops due to the qualitative nature of majority of the features associated to biotic and abiotic stresses. The environment and GxE interactions have an impact on oil quality and yield attributes[88]. Therefore, it is crucial to utilize the proper GS models to take the GxE effects into account for precise selection. Beche et al. revealed that the yield-related alleles were associated with the cultivated elite line, while the protein content alleles were from the wild progenitor, from a hybrid between domesticated and wild progenitors of soybean (G. max X G. sojae) [89]. Their predictive power is more affected by the variation in the distribution of trait-contributing alleles in such crosses. Hu et al. used GS to predict the capacity of soybean embryogenesis and reported a satisfactory prediction accuracy (0.78) [90].

iii. GS in Pulses

In the case of lentil, Haile et al. demonstrated that single-trait GS (STGS) is appropriate in the absence of large-effect QTLs, whereas multi-trait-based Bayes B is the optimum GS model if large-effect QTLs are present in the population [91]. They also claimed that MTGS increases prediction for low heritable traits with GxE interactions. In order to screen rapid culinary genotypes, Diaz et al. examined GS utilizing several populations (RIL, MAGIC, Andean, and Mesoamerican breeding lines) while taking into account quality attributes in Phaseolus, such as cooking time [92]. The variable was strongly heritable (0.64-0.89), and MAGIC population genomic prediction accuracy for cooking time was promising and high (0.55) compared to Mesoamerican genotypes' (0.22) accuracy.

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	Genome-wide association study (GWAS)-based tool for genomic prediction using genome-wide marker data, identifies SNP markers with the lowest *p*-values	R-based	freely available	(http://cassavabase.org/solgs)

		(e.g., top 100 markers) in the GWAS			
2.	solGS	Designed to store a large amount of genotypic, phenotypic, and experimental data.	Based on the Linux operating system.	open-source tool	https://github.com/austin-putz/GenSel.
3.	rrBLUP	Most widely used packages for genomic prediction in animal and plant breeding. This package estimates the marker effects from training datasets	R package based on BLUP, which is a mixed linear model framework	open-source tool	https://CRAN.R-project.org/package=rrBLUP.
4.	BWGS	It is an integrated pipeline based on R	Wide choice of totally 15 parametric and non-parametric statistical models for estimation of GEBV for selection candidates.	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 developed and implemented under the BIGS (Bioinformatics to Implement Genomic Selection) project	Used for estimation of molecular marker–based breeding values of animals for the trait of interes	Uses the Bayesian approach in the background	freely available user-friendly tool	https://github.com/austin-putz/GenSel.
7.	GSelection	Comprises of a set of functions to select the important markers and estimates the GEBV of selection candidates using an integrated model framework	R-based package	freely available	https://CRAN.R-project.org/package=GSelection
8.	lme4GS	Extension of the lme4 R package and can also be considered an extension of the rrBLUP used for fitting mixed models with covariance structures	R-based package	freely available	https://github.com/perpdgo/lme4GS
9.	STGS	Developed for genomic predictions by estimating marker effects, and the same is further used for	Performs genomic selection only for a	freely available	https://CRAN.R-project.org/package=STGS.

		calculation of genotypic merit of individuals, i.e., GEBV	single trait, hence named STGS		
10.	MTGS	MTGS performs genomic selection using multi-trait information comprehensive package which gives a single-step solution for genomic selection using various MTGS-based methods (MRCE, MLASSO, i.e., multivariate LASSO	R-based package, performs genomic selection 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) efforts performed for various traits in different crops using different statistical models, software packages, and next-generation sequencing (NGS) marker genotyping platforms.

S.no.	Species	NGS marker platform	Trait	Population size	Total SNP markers	Prediction accuracy	Model	Software packages	Reference
1	Rice	GBS	Grain yield, flowering time	363	73,147	0.31–0.63	RR-BLUP	R package rrBLUP	[95]
2	Rice	DArTseq	Grain 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	Grain yield, plant height, heading date and 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	Grain yield, Fusarium head blight resistance, 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

Model species like the human, yeast, Caenorhabditis elegans, Arabidopsis thaliana and rice have all had their whole genomes sequenced over the past ten years. Whole genome sequencing is likely to be done on a number of other plant species, including Zea mays, Sorghum bicolor, Medicago sativa, and Musa spp. The ability to control the features that lead to high agricultural yield will be revolutionized by systematic whole genome sequencing, which will provide crucial knowledge on the organization and function of genes and genomes [118]. Through conventional breeding, it takes five to six generations to transfer a trait from a species into high-yielding, regionally adapted cultivars, and selecting the plants with the right mix of features requires planting a lot of offspring. Before the farmers could choose a variety for cultivation, the enhanced lines had to pass a series of multi-location testing. This process takes at least 7 to 10 years. The ability to vary the degree of gene expression as well as the spatial and temporal pattern of gene expression is made possible through genetic transformation, which also gives access to genes from other species that can be used to create transgenic crops. The development of cultivars with stable gene expression requires five to six years after the transfer of the desired genes into the target crops or cultivars (Figure 5).

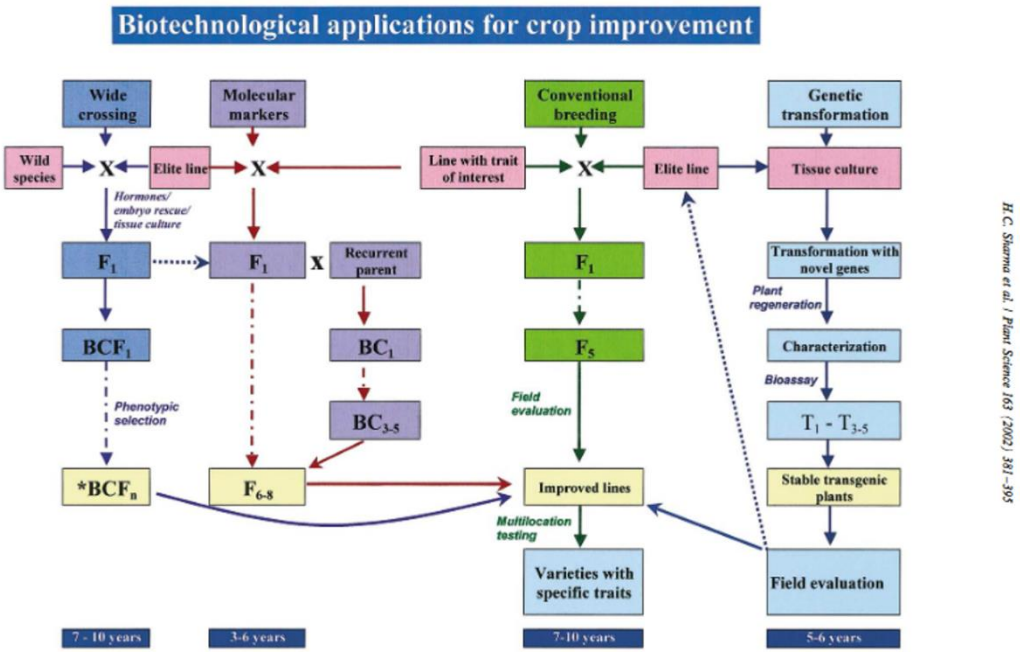

Figure 5 :- A schematic outline of biotechnological approaches in crop improvement. Lines derived through genetic transformation can be released as varieties or used as a donor parent in the conventional breeding. The lines derived from wide crossing can take many generations (BCFn) to obtain homozygous and stable lines, and such material can either be used as improved lines or as a donor parent in conventional breeding or marker-assisted selection.

Resistance against pests, diseases, and herbicides

In 1987, the first transgenic plants containing genes from Bacillus thuringiensis (Bt) were created. While the majority of insect-resistant transgenic plants have been created using Bt d-endotoxin genes, numerous experiments are currently being conducted to use non-Bt genes that disrupt the nutritional needs of the insects. These genes include lectins, chitinases, secondary plant metabolites, and protease inhibitor. Several transgenic plants have now been approved for field testing or on-farm production. Transgenic cotton has been used to successfully control cotton bollworms. The Bt genes have also been successfully expressed in tomato, potato, brinjal, groundnut, and chickpea against the lepidopterous pests. The Bt, trypsin inhibitor, and lectin genes for resistance to these insects are currently being inserted into sorghum, pigeonpea, and chickpea. Under containment glasshouse conditions, transgenic sorghum and pigeonpea plants with Bt and trypsin inhibitor genes are now being evaluated. Additionally, research is being done to create groundnut plants that are resistant to fungi and viruses. The use of transgenic plants with integrated pest management (IPM) techniques will have a significant positive impact on the ecosystem. The creation and use of transgenic plants with insecticidal genes will result in a reduction

in insecticide applications, an increase in the activity of natural enemies, and Integrated Pest Management (IPM) of secondary pests [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 their roots [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

Sucrose phosphate synthase (SPS) is a crucial enzyme in controlling the metabolism of sucrose. Transgenic plants that are regulated by a promoter from the tobacco small subunit to express the maize SPS. When grown with CO 2 enrichment, Rubisco has demonstrated enhanced foliar sucrose/starch ratios in leaves and lower quantities of foliar carbohydrates. This has created fascinating opportunities for modifying the chemical make-up of food grains to satisfy particular needs.

Enhanced yield and photosynthetic effectiveness

Introducing the C4 type of photosynthesis into C3 plants like Arabidopsis [63] and potatoes [64] is an attractive experimental strategy for dramatically increasing crop yield. Due to the oxygenase reaction of ribulose 1, 5-biophosphate carboxylase/oxygenase (Rubisco) and the accompanying loss of CO 2 from photorespiration, C3 photosynthesis is hampered by O 2 inhibition. The activity of phosphoenolpyruvate carboxylase (PEPC), an enzyme that fixes ambient CO2 in the cytoplasm of mesophyll cells, is a crucial component of this mechanism. The entire maize PEPC has recently been inserted into the C 3 plants via an Agrobacterium-mediated transformation method. The type I chlorophyll a/b binding protein of light harvesting complex II can be reduced down to degree oilseed rape that has undergone sublethal freezing during seed development

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, vitamins, iron, and amino acids. The selection of target traits is influenced by the end users, producers, and agro-based industry. transgenic rice with elevated levels of iron has been produced using genes involved in the production of an iron binding protein that facilitates iron availability in human diet. Decreasing the amounts of oligosaccharides (such as raffinose and stachyose) improves digestibility, and decreases the degree of flatu lence during digestion. Transgenic technology can also be used to remove anti-nutritional factors [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

In underdeveloped nations, where the need to enhance food production is most pressing, access to knowledge and experience will be a crucial element in the application of biotechnology for long-term food security. The Rockefeller Foundation, UNESCO, the International Cooperation Program of the European Union, the International Service for the Acquisition of Agrobiotech Applications (ISAAA), and the International Service for National Agricultural Research (ISNAR) are among the organizations attempting to play a significant role in the technology transfer from public and private sector institutions in the developed to the developing world. To address the needs of end-users in developing nations, particularly in Africa, international support for these efforts as well as the creation of several others will be required. The creation of appropriate regulations and a legal framework for the application of biotechnology in the production of sustainable food requires assistance and encouragement from the 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, understanding plant 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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