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Advancing Maize Improvement: A Review of Genetic Approaches and Breeding Strategies

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ABSTRACT

Maize (*Zea mays* L.), commonly known as corn, is one of the most important cereal crops worldwide, significantly contributing to food security, livestock feed, and numerous industrial applications. Major advancements have been achieved in identifying and applying genetic strategies to enhance maize production, stress resilience, and nutritional quality. This article reviews traditional breeding techniques, including crossbreeding and recurrent selection, alongside modern genomic approaches such as marker-assisted selection (MAS), genomic selection (GS), and Clustered Regularly Interspaced Short Palindromic Repeats/Cas9 (CRISPR/Cas9). These genomic tools complement traditional breeding to accelerate genetic improvement, enhance tolerance to abiotic and biotic stresses, and support the development of climate-resilient maize cultivars. Additionally, the roles of molecular markers, doubled haploid technology, and transgenic methods in maize improvement are discussed. Critical issues such as genetic erosion, sustainability challenges, and the preservation of genetic diversity are also examined, emphasizing their importance in sustainable maize breeding programs. Emerging trends, including multi-omics approaches, artificial intelligence, and participatory breeding, are explored as innovative solutions to meet evolving global agricultural demands. This comprehensive analysis provides an overview of the current state of maize enhancement research and highlights potential directions for future advancements.

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INTRODUCTION

Maize (*Zea mays* L.) commonly referred to as corn domestically and internationally, is one of the world's leading cereal crops being used as staple food, feed and raw material in several industries.

Maize has evolved and augmented in agriculture within the region of southern Mexico after having been tamed from teosinte about 9,000 years ago. In today's world, essential for billions of people, it plays a major role in

developing many countries' economies. The demand has increased for various uses such as populace growth, diet change, bio-energy, and climate change which are increasingly the trends in the world. This demand can only be met through sustainable improvement of maize, especially through the enhancement of genetic progress and further work on new techniques on breeding [1]. Modern selective breeding practices have however enhanced the yield and adaptability of these crops by a greater magnitude within the last century. The hybridization of Maize began in early 20th century and it transformed the production of the crop causing an increase in the yields and the ability to grow it in diverse environmental conditions. However, the prospects for further improving traits of cultivated crops, achieved by means of traditional plant breeding, are rather limited due to the above reasons. This paper lays emphasis on plant diseases, pests, heat, drought stress, and salinity stress which have been found to be on the increase in the backdrop of climate change. In addition, expectations from society from a crop have evolved over the years to include quality for feeding, health as well as endurance in the face of certain environmental conditions. Therefore, there is increasing pressure to apply technologies and superior breeding approaches toward the improvement of maize [2].

Molecular breeding was reported early but with improved technologies in improvement of this crop; the situation has improved. Through uses of MAS, QTL mapping, and GWAS, the breeders have been in a position to give a nod to favorable genes with desirable attributes such as yield, drought tolerance and disease resistance among others. They have also enabled breeding to be improved by making it easy that desirable characters be selected genetically as compared a functionalist approach where it takes time to select for the right traits [3]. Another ideal method that has been embraced diligently in maize breeding is the genomic selection (GS). This approach involves the use of tools such as marker-QTL link maps with erDNA's to facilitate the identification of optimal genotypes which means that the commercial traits that are ideal for crossing with the marker can be efficiently chosen. High-throughput phenotyping and computational methods have the capacity of shortening the breeding cycles and enhance selection accuracy for high-throughput phenotyping and computational methods difficult to phenotype traits [4]. Additionally, CRISPR Cas 9 system provides a high level of efficiency in the modification of target genes in the genome of the

maize. These methods allow for the generation of new phenotypes with great target gene specificity and low side effect impact, which may be of great value for the development of improved adaptation to biotic and abiotic stresses, diseases, and nutritional values. Likewise, transgenic technologies such as the genetically modified or GM maize has significantly contributed to pest resistance combined with herbicide tolerance to deprive biotic and abiotic stress impacts by availing instruments to the farmers. Nevertheless, there are still several obstacles regarding maize genetic improvement despite the benefits that stem from these modern development. One of the major threats advised by genetic issues is the emergence of genetic bottlenecks and loss of daring genes due to the increase in the number of purebred chicken lines. One of the other challenges includes climate change that alters factors such as temperature, water availability, and pests. To achieve its goal, maize breeding programs must not only increase the yield of maize but also vary the type of maize according to the changing climate conditions caused by climate change. Finally, there are socio- economic factors, such as lack of access to sources of advanced breeding technologies and the legal requirements of genetically modified organisms (GMOs) that still remain a barrier to the use of such innovations particularly in the resource-poor systems [5]. In this review, the current perspectives of maize growing are discussed based on the approaches and breeding techniques that have been applied during the development of improved genotypes. Most of the contents of the review are devoted to principles and application of molecular breeding, the strategy of genomic selection, potential of gene editing and consequences of transgenic approach. We also explore the problems facing the maize breeding programmes; the genetic diversity concerns, the adaptation to climate change and social economical factors to technology. In eng , this paper literally reviews and discusses the prospects of maize breeding based on the cutting edge technologies to meet the increasing global demands of agriculture and challenges posed by the growing problems associated with it.

Conventional Breeding Approaches

They have always been the oldest technique of breeding crops, and this equally applies to maize. These methods are the method of inheritance and the method of selection and have been used to breed the high yielding varieties of maize that is grown in the world today. Although

information on molecular breeding and other advanced techniques is increasing mass selection, hybrid breeding, and OPVs are also widely used in maize improvement. This section details these said traditional breeding programmes, covering issues such as historical background, methods, performances, and constraints by recording them to the number seven [6].

Mass Selection and Pure Line Development

If we are to categorise the methods of crop improvement, then mass selection could be accredited to being one of the oldest given that the practice of agriculture can be dated back to several centuries. This is one of the phenotypic selection techniques in that, the best individuals are selected from a population and used to breed the next generation. Farmers have been practicing mass selection unconsciously in early times by picking out certain plants from the maize plants that had better yield, better grain quality than others or even those plants that were resistant to a certain disease. With the increase in the process, the number of well-defined steps taken increased, and thus the process was more enhanced by giving rise to the development of the pure line. In case of mass selection, the breeder used to select 10-20% of plants with superior characters like larger ears or drought resistance and collected seeds to be used in the next season planting.

This goes on for several generations intending to increase the likelihood of the favored alleles in the breed. As mentioned above, although mass selection can be beneficial for the improvement of the population, it is not very efficient for complicated polymorphic traits where accurate genetic control is needed [7].

Pure line development is even more sophisticated than mass selection; it entails the picking of individual plants and reproduced through selfing for several generations. It is used to choose one genotype that is pure for all the genes of interest hence having a population that is genetically similar. A pure line variety is generally quite uniform and there is little differentiation between one generation and the other. But the limitation of mass selection and pure line development method exists only on the fact that they are unable to create new variation. Therefore, line varieties that are absolutely pure can lead to menace of inbreeding depression, hence reduced vigor after sometime [8].

Hybrid Breeding

This article being a contribution to the advancement of conventional maize breeding, this shows that hybrid breeding is a great improvement. From the early of twentieth century heterosis or hybrid vigor emerged thus changing the way maize is bred and produced. Heterosis in other words is hybrid vigor, generated through crosses between two genetically dissimilar parents, showing better vigor in terms of growth, yield, and resistance against diseases as compared to the parents. With this realization that crossbreeding could produce offspring that possessed better attributes, the advancement of hybrid maize came into the limelight in the modern production of maize [9]. Hybrid breeding in turn involves crossing two different inbred parental lines. Hence two types of hybrids arise. First generation hybrids commonly referred to as F1 hybrids are usually better than both parental lines in all aspects such as yield, resistance to pests and diseases, and hardness.

This situation can be attributed to genetic improvements caused by cross breeding since it boosts up the total fitness of the hybrid crops. The concept of hybrid vigor can be most beneficial for maize since this crop receives additional resistance to various diseases, enhanced usage of resources, and increased endurance to harsh environments. A significant innovation that transpired in the early part of the twentieth century was the cultivation of hybrid maize. However, the commercial production of hybrid cultures of maize began in the 1930 and 1940 and has been quickly adopted by farmers in the United States. Hybrid maize enjoyed relatively high demand from the market due to higher yields as opposed to the OPVs or local varieties known as land races. Yields of hybrids, for the same period of time, were 20-30% higher than those of OPVs; hybrids provided better and more uniform fruits which were also less susceptible to disease [10]. However, this sort of breeding comes with its own set of problems as well. The biggest disadvantage being that hybrid maize used in breeding must be crossbred every generation since hybrids themselves are not true breeding plants. It implies that farmers require to use hybrid seed each season, making hybrid maize to be more expensive than OPVs. Moreover, the performance decreases in further generations if hybrid seed is sown rather than bought and planted in the soil again. This increases the probability of reliance on commercial production of seeds which is expensive and thereby puts off the producers in areas of low resource endowment.

since they may not afford the hybrids' expensive seeds.

Open-Pollinated Varieties (OPVs)

Various approaches for male sterility, especially open-pollinated varieties (OPVs) are also playing significant role in maize improvement. OPVs are those that reproduce through wind or insects brought pollen, and while certain plants in each particular category are used, the seeds are not deliberately crossbred with other desirable plants. These varieties are genetically polymorphic, that is more than one genotype is found in the population which make them to fit in this environment. OPVs have served for decades as the basis of breeding for smallholder farmers especially in low HLPE farms because of their low cost and possibilities of seed saving from one postharvest season to another [11]. The importance of OPVs resides in its availability, specifically the flexibility of this type of vessel. When farmers do not have the capital to secure hybrid seed yearly, OPVs are a cheaper solution available in the market. Farmers can therefore use their produce seeds in subsequent planting seasons, this will help them cut on the costs of buying seeds from other parts. Hybrids on the other hand are less genetically diverse than OPVs and therefore have less opportunities to adapt to the ecological changes like drought or high temperatures. This flexibility makes OPVs desirable in varying climate conditions outperforming in case of complementary stresses that affect farmers. Nevertheless, OPVs also have certain disadvantages. Since OPVs are self pollinated, they possess more genetic variation with the population thereby having some vices like fluctuation in yield, disease resistance and maturity. Hence, OPVs are less uniform than the hybrid types and may not do so well under high input, commercial production. Moreover, to make sure that OPVs produce desirable characteristics, it becomes relevant to continue selecting them and managing their genetic quality. There are circumstances that OPVs may need more attention in terms of management to ensure that they are not genetically deteriorated due to the seed saving practice [12]. However, OPVs still have significance in maize production especially in the low input African farming systems. More recently, traditional breeding techniques which have been used to develop OPVs in the past have again come under focus; this is mainly in a bid to develop recurrent selection for desirable characteristics that will increase the stocks' beneficial traits without too much loss of genetic variation. Hitherto, the release of improved OPVs with

higher yield potential and resistance to those pests and diseases could go a long way to solve the problem that hybrids denied by smallholder farmers due to high cost.

Molecular Breeding Techniques

This paper discusses how molecular breeding has provided a fast, accurate and scientifically informative way of improving crops as compared to traditional plant breeding methods. These have include marker and genomics for early generation realizing marker aided selection and speeding up the breeding process for the introgression of the desirable traits into the elite varieties. In the case of maize, the use of molecular breeding has been used in combating some of the most important constraints like drought, diseases and yield instability. This section gives a comprehensive account on the fundamental molecular breeding approaches that have been used in maize; including marker-assisted selection (MAS), quantitative trait loci (QTL) mapping, genome-wide association studies (GWAS), and marker-assisted recurrent selection (MARS) [13].

Marker-Assisted Selection (MAS)

MAS is one of the oldest and most frequently used molecular breeding techniques. It employs the means of identification and utilization of Molecular Markers which are in a close linkage to the traits of interest. The fundamental concept of MAS is that simple sequence repeats (SSRs), single nucleotide polymorphisms (SNP), or insertion-deletion polymorphisms (Indels) can be mirror images of the wanted alleles so that selection can be made for individuals for favorable genotypes without necessarily requiring phenotypic data. This reduces breeding cycles and raises selection intensity particularly when the phenotypes cannot be effortlessly measured or have low heritability or latent appearance at the later development stages of the plant. MAS has proven very useful in maize improvements especially on the aspect of disease resistance and abiotic stress. For instance, the MAS for the introgression of resistance genes against the maize streak virus and northern corn leaf blight has led to the production of relatively resistant genotypes with some yield discount. Likewise, other markers associated with drought tolerance QTLs have been used in breeding of high yielding drought adapted germplasm in maize [14]. An example is the Water Efficient Maize for Africa (WEMA) that adopted MAS to incorporate the drought resistant genes into easy-adaptable commercial hybrids

resulting in improved yields in the sub-Saharan region [15]. Another good example is use of MAS in biofortification for instance, on provitamin A content in maize. After several marker-assisted backcrossing procedures, breeders were able to incorporate the desirable alleles of the crtRB1 gene resulting in the development of new maize lines containing improved provitamin A. In general, MAS has become an integral part of the modern maize breeding process proving that although molecular approaches can substantially supplement traditional selection methods, they can also bring about significant positive changes to the maize yield.

Quantitative Trait Loci (QTL) Mapping

Hence, Quantitative Trait Loci (QTL) mapping is considered as one of the basic approaches used in the identification of traits regulated by more than one gene. QTL mapping is a process of identifying and mapping those loci in a particular organism which are responsible for the majority of the distinctions in the phenotype of an organism belonging to a specific population, generally descendent of a cross between two genetically disparate lines of that species. By one, there are two main approaches towards the analysis of QTLs and these are linkage mapping and interval mapping [16, 17]. Linkage mapping makes use of a molecular linkage of markers and traits within the pedigree based population while on the other hand; interval mapping, uses statistical models to infer the probability of the existence of QTLs in any marker intervals, which offers more magnitude and precision on the localization of QTLs [18]. In maize, QTL mapping has been very useful in identifying the genetic control of some traits like drought tolerance, resistance to diseases or even grain yield. QTLs linked to drought tolerance has been developed-the most important plant characteristic as climate change occurs. For instance, identification of 'qDTY1.1' and 'qDTY2.2' has helped the breeders to use marker assisted selection to introduce desirable trait in elite drought tolerant varieties. These QTLs give access to such abiotic stress-aided high grain yield by increasing the field if factors such as root structure, flowering profusion, and kernel stuffing [19]. Additionally, will QTL mapping helps in the understanding of complex alternatives as polygenic and interactive in the presence of environmental factors. Meta-QTL studies that combine results of different studies have also helped to fine map some of these important QTLs and increase the value of this approach

for breeding purposes [20]. Most of all, the genetic dissection of flowering time escalates the understanding of QTLs that govern photoperiod sensitivity and adaptation in different agro-ecological environments helping expand the boundaries of growing environments for Maize. Though the QTL mapping has given the foundation for plant breeders, the outcomes from this methodology suffers from low resolution and limited transferability across different germplasm; this led to the simultaneity of high-density genotyping and use of sophisticated statistical methods that pointed towards genome-wide association studies (Gwas) that enabled plant breeders [21].

Genome-Wide Association Studies (GWAS)

As a result, whole-genome association study (GWAS) can be consider as a revolutionary approach which provides a combination of high-resolution trait locus mapping by capturing natural variation among germplasm collections. Another advantage of GWAS compared to the QTL Mapping method is that it does not require construction of special population but analyze the historical close- inbred individuals recombination. The statistical basis of a GWAS is to find the significance of the link between genetic markers (preferably SNPs) and a given phenotype and to control for confounding factors such as population stratification and relatedness to reduce false positives [21]. In maize, GWAS has been especially important because it has revealed the genetic control of many traits associated with agricultural production, abiotic stress, and biosynthesis of various compounds [22]. A panel of 200 loci was newly implicated in drought tolerance, some of which were confirmed in the previous QTL mapping approach and the others which for the first time have been mapped in the bi-parental populations. These have also added value in the breeder's arsenal, which makes it possible to use multiple desirable alleles in the development of the organism through genomic selection techniques. Moreover, GWAS has enabled the segregation of yields' features that are consistent with the nutritional value. For instance, association mapping of kernel carotenoid content led to identification of specific genes like lycopene epsilon cyclase (lcyE) and crtRB1 which can be used for the marker-assisted biofortification. Moreover, GWAS research on root traits have identified potential genes that are linked to improved water and nutrient uptakes which are important in the development of drought and low input tolerant maize [23]. GWAS in maize improvement has

beneficially relied on availability of large amount of genotypic data such as MaizeSNP50 BeadChip and GBS techniques in combination with the large phenotyped mapping populations like MAPs and NAMs. However, the use of GWAS also has some limitations that come in form of detecting rare alleles and establishing causality between SNPs and traits. And so to overcome these limits, other lines of studies such as fine mapping and functional validation are used to bring the identified associations into targets that can be used in breeding processes [24].

Marker-Assisted Recurrent Selection (MARS)

Marker assisted recurrent selection (MARS) is a strategy considered to be closely associated with both marker assisted selection and recurrent selection. In MARS, multiple QTLs linked to a target trait are grouped and recombined over generations so that the action of the multiple genes on the polygenic trait is accumulated. Different from the traditional MAS that has limited coverage at few QTL, MARS operates throughout the whole genome and keeps the genetic variation for continuous genetic improvement [25]. This approach entails typing the first generation of the plant for all the favorable allele at multiple loci, to arrive at the plant with the best possible set of genes and then cross them to generate the next round of breeding population. This process continues for successive generations and this gradually gets loaded into the populations the desired amount of good alleles. In maize breeding, however, MARS has many uses in increasing yield under both favorable and sub-optimal environments as a sign of its prowess to solve complex polygenic traits that inform agronomic value [26]. For instance, CIMMYT and other collaborators have used MARS for identifying drought adaptive maize that is suitable for SSA. Surely, they constructed multiple cycles of selection and recombination and created substantial yield gains under water-limited environments with a reduction on its yield under water ample conditions. Likewise, MARS has been used with diseases, like maize lethal necrosis (MLN) where the assembly of minor resistance genes of the genome has been shown to be more effective and wide ranging as opposed to the main resistance genes. However, as a consequence of interacting with MARS protocols, GS is becoming more incorporated with equally higher precision and selection effectiveness. Through the use of high-throughput genotyping, state-of-art statistical methods and recurrent selection cycles,

modern MARS programs can be highly effective and progressive approach for enhancing maize genetic improvement [27]. Techniques of molecular breeding such as MAS, QTL mapping, GWAS and MARS have played a great role in improving maize breeding that has given a genetic improvement of the plant through aiming and targeting particular genes. Each of them is valuable and focuses on different aspects of genetic work, and their further interaction will help to achieve greater results in addressing the modern challenges of food security and climate adaptation in the coming decades [28].

Genome Editing and Genetic Engineering

Genetically modified crops or the technique of genetic manipulation of genes has changed the modern crop improvement by opening a way to control the plant genome more accurately and doing it at a faster rate. These technologies add value to the improvement of desirable qualities in the quality of MAIZE such as stress tolerance, disease containment, and nutritional improvement apart from reducing on the use of chemicals and adopting sustainable resource use. The chosen prominently anti-GMO writer is engaged in detailing the major genome editing techniques such as CRISPR-Cas9, transgenic approaches to maize genetic engineering, the regulatory systems, and the social aspects of modifying genes in maize [29].

CRISPR-Cas9 and Related Systems

Maize (*Zea mays* L.) can be said to be the most cultivated grain crop all over the world. It has also been adopted mostly in various parts of the world due to its flexibility for use as well as its ability to grow in different environmental and other conditions of the soil. Due to the aforementioned limitations of random mutagenesis, relevant targeted genome-edited methods began to be explored in the last decade and have now advanced significantly. These have enhanced the fidelity of gene editing by nearly one thousand times through improving the methods mentioned above.

Some of the first targeted editing techniques such as the zinc-finger nucleases (ZFNs) and TALE nucleases (TALENs) were only partly effective but they possessed certain constraints [30]. Traditional methods include those that have been in use for a longer period, they are complex, rigid when it comes to operation and very

expensive relatively to the advances methods such as the CRISPR/Cas9 system. The system is composed of universally used Cas9 nuclease protein and a single guide RNA (sgRNA) that includes a target site of 20 bp and a hairpin junction (23). With the help of the sgRNA, Cas9 endonucleases make a double strand break (DSB) at a specific twenty nucleotide target sites called genome locus which is near the NGG sequence known as the protospacer adjacent motif (PAM), where N could be any nucleotide. Cas9 contains two catalytic nuclease ends:

RuvC end and HNH end which is involved with the creation of DSB at precise locations due to which the specific target site is identified by sgRNA.

These DSBs can be repaired in two ways mainly non-homologous end-joining (NHEJ) and Homology-directed repair (HDR) as depicted in figure 1. In organisms like maize it is pertinent to note that a 20 bp sequence is sufficient to be allele specific in single copy genes. The small sized sequence makes it easy to design the sgRNA [31].

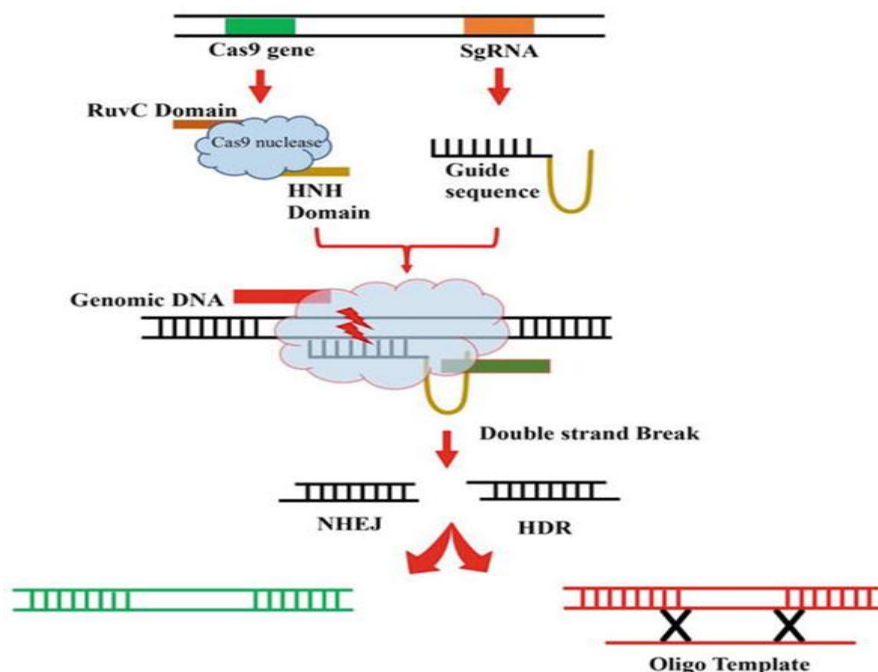


Figure 1: A Visual Model Depicting the Genome Modification Process of the CRISPR/Cas9 System [14]

Compared with TALENs which were 9.1%, the CRISPR/Cas9 system was 13.1% in maize protoplasts. The targeted Org 15 gene mutation efficiency of the two systems was added in supplementary table S2. Moreover, usage of the CRISPR technology to mutate the maize depicting a rate 10-20 times more than that of homing endonucleases. A recent development involves the creation of a convenient public system for maize known as “ISU Maize CRISPR” that is meant to be used in site-directed mutagenesis in maize. It uses both *Escherichia coli* cloning vector as well as *Agrobacterium* binary vectors and it can accommodate up to four sgRNAs for single or multiple gene editing. It has brought a new advancement on how CRISPR/Cas9 needs to be adopted in crops, based on a study on maize specifically [32]. To deliver the CRISPR/Cas9 system that includes the sgRNA and Cas9 protein, it is possible to use transient methods or a stable transformation method in maize cells.

Moreover, this method permits the multiplexing type of operation as it combines the ability to mobilize multiple modes of analysis to access different addresses at the same time. This is an advantage over some other nucleases since CRISPR/Cas9 is able to target methylated DNA, making it suitable for use in plants [33].

Transgenic Approaches

Genomics is dedicated to the sequencing, characterization, and comprehensive exploration of a plant’s genetic makeup, encompassing its composition, structure, functions, and intricate networks within the genome. Novel approaches to plant breeding have been made possible by developments in plant genomics, which effectively enhance and expedite various aspects of the breeding process. These innovations include techniques such as marker-assisted selection, gene pyramiding,

association mapping, breeding by design, genomic selection, and more [34]. Genomic regions linked with fodder traits were pinpointed, and a prediction study on genomic regions was carried out using 1026 DH lines and 276 elite lines as prediction sets from bi-parental crosses [35]. Proteomics involves a comprehensive investigation of proteins within a biological system, encompassing plants and animals, at a specific moment in time. The analysis of proteomics serves the purpose of quantifying the abundance of various proteins, discerning alterations resulting from diverse post-translational modifications, and elucidating their functions and localization. It offers a snapshot of diverse metabolic processes, their ensuing interactions, and their impacts on other regulatory pathways. Consequently, proteomic studies are indispensable for deciphering the diverse reactions within pathways under various stress conditions and timeframes [36]. The Proteomics field has attracted considerable interest from scientists seeking to examine physiological differences at the proteomic level under varying stress conditions. Plants use the development of defense-associated proteins (DAPs) in conjunction with the down-regulation of redundant proteins as a stress-reduction and energy-saving strategy. Metabolomics is a cutting-edge biotechnique that seeks to identify functionally active metabolites, clarify their functions, and provide insight into the various biochemical processes that occur in plant genotypes and the phenotypic expressions that follow. All metabolites, primary and secondary, with a molecular weight of less

than 1500 Da, as well as their precursors and intermediates within the corresponding metabolic processes, are included in the metabolomes. Based on their particular goals, metabolic investigations can be divided into two categories: targeted and untargeted. The goal of targeted metabolomics is to precisely quantify one or a small number of metabolites from a predetermined list of recognized compounds [37]. This method helps identify metabolites linked to particular features because of its high sensitivity and quantitative nature [38]. Untargeted metabolomics, on the other hand, increases the possibility of identifying unintentional impacts by measuring the mass spectrometric properties of metabolites with unknown identities. The application of metabolomics has proven invaluable in understanding how maize plants respond to various stress conditions i.e., heat, salinity and drought. More importantly, a study by Ganie et al. revealed metabolic pathways impacted by phosphorus stress situations, offering insights into strategies for improving phosphorus efficiency. The analysis, conducted using gas chromatography-mass spectroscopy, the investigation revealed a drop in fatty acids like cholesterol and stigmasterol, which are critical for membrane fluidity, and an increase in sugar alcohols like glucitol and mannitol under P-limitation, which are essential for membrane fluidity. In cases of severe phosphorus starvation, plants will scavenge phosphorus from these fatty acids, disrupting membrane fluidity. Additionally, elevated levels of serine and glycine indicated an increase in photorespiration rates [39].

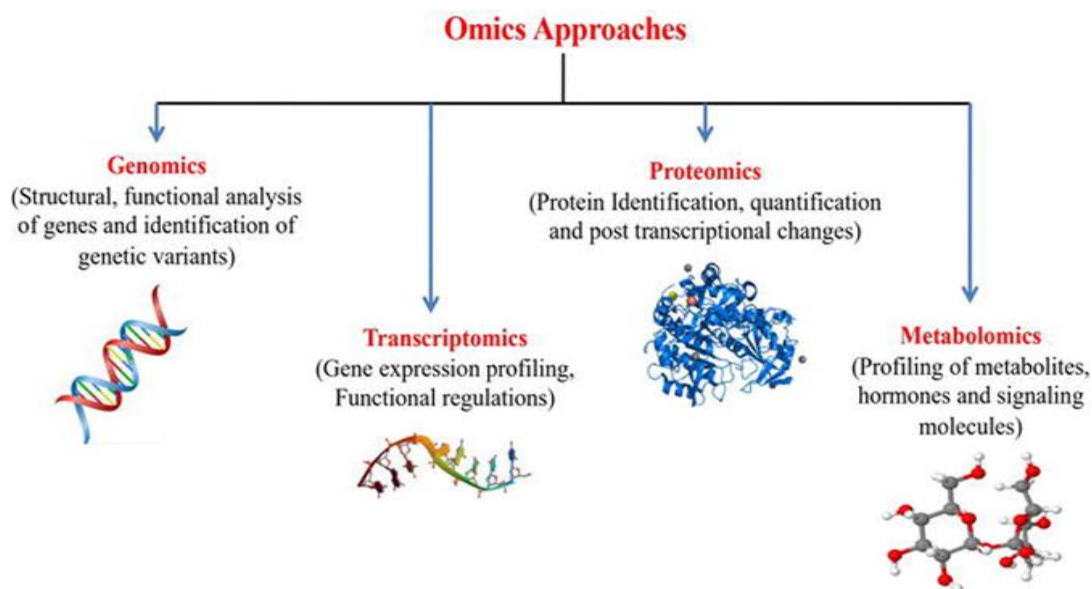


Figure 2: Representation of Different Omics Approaches used for Maize Crop Improvement [14]

Emerging Technologies and Future Directions

As of now the field of maize breeding is relatively young and the new solutions are opening new possibilities in increasing productivity, as well as develop resistance in the face of current problems and challenges. These are some of the technologies, which on the frontier of genomic, data and system biology, and engineering hold the potential to redefine maize breeding for increased vigour, rates of improvement, and directions. Such technologies as systems biology and multi-omics integration, high-throughput phenotyping, and synthetic biology are proposed in this section as important candidates of post genomics technologies likely to influence the transformation of maize breeding in the future [40].

High-Throughput Phenotyping

High-throughput phenotyping is another technologically innovative development in maize breeding that involves the mass evaluation of plant characters. Phenotyping has many years now being a time-consuming exercise which has called for field trials and measurements on standards such as height of plant, size of a leaf, yield of a grain, and stress resistance. With the development of new technologies in phenotyping it has been easier and accurate results has been achieved in phenotyping hence reduced time and cost that was used in the traditional phenotyping. Drones and unmanned aerial vehicle (UAVs) which are also referred to as unmanned aerial systems (UASs) are also actively employed in high-throughput phenotyping to acquire big data from maize field. Multispectral, hyperspectral, thermal imaging will be mounted on the drones that are used for to monitor plant health, growth patterns and stress levels [41]. For instance, due to hyperspectral imaging, there is the likelihood of identifying differences in plant health status which is usually preceded by differences in genetics such as chlorophyll content or water stress or nutrient stress. The data can then be analyzed by the use of machine learning techniques to predict the relationship between genotype and phenotype from the genotype data [42]. Besides drones, other GBSs include phenotyping trolleys, automatic cameras, and sensors for soil moisture among others that are also used to monitor the growth of the maize plants in a real-time basis. These can record all different phenotypes such as the area of the leaf, architecture, height of the plant and besides this, it can

record the climate data such as temperature, humidity of the soil etc. The use of these sensors in phenotypic data together with artificial intelligence and big data analysis in particular help breeders to identify superior plants that harbor desired phenotypic attributes [43]. This article has, therefore, found machine learning to be of great importance in high-throughput phenotyping since it aids in analyzing a large amount of data [44]. The traditional phenotyping techniques face a lot of challenges especially on the wave of high-throughput phenotyping systems simply because of the amount of data handled. The CNNs and random forests can be trained to learn images and sensor data, subsequently determining critical features of plants and make forecasts of the performance. The use of such phenotyping platforms with machine learning in plant breeding can therefore offer the opportunity to speed up the rate of selection for the desirable plant characters especially in the case of complex traits such as yield and tolerance to stress [45]. Moreover, HT phenotyping can be linked with genomics data to make genomic-phenotypic prediction models. These models can anticipate the performance of the various genotypes and phenotypes of maize varieties availed to the breeder who in turn selects the best ones that will be used for the next generation. Another advantage of having this environmental data incorporated in such models is that breeders can also estimate the performance of various maize varieties under varying climatic conditions hence enhancing the breeding programs.

Synthetic Biology and De Novo Domestication

System biology was defined as an emerging discipline that focused on engineering biology to design and construct new biological components, devices and systems. Synthetic biology can be the most effective strategy in maize breeding, not only because additional genes can be introduced in the genome but also because the desired traits can be complex and difficult to breed for or modify. For instance, synthetic biology can be applied to designer metabolic pathways or revamp existing ones with the purpose of synthesising useful commodities from maize plants including biofuels and pharmaceuticals. This could change the position of maize from being just a food grain to the unlimited production of industrial and medical commodities [14]. Another one of the ideas proposed in connection with synthetic biology is that of de novo domestication. De novo domestication means that one takes a wild plant and creates in it factors that are found

in domesticated plants such as high yield, disease tolerance and nutrition value. This could be applied in order to develop new varieties of maize suitable for particular conditions or with characteristic that are nonexistent in the ordinary varieties. For instance, it has been sought to genetically manipulate maize plants to grow in conditions of salinity or extreme temperatures since genes from other related species can be used to achieve this [46]. It also allows for the design of artificial metabolic pathways that can produce other useful substances, which have their uses in industries. For example, maize can be developed to contain higher production rates of bioplastics or other bio products as a substitute to those produced from fossil fuels. third, through increasing some specific bioactive compound in the stubble, synthetic biology contributes to increase nutritional quality of maize for utilization in mitigating malnutrition in developing countries [47]. The use of the biotechnology combined with GE technologies such as CRISPR-Cas9 may help in the early development of new maize varieties with desirable characteristics. Through gene editing and synthetic biology, there is creation of high value new plant architecture maize crop in the desired improved attributes of resilience, productivity and sustainability. This has opened up new vistas of opportunities for maize breeding for enhancing the quality and increasing its adaptation to changeability, beside, as it has been posed as the world's largest food the ever-growing issues of the global climate change, food security and sustainability [48]. In the lights of development reality, the new technology changes the maize breeding as systems biology, high through put phenotyping, and synthetic biology. These technologies have made it possible for the breeders to gain new ways of dissecting the molecular genetics of the requisite traits, increase the rate of breeding and create new traits that can improve maize production results and resistance to biotic and abiotic stresses. As these technologies develop more and more, they have the possibility to help increase the progress in maize breeding, solving the current problems of the world agriculture.

Challenges in Maize Genetic Improvement

Over time, genetic improvement in maize has recorded tremendous growth but studies have revealed some of the challenges that are likely to affect the crop. The others include genetic bottlenecking, climatization, and socio-economic factors that hinder the spread of new forms of

technologies. These challenges have to be overcome to guarantee that maize breeding remains on par with issues of food security, sound environment and resilience in the face of the challenges the world is most likely to present now and in the future [49].

Genetic Bottlenecks and Loss of Diversity

Another problem indicative of threats to genetic improvement of Maize is the problem of/with genetic drift which leads to genetic bottlenecks. Since breeding programmes concentrate on such qualities as yield, resistance to pests, and tolerance to stress, it is possible to speak about genetic Uniformity. This can lead to low genetic variation which is important for the long term productivity of the maize crop for adaptation to new pests, diseases and any adverse ecological conditions. Using few and preferred varieties or breeding lines in cultivation and breeding reduce the gene variation that can be used in breeding in the future and the crop's capacity to adapt to new problems [50]. Genetic bottlenecks can also lead to inbreeding depression whereby increase in homozygous deleterious alleles causes vigor, fertility, and stress resistance to decrease in the population. This is prevailing for maize because it is a self-pollinated crop, implying that the prospects of inbreeding is higher. To avoid this, breeding programs must ensure that the landraces, wild relatives or germplasm from the distant sources are incorporated in its programs. To overcome these challenges, molecular markers, genomic selection as well as use of wide crossing methods can be used to incorporate new sources of variation [51]. However, the Maize diversity is also lost when farmers switched to commercial hybrid seeds from traditional methods of growing maize or adopting the improved seeds. Recently people began using hybrid varieties that belong to new plant type which have high yield potential resulting in a decline in the use of other traditional varieties suitable to local environment. It will be crucial to make use of the preserved existing germplasm in landraces in order to ensure that the corn plant is able to adapt to future problems [52].

Climate Change Adaptation

Other factors that pose a challenge in the improvement of maize genetics include the effects of climate change. As a crop, maize is highly susceptible to environment conditions especially temperature and water stress and therefore is exposed to the increasing instances of abiotic

stresses like drought, floods, heat and others. In light of the changing climate conditions, seed producers need to produce maize varieties that will grow in the new conditions and in new wave of changes. However, selection for climate change adaptation involves dealing with genotype by environment by management interactions (Genotype $\times$ Environment $\times$ Management Interactions, GEMs) [53]. However, the nine most necessary priorities out of the 38, garnered strong conversation in the article include the following; One of those was the development of drought tolerant maize varieties. Drought is one of the main factors of reduced yield in maize, especially in areas where irrigation is not possible. Although, maize breeding endeavors have advanced in identifying and incorporating genes responsible for drought tolerance, developing a drought-resistant maize is still a challenge. Moreover, the stress factors that need to be taken into consideration by the breeders are heat stress and waterlogging since these characteristics have become critical in the future [54]. For the second sphere of adapting to climate change, there is the need to work on enhancing resistance to disease/pests affecting maize. Due to climate change, climate conditions for pests and diseases are likely to change hence bring new risks in production of maize. For instance, climate change may put pressure on the fall armyworm which affects maize by increasing temperatures and therefore causing the spread of the pests in areas it would have been uncommon before. Developing new varieties of maize that are immune to all these increasing threats will be crucial in feeding the world in the future climate [55].

Socio-Economic Barriers in Technology Adoption

Yet socio-economic constraint continues to foster the limits in the use of improved varieties of maize genotype especially in the developing world in spite of the gains registered in genetic improvement. There is also the problem of the tendency to high cost of the new technologies, for instance in the case of GM crops for situation may be too expensive for most of the smallholder farmers. For instance, genetically modified maize seeds that are resistant to pests or herbicides are usually costlier than traditional seeds this denies the resource scarce farmers the chance of affording them [56]. Besides the issue of seed costs, there are other factors likely to hinder the implementation of new technology such as lack of information, physical facilities and other

services required for the change. For instance, high yielding maize varieties or genetically modified crops may be seized to result in enhanced yields if accompanied by proper package of practices, knowledge, and advise as well. In a place that such resources are scarce, the farmers may be discouraged from adopting new technologies despite the fact that these technologies have some benefits in terms of yield and resistance to pests [57]. There are also regulatory disadvantages which restrain the use of improved maize variety breeding techniques especially those involving the use of genetically modified crops. The approval systems in many countries is long, costly, and uncertain when it comes to GM crops. This makes it influential for both the breeders and farmers and may actually result to the delay in the adoption of new, maybe improved, varieties. This is another factor of the adoption of GM maize because the public has a perception of genetically modified organisms. In environments where consumers and other stakeholders have negative attitude towards GMOs, there is need for attitude change through awareness creation [58]. Furthermore, the capacities that large agricultural industries hold in the seed market has been a cause for worry due to monopolistic control of the seed industry hence resulting to high prices for seeds as well as greatly relying on technologically patented seeds. This can worsen socio-economic inequity for such reasons; this is, especially in the developing nations, and smallholder farmers may not be in a position to afford the fertilizer or any quality enhanced seeds [59]. All these socio-economic barriers call for combined strategy of cost reduction for new technologies, increasing access to training and extension as well as favorable policies and regulations. Technological policies that provide equal opportunity and mechanisms that would allow smallholder farmers to apprise themselves with new development in maize improvement should therefore be in place for enhanced agricultural development.

Conclusion

In conclusion, remarkable progress has been achieved in improving the genetics of maize crop using superior breeding coupled with genetic engineering to improve the crop productivity and quality. Selecting method and hybridization have been useful tools in developing high yielding qualities of maize with good quality characteristics. However, the development of MAS, QTL, and GWAS has equipped the breeder with tools to select specific genes for improvement of the quantitative traits. With the help of modern tools for genome selection as

well as the method of predicting breeding genomic selection has advanced the breeding process much further in as much as it accurately identifies superior genotypes. Furthermore, as a result of genome editing technologies such as CRISPR-Cas9 and transgenic technologies, there are possibility to develop new traits in maize that cannot be developed through breeding process. However, there are some key issues; genetic limitation, climate change and other socio-economic factors that are still a huge hindrance to embracing the novel technologies. A deal with these challenges will go a long way in sustaining maize breeding in the face of such global tasks as food security, climate change, and sustainability. Development of new and better quality varieties of maize can be sustained only through introduction of new and better technologies and effective policies and practices that shall facilitate these improvements.

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