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MODERN CROP BREEDING AND GENOME ENGINEERING FOR CROP IMPROVEMENT FOR FUTURE FOOD SECURITY

Anjali[1] and Aditya Kasaundhan[2]

Abstract

Global food security has come under scrutiny due to these catastrophic weather occurrences and the necessity to feed a population that is expanding quickly. Despite the fact that plant breeding has produced the extremely productive crop varieties we have today, to fulfil anticipated future demands, the rate of genetic improvement must double. Extremely high heat and drought have caused huge crop losses for farmers all around the world.Here, we go through the fundamental concepts and characteristics of crop breeding as well as the effective application of contemporary technologies to advance crop development in the face of progressively more difficult production conditions. In order to meet the growing need for food, sustainable agriculture must develop crops with high yields, high nutritional content, and little need for human intervention throughout growth.The primary objective up to now has been to alter plants by adding genes that give them new characteristics that neither they nor their ancestors ever possessed. Contrarily, we recommend another potentially advantageous and probably less contentious approach that contemporary plant biotechnology might employ., which broadens earlier methods, tries to give crops the lost traits that their ancestors originally held in order to withstand harsh environmental circumstances.

[1]Department of Genetics and Plant Breeding
Sardar Vallabhbhai Patel University of Agriculture and Technology, Meerut
[2]Dept. of MBA Agriculture Business Management
CSA University of Agriculture and Technology, Kanpur, Uttar Pradesh
Email – anjaliojre@gmail.com

Introduction

The current number of 7.6 billion people on this planet is estimated to increase to about 10 billion by 2050. With this rapid population growth the world has become increasingly urbanized and the ratio of food producers to food consumers has significantly declined. This has placed pressure on food production globally, but intensified, more efficient agricultural production has met these demands. There are, however, serious concerns that the forecasted increase in demand for plant-based products by up to 70% within the next three to four decades cannot be met through increased production using current crop varieties and farming practices. For all associated agricultural and environmental research sectors, this poses an unprecedented challenge. Only a small portion of the approximately 300,000 edible plant species are employed for human nourishment. Only three species—rice, maize, and wheat—provide 60% of the energy in the typical human diet out of the 200 species that are usually consumed. Roots and tubers, sugar, legumes, nuts, oil-bearing crops, vegetables, fruits, spices, and other items like tea and coffee are some more key food crops in addition to cereals. Although many wealthy nations raise and harvest food crops for financial gain, they nevertheless make a significant contribution to world trade and food security. In developing nations where hunger is still a major problem, subsistence farmers frequently produce food crops. Orphan crops, such as sorghum, finger millet, and cassava, are important for local diets in developing countries but have received little investment. With some rapid genetic improvement, they could be cultivated more widely to help diversify human diets and improve farming systems through better crop rotation. Yield is one of the key characteristics that plant breeders work to enhance. This can be "grain yield," "total biomass," or "total amount of sugar" per harvested area, depending on the species. Yield is a highly quantitative attribute, therefore it is influenced by a variety of variables, such as the interactions of several underlying genes, which often have little effects (G), the environmental conditions in which the plants are produced (E), and the management techniques used (M). Most of the time, the G, E, and M interact strongly, leading to a high degree of complexity at the level of trait expression. [4]. Each of those main complexes decomposes into a number of parts, each of which is a complex in its own right. For instance, in cereals, the G component for grain yield can be viewed as a higher-level complex made up of various genetically determined components that collectively influence yield. Important production factors for a crop like wheat include the quantity and size of kernels per ear (for example, each spike or panicle) and the number of ear-producing tillers per plant. The number of spikelets per spike and the number of kernels produced per spikelet are two examples of the major yield components that break down into a variety of lower-level physiological components.A variety's yield potential is directly influenced by its genetic makeup, such as when taking into account genetic resistance to bacterial or fungal infections that cause plant illnesses. The amount of water that is available for the plant (primarily governed by the frequency and distribution of precipitation), soil composition, radiation intensity, and temperature are major environmental factors that are important to plant breeding. Extreme G and E interactions occur when the ranking of various types varies according to the environmental conditions they were produced in.For instance, if two varieties of maize are grown in a location with

sandy soils, low water storage capacity, and frequent rainfalls throughout the growing season, the maize variety with a very shallow root system and a relatively small allocation of resources to below-ground plant development may be able to yield significantly more than the other variety. However, when both types are cultivated on production sites with deep soils that have a high water-holding capacity and very little precipitation during the crop-growing season, the situation completely shifts and results in severe droughts.

Crop Improvement Programs

Both the public and private sectors operate programmes for crop enhancement. Generally, germplasm is produced by public plant breeding programmes and made freely available to farmers, scientists, and other breeders, though there are intellectual property laws and material transfer agreements in place. Conversely, seeds created by private plant breeding projects are subject to more stringent intellectual property restrictions and must be obtained through the breeding business or the designated seed distributor. Public crop breeding initiatives are carried out by numerous international research institutions. For instance, the CGIAR is a sizable international cooperation made up of 15 agricultural research organisations whose shared goals are to increase future food security globally, combat poverty, and enhance human health and nutrition. Their combined investments in crop enhancement amount to Billion us dollars. The International Maize and Wheat Improvement Centre (CIMMYT), which is situated in Mexico and is in charge of the initiatives for improving wheat and maize, is one of the partners. Numerous kinds created by CIMMYT are produced on millions of hectares of land globally. The International Rice Research Institution (IRRI), the largest non-profit agricultural research organisation in Asia, is situated in the Philippines and is another significant public crop improvement organisation that actively works to improve rice varieties.In order to bridge discovery research and applied crop breeding, public agricultural improvement projects are also crucial. The private plant breeding market, on the other hand, is dominated by large, multinational corporations like Bayer, Syngenta, and Corteva. Farmers can purchase seeds from these companies that are produced and commercialised from highly productive types. For instance, a strong mid-tier for plant breeding exists in Europe and is made up of small to mid-sized businesses. Smaller businesses often rely on collaborative R&D activities with public research institutions and/or other small businesses while the major firms typically perform breeding research using their own facilities and internal resources.

Genomics Era of Crop Improvement

Crops have improved over the past 10,000 years mostly by selection of superior individuals who displayed traits beneficial for human nutrition and production, but without the use of forced crossing. Mendelian laws marked the start of modern plant breeding, which has evolved significantly over the past 150 years. Plant breeding has become a tremendously complicated profession as a result of the introduction and ongoing development of theoretical frameworks, including quantitative genetics principles and the quick advancements in modern biotechnology and genomics. [11]. Modern plant breeding initiatives employ expert teams that combine very diverse and broad skill sets, making them highly interdisciplinary. These skill sets include genetics, statistics, agronomy, biochemistry, physiology, bioinformatics, molecular biology, and economics. The "genomics

era" of crop development has begun as a result of advancements in DNA sequencing technologies, which have completely changed crop breeding and research. For the majority of significant crop species, whole-genome reference DNA sequences are already available, and highly affordable genotyping tools to "DNA fingerprint" plants have also been developed. Single-nucleotide polymorphism (SNP) markers are frequently used as DNA markers because they are common in crop genomes and can be scored quickly and cheaply. In order to improve crops today, it is already common practise to genotype vast populations of plants using tens of thousands to a million markers. Even whole-genome resequencing data are become easier to get and are revealing previously unheard-of structural variation in crop genomes. [22]. Countless genotype data are employed for a variety of reasons using the most recent statistical genetics methods. For instance, "genomic selection" is a very promising contemporary selection approach that uses data from genome-wide DNA markers. In this method, statistical models or machine learning algorithms are used to establish a connection between genomic polymorphisms and phenotypic variation. The approach's theoretical underpinning holds that genes (or more broadly speaking, quantitative trait loci (QTL)) that influence the trait of interest (for example, grain yield) are marked by DNA markers, enabling one to estimate the effects of each of those QTL on the target trait.Without actually evaluating those genotypes in field trials, the genomic estimated breeding value for each genotype is determined using a prediction equation based on whole-genome marker profiles. As soon as DNA marker profiles can be created, this enables breeders to forecast genotype performance (i.e. at seedling stage). In the end, there is a large reduction in the time until selection decisions are reached, which increases genetic gain per unit of time. Since its official debut in 2001, genomic selection has significantly increased genetic gain in animal breeding (for example, dairy cattle) and holds great promise for crop development.

Overview of Association Mapping Methodology

Association mapping, also called linkage disequilibrium (LD) mapping, refers to the analysis of statistical associations between genotypes, usually individual SNPs or SNP haplotypes, determined in a collection of individuals, and the traits (phenotypes) of the same individuals (Figure 1). As this definition implies, association mapping is closely related to well established genetic methods, such as quantitative trait loci (QTL) mapping [18]. Prior until recently, genetic mapping was typically done in defined pedigrees or purpose-created populations, such as the offspring of parents who were selected based on their differences in the trait(s) of interest (families). In contrast, genetic association mapping makes use of a group of people, such as those from wild populations, collections of germplasm, or subsets of breeding material. As a result, many alleles at each locus may be examined for association at the same time in a varied community, whereas only two alleles segregate in every biparental population. Candidate gene association and Whole Genome Scan, often known as Genome-Wide Association Study, are the two association mapping approaches now in use. The question "is there an association between DNA polymorphisms in gene A and the plasm gathering There is a relationship between the carotenoid content of seeds and the DNA sequence alleles of phytoene synthase (or any other gene involved in carotenoid production). [10,17,20,]. This strategy presupposes a solid grasp of the trait's biochemistry and genetics, and many genes might go unnoticed.

Therefore, the whole genome scan, which is discussed in more depth below, is a superior option in the lack of full information of the relevant metabolic process, including regulatory genes. Genome scanning entails genotyping densely distributed genetic marker loci that span all chromosomes and testing for associations with the majority of the genome's segments (Figure 1). One (or more) of the genetic loci under examination are either causal for the trait or in linkage disequilibrium with the causal locus, according to the simple hypothesis under consideration. Candidate gene association could be viewed as a subset of a more comprehensive genome scan technique since it presupposes some knowledge of the genetics of the trait

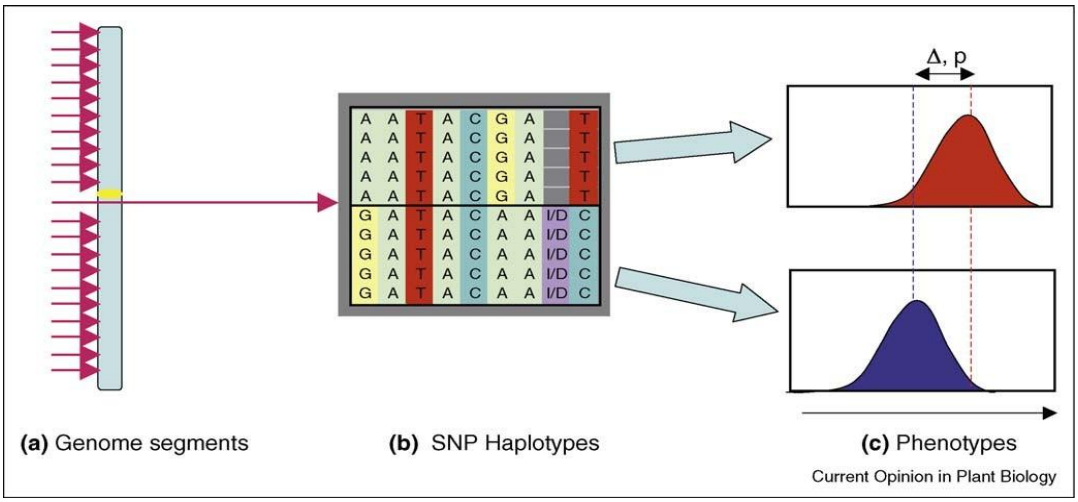

Fig 1. Principle of association analysis

(a) A collection of genetically diverse individuals is genotyped at densely spaced loci distributed throughout the genome; (b) the genotypes are divided into groups sharing SNP haplotypes (shown) or individual SNPs, at each locusin turn; (c) the distributions of phenotypic values for each of the haplotypes (oralleles) are compared and probability of null hypothesis (the distributions are equivalent)is evaluated

Genetic Modifications Generated by Genome Editing In Plants

The emergence of the CRISPRCas system has sped up the development of plant genome editing in addition to ZFNs and TALENs. The Cas9 and Cas12a complexes, which are both single effector proteins that carry out nucleic acid cleavage, are the most used CRISPR-Cas systems.[9 Figure 2A]. Recently, the Cas12b system was also developed for plant genome editing [16].For the Cas protein to locate its target sequences, all of these systems depend on crRNAs. A trans-acting crRNA (tracrRNA), which can be intentionally joined with the matching crRNA to generate a sgRNA, is an extra RNA molecule that the Cas9 protein needs. [12].Simply including the DNA target protospacer sequence into the crRNAs or sgRNAs allows CRISPR-Cas systems to be programmed. To broaden the editing potential of these tools, various Cas orthologs and variations with various PAM

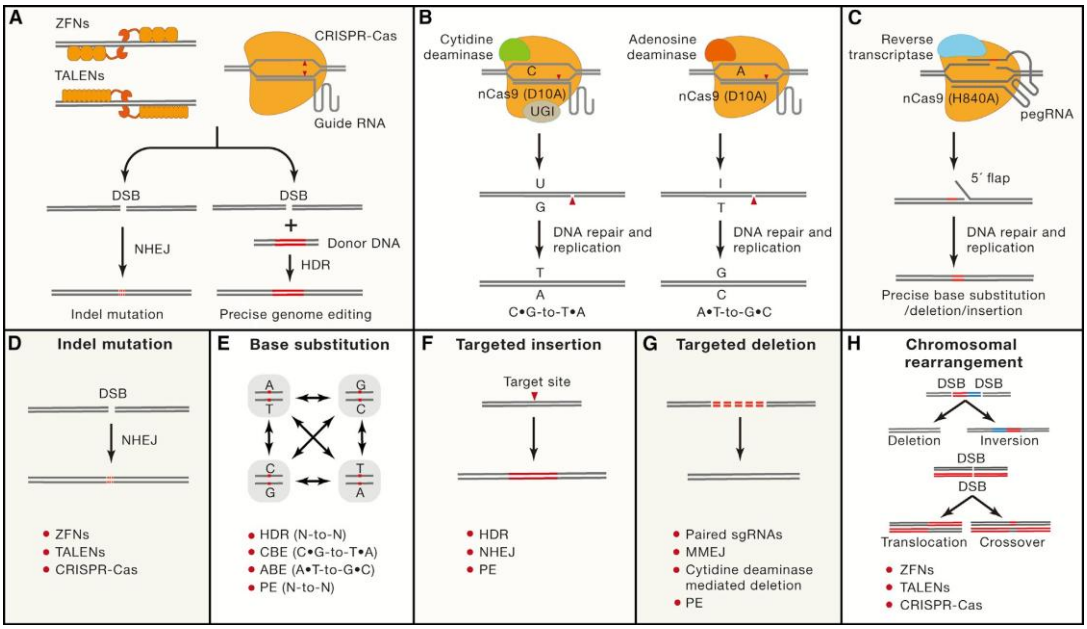

Figure2. Genetic Modifications Generated by Genome Editing In Plants

(A) Schematic diagram of the NHEJ and HDR DNA repair path ways when DNA double-strand breaks (DSBs) are produced by sequence-specific nucle-ases (SSNs).

(B) Base editing technology. Cytidine oradenosinede amina seisfused with Cas9 nickase (nCas9(D10A))to generate acytosine base editor(CBE) oradenine base editor (ABE), respectively. The CBE generates C$G-to-T$A base substitutions, and the ABE generates A$T-to-G$C base substitutions. UGI, uracil DNA glycosylase inhibitor.

(C) Prime editing technology. Theprimeeditor (PE) is composed of a fusion of nCas9 (H840A) with reverse transcriptase and a prime editing guide RNA (pegRNA).

(D) ZFNs,TALENs, and theCRISPR-Cas system induce small random indels mutation via the DNA non-homologous end joining (NHEJ) repair pathway.

(E) Base substitutions can be created by HDR,CBE, ABE, and PE.

(F) Target edinsertion editing by HDR,NHEJ, and PE.

(G) Targeted deletion editing by paired gRNAs, cytidine deaminase-mediated deletion, MMEJ, and PE.

(H) Pairs of DSB sare introduced simultaneously into chromosomes, inducing chromosome deletions, inversions, translocations, and crossover.

(protospacer adjacent motif) specificities have been discovered and utilised.[2].The CRISPR-Cas system and newly developed tools such as base editors [9 Figure 2B]and prime editors [3 Figure 2C]. have greatly expanded its potential applications. To date, genome editing has been used to generate a variety of heritable genome modifications in plants including (1) small random insertions/deletions (indels) [Figure 2D] (2) point mutations or nucleotide substitutions [Figure 2E] (3) DNA fragment insertions [Figure 2F] (4) DNA fragment deletions (Figure 3G); and (5) targeted chromosomal rearrangements

[Figure 2H]. In traditional genome editing, DSBs at target loci are repaired. SSN reagents recognise and cleave target DNA when they are introduced into plant cells, creating DSBs that are then repaired by endogenous DNA repair pathways like non-homologous end joining (NHEJ) and homology-directed repair (HDR). The primary pathway for repairing DSBs is NHEJ, and during this process, indels may be added to the junctions of the rejoined chromosomes. [5,24Figure 2D]. Due to frameshift mutations, the resulting indels are stochastic, vary in length and sequence, and frequently lead to gene knockouts. In contrast, HDR can happen if a homologous DNA template is offered or made available. HDR-mediated genome editing can result in precise gene substitutions, point mutations, and DNA insertions and deletions [Figure 2A] although the effectiveness of HDR in plant cells is very low.

Breeding for Resource Use Efficiency and Stress-Prone Sites

Crop cultivars with high nutrient use efficiency (NUE) will help to sustain production in lowinput agriculture by increasing the efficiency of uptake and utilization of nutrients by breeding for suitable root systems. NUE for seed crops is dependent upon the efficiencies of nutrient acquisition (or nutrient uptake) and nutrient utilization. The evidence to date suggests that natural variation for NUE is present in modern germplasm pools and that its exploitation in breeding programs has potential in developing nutrient-efficient crop cultivars [15,19]. For instance, the Pup1 mutation boosts P uptake and significantly improves grain output in rice grown in P-deficient soils. [23]. Introgressed lines containing Pup1 allele significantly increased grain yield on P-deficient soils [6]. Grain yield in P-deficient soils is considerably increased by overexpression of a Pup1-specific protein kinase gene (PSTOL1). By encouraging early root development, POSTL1 enables plants to absorb more P and other nutrients. [8]. 160 varieties of maize resistant to drought in sub-Saharan Africa were distributed to farmers through the breeding of stress-resistant maize. [1,7]. Expectational analysis of the introduction of drought-tolerant maize in southern and eastern Africa anticipated significant gains in average grain yield and yield stability. [13], Despite having a yield advantage of 4–19% over commercial control crops according to post ante analysis of drought-tolerant maize hybrids of early to medium maturity period, with larger benefits under stress situations [21]. Therefore, there is enormous potential for the production and sale of drought-tolerant maize seeds in Africa. However, the lack of improved seed, insufficient knowledge, a lack of resources, the high cost of seed, and the perceived qualities of various cultivars are some of the adoption barriers [14]. Increased adoption in eastern and southern Africa will result from a sufficient supply of affordable micropacks (1 or 2 kg) of drought-tolerant maize seed sold in local marketplaces [7].

Conclusions

Plant breeding has a wide range of options thanks to the advancement of genome editing technology in plants. Genome editing's effective, focused, and targeted mutagenesis has created the groundwork for a number of next-generation breeding techniques that will transform agriculture in the future. All methods must be investigated in order to utilise plant genome editing to its fullest potential. Crops can be intelligently developed with a combination of genetic features thanks to genome editing. When

employed for quick plant breeding, these accurate and effective approaches produce results that are comparable to those of traditional breeding. It is unlikely that genome editing-based next-generation breeding will entirely replace current methods; instead, we can only ensure their widespread adoption by combining them with other technologies like high-throughput phenotyping, genomic selection,

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