Advances in Genomics: Crops Adapting to Climate Change

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Abstract

In a world where food consumption is rising, climate change poses a severe danger to feeding a growing population. Previously, increased agricultural output was achieved by using fertilizer and insecticides for improved weed and pest control. However, these techniques rely on exhaustible resources and are frequently unstable. Current developments in advanced genetics are paving the door for long-term agricultural intensification and greater global warming crop adaptability. The amount of quality genomic information accessible has been rapidly increasing as a result of the widespread usage of genome sequencing technology. The increasing availability of genomic data has facilitated the shift to plant pan-genomics, allowing researchers to easily know the diversity and available traits for crop improvement and cultivar development. These advancements enhance genomic-assisted breeding, which allows for the quick engagement of candidate genes in climatic conditions and agricultural characteristics, enabling the development of resilient crops.

Keywords: Advance Genomics; Agronomic Traits; Climate Change; Genomic Selection

Introduction

Providing enough food to sustain the world's high rate of growth would be a major challenge for farming, particularly in light of climate change's catastrophic results [1]. These changes may result in increased environmental stress on plants, higher pest and disease prevalence, and a drop in crop production. In recent decades, increased agricultural production has primarily been obtained through improving agricultural practices and developing superior seed varieties [2]. Adopting these technologies to ensure agricultural production by maintaining a continual increase in crop output is unstable, as most of them depend upon exhaustible resources such as phosphate or nitrate fertilizer, and there's very little room for further improvement [1,2]. By modifying existing crops to physical and biological pressures and breeding improved crop types, genomic-assisted development is thought to have the potential to address these issues and ensure a sustainable increase in the food supply.

Crop genome sequences offer gene composition, genomic variability, as well as the biological function of agricultural variables, making them the foundation of plant genetics research. A growing number of plant genomes, both crops and wild crop relatives, have been constructed since the widespread use of genome sequencing technologies [3]. Unlike many other mammalian genomes, plant genomes are usually large, repeating, and compartmentalized [4]. As more genome sequence data becomes available, it becomes obvious that the genetic makeup stored in a specific plant species doesn't properly reflect the organism's diversity [1]. Genotyping at

the population level has provided the opportunity to reveal broad genetic diversity within species. Crop pan genome research, which tries to capture genetic variation inside one species accurately, has also helped researchers better understand crop diversity [5]. Furthermore, genome editing techniques hold a lot of potential in generating weather patterns in plants and speeding breeding [6]. Because of the rising number of genetic information and developments in genetic modification, genomic-based agriculture may play a significant role in guaranteeing agricultural production in a changing climate.

Effects of Climate Change

The price of agricultural goods is increasing as a result of human population growth and better nutritional consumption per person. Patterns of land use and rising temperatures are increasing resource stress [1,7]. Floral growth of the plant, rainfall patterns, soil quality and degradation, disease transmission, and hosting sensitivity are all affected by climate change [8], as are much more modest variations in crop diversity and variation [9] and crop pollination interaction [10]. The cumulative effects of global warming on our agriculture systems worldwide may result in crop failures and food poverty. A collaborative effort that highlights the need for productivity improvement (i.e., output) and variety in our plants, as well as performance (i.e., moisture, space, and fertilizer consumption), is the best way to address the complex challenge [1].

Priorities for Adaptability in Regional Areas

Despite the fact that climate change is a worldwide issue, the severity and direction of a problem aren't evenly distributed among countries, or perhaps even countries. The North Region is expected to adopt a warm summer, despite the fact that Mediterranean countries in Europe will be prone to regular droughts. Flood waters are expected to rise in Bangladesh as the rainy season in Asia intensifies, while others may see a decrease in precipitation. Desertification is likely to worsen throughout Africa as temperatures rise [11]. According to Kotir [12], less developed countries are the most exposed to global warming danger according to the Global Temperature Risk Rating report [13], and their agriculture and food production would suffer as a result. Even though the unpredictable nature of such areas makes them a primary focus for preserving crop yields, ecological integrity must also be considered when developing effective programs and ensuring the best use of resources. Proposed various global and regional adaptability targets based on changes in the agronomic suitability of 15 important rain-fed farming systems and also alterations in the biodiversity of 1,263 species of birds, according to Hannah, et al. [14]. Combining weather patterns changes in crop wilder relative

(CWR) biodiversity with agricultural adaptation, on the other hand, allows for a far more integrated approach to developing prioritized crop improvement and breeding programs.

Important Traits for a Breeding Target

Despite the fact that output is frequently the primary breeding goal, adaptation features such as blooming period, alkaloids concentration, and capsule indehiscence have been the subject of extensive selection studies because they increase total yield and quality. Because of its multifaceted role in ecological, evolutionary, and adaptive processes, flowering time is unusual among variables that affect plant fitness [15-17]. In a worldwide search of 116 Northern Hemisphere plant families, including numerous legume species, worldwide evolutionary indications in the orientation and degree of blooming time alterations, guided by choice during rising temperatures, were discovered [18]. However, it's still unclear what causes variability across within species, or if these alterations are adequate for longevity. Understanding the genetic component of blooming variability is therefore crucial for breeding purposes [19,20].

Measures to mitigate the effects of climate change have resulted in more research into dryness and high temperatures, as well as biological stressors [1,21]. One of its primary constraints for legume production is increased salt in soil and water, which is induced by climate change-related phenomena including ocean warming and rainfall changes [22]. Humans are breeding for unique attributes in combination with all these desirable traits as a result of climate change. To reduce carbon dioxide emissions, researchers are looking for traits that reduce methane generation in grazing animals in pastures, such as underground clover (*Trifolium subterraneum*) [23]. Theoretically, improvements facilitated by genetic studies can also have practical implications, including allowing breeding programs to speed the adoption of potential wildlife.

Identifying Genetic Variation

Understanding the scope and dispersion of genetic diversity is critical for making better using such sources in crop development. We need to learn more about mutations, the genetic variety of adaptive characteristics, the phenotypic implications of genetic variations, and the link between the environment and genetic variation to best explain the transition process. Darwin [24] saw domesticated as a template of adaptability wherein the origins of variability and choice might be deduced. Plant adaptation has been critical to the growth of mankind's development since it requires an adequate supply of food [25]. As a result of human interventions and earlier population bottlenecks, the genetic diversity of most domesticated crops has been

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greatly reduced in comparison to their wild progenitors.

Through Classical Mutagenesis, Generating Novel Diversity

Induced mutations are increasingly being used to broaden the genetic basis of crops in order to generate genetic variations to use in agricultural development initiatives [26]. In crops such as legumes, radioactivity (including X and gamma radiation) and chemical-based alterations (such as related compounds sulfonic acid and methane nitrous urea) were widely used. More than 442 mutant legume cultivars were legally or economically released worldwide, as per the FAO/IAEA Mutant Variety Database, with soybean accessions leading the way, followed by faba bean and groundnut. These mutations have been associated with increased yield, resistance to viral and fungal infections, early maturity, and drought tolerance [27]. By introducing new genetic diversity into the breeding program, mutation rearing has significantly impacted novel characteristics.

Opportunities

Improvements in Crop Diversity Collection

Genotyping by Sequencing: GBS has transformed crop genetic analysis by offering advanced tools to quickly and accurately identify genomic variation underlying agronomic factors [28,29]. Because of their expanding popularity, single nucleotide polymorphisms (SNPs) have become the genotyping markers of choice. These markers are hereditary, extensively distributed throughout the genomes, and provide solitary precision, making causal, or "perfect," markers easier to detect. There are two types of GBS methods: whole genome resequencing (WGR) and reduced representation sequencing (RRS). Huang, et al. [30] found that WGR generates a high density of SNPs and is often carried out at 1x coverage, which is sufficient for successful SNP calling in recombinant populations with a high-quality reference genome [31]. However, it is still prohibitively expensive to sequence populations with large genomes, such as wheat. RRS, on the other hand, saves money by concentrating on a small number of variables.

RRS has lower SNP densities and frequently massive quantities of missing data owing to limitations on genetic polymorphism and the probability sampling process. However, incomplete data infers that technologies are improving, so they may be able to help alleviate these issues. Genotyping by sequencing (GBS) technologies are commonly utilized for crop sequencing, resulting in SNPs that may be exploited in molecular marker techniques. GBS data for both large and small cereals will become increasingly available as sequenced prices steadily decline, and all these sources

will be important for agricultural adaptation to climate change. The options for adapting GBS to every breed or use are nearly limitless. A variety of enzymes have been examined in corn to see whether they can alter the extent of complexity reduction. It is feasible to extend the coverage of a given gene or the doubling degree of a research population using various levels of complexity reduction. The interaction of these two elements will define the best strategy for the species under inquiry. In species with large genomes or no benchmark genomes, the employment of atypical restriction enzymes (i.e., 6 bp or larger target location) with methylation sensitivity can help to reduce complexity by targeting fewer sites. As a result, sample depth in the same genomic areas will increase, and the number of missing data points will decrease.

Genotyping Arrays: Genetics has significantly benefited from single nucleotide polymorphism (SNP) array technology, which allows for rapid genotyping of numerous markers across the genome without the need for sequencing. While commercially available SNP microarrays were first designed to detect genetic change in people, the technique was quickly adopted for non-human species studies and is now widely used in crop genomics [32]. Despite the fact that probes were expected to be phased out a year ago due to lower sequencing costs, new and larger crop arrays are constantly introduced. Illumina and Affymetrix's commercialized SNP arrays now enable the testing of numerous samples with hundreds of thousands to millions of SNPs (http://www.illumina.com; http://www.affymetrix.com). Even though they provide for the focusing of specific loci, the generation of this objective, and simple computer analysis, these arrays remains popular. These two genotyping methods complement each other since SNPs utilized in arrays are typically derived from GBS data. Several major crops, such as canola [33,34], maize, rice, and wheat, have commercialized SNP arrays that would provide excellent data for gene mapping, correlation research, and genome selection [32].

Pangenomics: The pangenome is a collection of all a species' genes, including both core genes located throughout all individuals and variant genetic material present in a select few. *Brassica rapa*, maize, rice, and soybean have just been published, despite the fact that the term was coined for bacteria and is much more widely used in microbiological studies [35]. The trend toward using crop pangenomes as molecular breeding resources, rather than single-sample reference genomes, would minimize biases and improve variability coverage. Understanding the presence and lack of variation in crop genes has been demonstrated to influence climate-relevant agronomic properties such as submergence tolerance and phosphor absorption efficiency in rice and responses to environmental stresses in numerous species, including muskmelon and soybean.

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Pangenomics, in general, provides a way for a more comprehensive understanding of diversity, which will be critical in identifying genetic differences beneath the several sophisticated agricultural traits that can help farmers adapt to climate change. Although reference genomes have tremendously helped crop genetics research and breeding, they only contain a small portion of the variety's variability. One approach is to create pan-genome components, which contain sequencing and structural variation in an organism in greater detail. For legumes, pangenomes have been produced for soybean Lam, et al. [36] Li, et al. [35] and *Medicago truncatula*, for example [37]. Pangenomes, instead of a specific reference genome, accommodate structural changes, allowing for a more comprehensive capture of a species' genetic variety. They also provide for the precise identification of SNP variations. This makes it easier to identify uncommon variants that can be linked to quantitative agricultural characters. SNPs found in core (all members of a species) and variant (a subset of individuals) genomes have been reported to influence adaptability to biotic or abiotic stress factors in various studies using pangenomes [38]. Based on new gene discoveries and nucleotide diversity discoveries, these resources can be valuable for plant breeding, enabling the development of molecular markers for introducing previously untapped genes into crop improvement programs, depending on new gene discovery and nucleotide diversity discovery. Because a successful pangenome study requires the selection of suitable individuals with good variety [39], Furthermore, pangenome creation needs a large amount of sequencing data and computational resources, and assembly precision determines the quality of the final product. This makes building pangenomes difficult in plants with complicated and enormously repetitious genomics, such as peas, as well as polyploid genomes, such as tetraploid alfalfa (Medicago sativa).

High Throughput Phenotyping

Accurately assessing crop characteristics and discovering genomic regions linked with those attributes are also essential components of successful crop development schemes. Transcriptomic, metabolomic, and proteomic approaches can be used to extend analysis to the molecular phenotype, in addition to advanced and high phenotyping techniques (such as near-infrared spectroscopy on crop harvesting processes and spectrum reflection of forest canopy) [40,41]. Collectively, this will enhance our understanding of how to examine the phenotype spectrum utilizing massive multi location field trials [42]. A recent study that used both field-based high throughput phenotyping (HTP) and subjective profiling on a massive population of rice (consisting of 1,568 specimens) validated the effectiveness of HTP in detecting QTLs linked to yield components and yield parameters

[43]. The development of an elevated morphological characteristics method to examine root systems Gioia, et al. [44] is also relevant, and combining HTP approaches with elevated testing holds the promise of uncovering the genetic cause of different traits like hot and water stress.

Genomics Applications in Crop Improvement to Mitigate Climate Change

Genomics-based Selection: Genomic selection (GS) is amongst the most potential advances for next-generation sequencing selection, leading to quick crop improvement without extensive genetic research. The estimation of genomic estimated breeding values (GEBVs) for different pieces in a phenotyped and genotyped trained group is the basis of GS. As a result, a breeding population could be generated from a sample population and reproduced across successive generations without the need for additional time-consuming morphological characteristics. According to computational methods with the grazing grass *Lolium perenne*, GS reduces the breeding season by 4 years when compared to conventional breeding. Empirical investigations of GS in the oil palm industry have shown its use in improving breeding efforts [45]. Cassava GS in concentrates on performance and yield parameters revealed conceptual increases of 39.42 percent–73.96 percent when compared to phenotypic selection for this crop [46], which is possibly extremely adaptive to forthcoming climatic variations [47]. Crop researchers have indeed begun to conduct empirical GS investigations in wheat using GBS methods [48].

GBS was applied to a set of superior wheat parental lines, and GS designs with higher-yielding and stem rust-resistant forecast accuracies were generated. GBS was applied to sets of elite wheat parental lines, and GS designs with excellent prediction accuracy for yield and stem disease resistance were generated. In maize, genomic indication based on GBS data worked and more documented SNP arrays, indicating that GBS may be utilized to capture variability for breeding programs [49]. The use of GBS for GS helps in increasing marker density at lower costs, improving the usefulness of GS in genetic improvement even further. Furthermore, GS can assist in the selection of distinctive properties like frost, hot, droughts, subsidence, and biotic stress tolerance, implying that GS techniques have the ability to assist in agricultural climate change adaptation.

Genome Editing
- **The CRISPR/Cas9 System for Crop Genome Engineering**

The clustered regularly interspaced short palindromic repeat (CRISPR)/CRISPR-associated protein (Cas9) method for directed genetic manipulation is a low-cost and versatile technology. The growing popularity of this novel method

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has spurred a "CRISPR fever," with great importance in plant genome editing for fundamental studies and agricultural development. CRISPR/Cas9 is a genome editing technique that originated in the immune systems of bacteria and archaea and was recently repurposed for higher organisms. CRISPR/Cas9 genome editing has a high level of specificity, which can be further increased using Cas9 nickase [50]. Indeed, cleavage success and specificity can be higher than with other genome editing approaches. The CRISPR/Cas9 technology has been shown to be successful in a variety of crop varieties over the last three years, including maize, orange, potato, rice, sorghum, tobacco, tomato, and wheat. The majority of breeding procedures rely on natural genetic variability or alteration frames to incorporate favorable loci into top genotypes via time-consuming back-crossing processes. CRISPR/Cas9, on either side, can directly introduce naturally occurring or novel changes into elite genotypes. This has the potential to significantly expedite plant breeding initiatives. A single nucleotide mutation, for example, is responsible for the pod-shattering resistance of the commercial canola cultivar PodGuard. The cultivar was chosen from a panel of several mutant genotypes that were cultivated and evaluated for pod-shattering resistance.

The use of CRISPR/Cas9 to alter the target locus, yielding the desired genotype without alteration frames, could significantly reduce turnaround time for comparable breeding programs. Although no commercially available crops have been transformed using genetic modification technologies such as CRISPR/Cas9, the technology has been used to enhance weather patterns and agricultural attributes such as disease resistance in crops. Rice's blast resistance has been increased by using CRISPR/Cas9 to address the *OsERF922* gene. Powdery mildew resistance was provided in wheat using the genome editing approach by inducing a functional impairment in the susceptibility locus TaMLO. Cucumber's *eIF4E* genetic expression was disrupted to create broad viral resistance. Finally, utilizing CRISPR/Cas9 to disrupt the SlDMR6-1 gene in tomato resulted in wide-ranging resistance to disease. These findings suggest that genome editing might be applied to enhance other agricultural attributes as well. DuPont Pioneer will release the first commercialized crop modified using CRISPR/Cas9, a rich amylopectin corn variety [51].

CRISPR genome editing employs a complementary guide RNA, a Cas9 nuclease to cause double strand breaks, and, more recently, a nonhomologous end join or homologous directed recovery process [52-54]. In a recent work by Medicago truncatula, the MtPDS gene, which is important in carotenoid biosynthesis, was successfully disrupted by an enhanced Agrobacterium-delivered CRISPR/Cas9 platform [55]. The foregoing examples, together with the access to high reference genomes, demonstrate that CRISPR/potential

Cas9 has applications besides modeling legumes. CRISPR has been a popular alternative for genetic modification in crops due to its ease of use, low cost, and capacity to edit many sites, allowing genes to be pyramided into a novel variety in a single generation. Additionally, unlike conventional breeding techniques, CRISPR is not limited by current varieties because it can directly introduce new mutations. This might be advantageous, particularly for crops with limited variety for desirable characteristics and where natural changes do not exist. Furthermore, while crossings or backcrossing approaches may introduce harmful genes, genetic modification is likely to do so. Though CRISPR provides unparalleled possibilities for crop improvement, implementing a CRISPR strategy requires a thorough understanding of the target gene (s), their role, and expression. This could limit CRISPR's application in crops due to a lack of understanding of the genes associated with adaption processes. Nonetheless, the lower cost of genetic analysis, together with advances in genomic assembling accuracy and functional annotation, may enhance gene predictions, although it should be noted that empirical evaluation of genetic material is still required for promising findings [53].

Difficulties in Applying Genomic Research for Improved Crop Varieties

Because farmers are still unable to transplant produced seed and should acquire fresh seed every year, the introduction of hybrid crops and genetically modified (GM) seeds has allowed seed businesses to gain an advantage in seed manufacturing. While the general population usually perceives this as contentious, it is barely discussed that this approach does not preclude farmers from producing conventional types and has produced major advancements in agricultural germplasm. Maize yield, for example, has increased dramatically in the United States over the last seven decades, with genetic gains achieved through a number of strategies, including hybrid and GM seeds, accounting for more than half of the increase. Between 1930 and 2011, genetic gain accounted for 79% of the increase in Iowa maize yield [56]. Increases in genetic improvement, on the other hand, have been significantly smaller in different crops such as wheat, where agriculture seeds have always been frequently employed and hybrid and GM seeds are not generally used. Between 1961 and 1990, global average wheat yields increased by 2.95 percent per year. Nevertheless, the annual rate of increase for the following 22 years was just approximately 1%. Although genomics can speed up the creation of climate-adapted crops, the practice is still costly, and crop performance advancements would fail to meet food demands unless there is a system for crop production to see a return on investment. Growing acceptance of GM or hybrids, which force producers to purchase new seed annually, or

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actual end licensing schemes, which compensate breeders when the product is marketed, would allow breeders to securely engage in the breeding of superior varieties, expediting crop species' climate adaption [58-60].

Future Perspectives

Improvements in genomic technologies are enabling genomics-assisted breeding, which is being used to combat climate change. Combining the capabilities of these tools, which include sequencing, genome assembly, genotyping, marker identification, and genetic modification, as well as better bioinformatics techniques and high-throughput phenotyping, will enable the development of climate-ready crops.

Conclusion

Several factors influence the approach used to develop new cultivars, including crop knowledge, the accessibility of genomics and phenotype information, the type of characteristics (simple or polygenic), and country regulations. Classic and contemporary breeding practices have contributed to the development of better crop cultivars (and will continue to do so). Meanwhile, the pressure for crop development, prompted by the rapid rate of climate change and population increase, emphasizes the significance of looking beyond the frame. These advances help genomic-assisted breeding by providing for the quick discovery of candidate genes in weather patterns and agricultural traits, while CRISPRs allow the creation of new cultivars containing numerous genes in a single generation for developing plants suited to a changing climate. This significantly speeds up the process of generating crops that are adaptive to the continually changing environment, ensuring that agriculture can maintain pace with the rapids of climatic change.

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