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13. Crop Breeding Strategies for Climate Resilient Agriculture

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Abstract:

Climate change is a danger to global food security because of the decline of crop productivity around the world. Stakeholders and policymakers are worried about food security because it's expected that the world's population will exceed 10 billion in the upcoming years. The best path ahead for meeting future food needs is crop development through current breeding techniques, effective agronomic practises, advances in microbial applications, and leveraging the natural diversity in neglected crops. In this study, we outline the next-generation breeding techniques that can be utilised to boost crop productivity by creating superior genotypes that are climate-resilient to meet the problems of future global food security. The creation of fully annotated crop pan-genomes is now possible because of recent advancements in genomic-assisted breeding (GAB) techniques, which provide a picture of the whole spectrum of genetic diversity (GD) and restore a species' extinct gene repertoire. Pan-genomes offer fresh ways to take advantage of these distinctive genes or genetic variation for breeding programme optimisation. The idea that genome editing is being redesigned for crop improvement has become institutionalised with the introduction of next-generation (CRISPR/Cas) systems, including prime editing, base editing, and de nova domestication. Moreover, the editing process was made more effective by the availability of adaptable Cas orthologs such Cas9, Cas12, Cas13, and Cas14. CRISPR/Cas systems are now widely used in agriculture research, successfully editing major crops to enhance resistance to abiotic and biotic stress. Agriculture is moving towards automation or digitalization by utilising high-throughput phenotyping methodologies and big data analytics tools such as artificial intelligence (AI) and machine learning (ML). When speed breeding is combined with genomic and phenomic technologies, it is possible to identify genes quickly and thus accelerate crop improvement programmes. Furthermore, the integration of next-generation multidisciplinary breeding technologies can open up new pathways for developing climate-ready crops that contribute to global food security.

Keywords:

Climate resilient, food security, climate change, CRISPER/Cas9, next-generation breeding, pan-genoms, genome editing.

13.1 Introduction:

Climate resilient varieties are crop varieties that are developed and selected to withstand the impacts of climate change such as increased temperatures, droughts, floods, and pests. These varieties are bred using techniques such as conventional breeding, molecular breeding, and genetic engineering, among others. Modern agricultural practise is struggling to get the level of primary output required to feed about ten billion people by 2050 since land is becoming scarcer and population is increasing rapidly [1].

The development of climate-resilient varieties is crucial to ensure food security and to adapt to the changing climate. Climate change is expected to cause significant yield losses and affect the quality of crops, making it difficult for farmers to feed growing populations. Some of the characteristics of climate-resilient varieties include drought tolerance, heat tolerance, pest and disease resistance, and the ability to adapt to changing climatic conditions. They can also have higher yields and better nutritional content. According to predictions, severe climatic circumstances will generally result in lower worldwide yields of economically significant crops like maize (7.4%), wheat (6.0%), rice (3.2%), and soybean (3.1%) for every degree Celsius that the world's average temperature rises[2].

Developing climate-resilient varieties requires collaboration between scientists, farmers, and policymakers. Farmers need to be educated about the benefits of these varieties and provided with access to the necessary resources and information. Policymakers need to support the research and development of climate-resilient varieties and ensure that they are widely available to farmers.

Some important methods that may support in adaptation to climate change include in-situ moisture conservation, water harvesting and recycling for supplemental irrigation, residue incorporation other than burning, growing cultivars that are both abiotic and biotic stress tolerant, appropriate agronomic and nutrient management, and breeding for multiple traits of interest, including quality.

Promising technologies for climate-resilient agriculture:

Some significant actions that aid in adjusting crop output to climate change including

- **Adapted cropping techniques and cultivars:** (crop diversification, a shallow-deep root system that combines legumes and cereals, and enhanced short-duration crop cultivars that are tolerant to heat and drought),
- **Developing soil strength and resilience**: (Avoid bare soil, provide fertiliser after required soil testing, regulate tillage, add organic manure to the soil to boost soil carbon, rotate crops or intercrop with legumes, and use green manuring),

- **Farm machinery:** (Opening the furrows with a chisel and mb plough conserves rainwater, and using a laser leveller to increase nutrients and increase water use efficiency),
- **Rainwater harvesting and recycling:** (Farm ponds and reservoirs with inter-plot and inter-row water collection systems),
- **Crop contingency plans**: (Fishery interventions and livestock
- **Weather based agro advisories**: (Time specific weather data, like as rainfall, temperature, and wind velocity, are recorded by automated weather stations set up at experimental farms and small weather observatories).

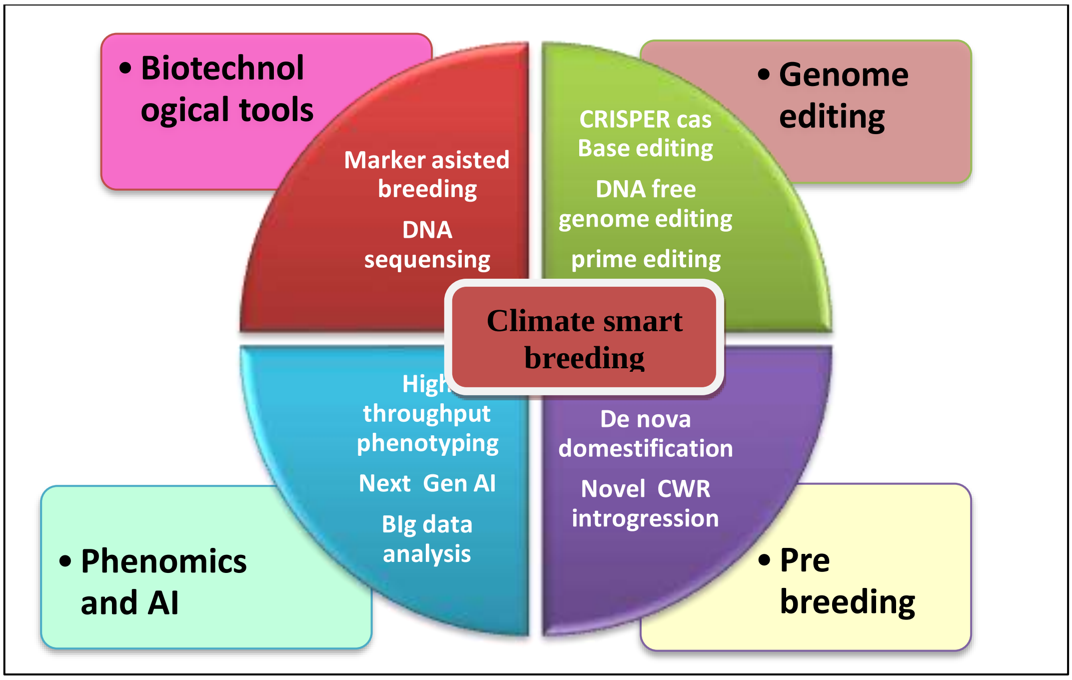

Figure 13.1: Climate Smart Breeding

13.2 Pre-Breeding and Crop Wild Relatives (CWR):

Crops would be subjected to higher biotic and abiotic pressure due to the introduction of plant diseases and pests brought on by adverse climate condition. Crop resilience in the era of climate-change is made feasible by breeding crop plants with diverse genetic backgrounds.

For the purpose of supplying the mushrooming population with food, it is vitally important to use crop wild cousins to develop larger spectrum kinds to address various biotic and abiotic challenges. Modern crops have a restricted genetic history as a result of selection preferences throughout the domestication era. This limits their capacity to adapt to their environment and to reproduce using modern germplasm.[3] Wild relatives and ancestors typically have wide climatic and environmental adaptation, which results in a better potential for agricultural development.

Pre-breeding activity connects the beneficial qualities of crop wild relatives to the production of current cultivars by giving breeders access to more readily exploitable wild genetic variation[4 ,5]. Pre-breeding is one of the opportunity to insert desired genes into the primary, secondary, and tertiary gene pools of elite breeding lines, and genotypes from wild species in order to reduce linkage drag. As domestication naturally reduces genetic variation, nearly all agricultural crop species were domesticated from wild plants species at some point[6]. In a variety of crops, including cotton, sugarcane, triticum, paddy, maize, potato, chickpea, tomato, tobacco, and pigeon pea, the genetic capacity of wild forms has been documented.

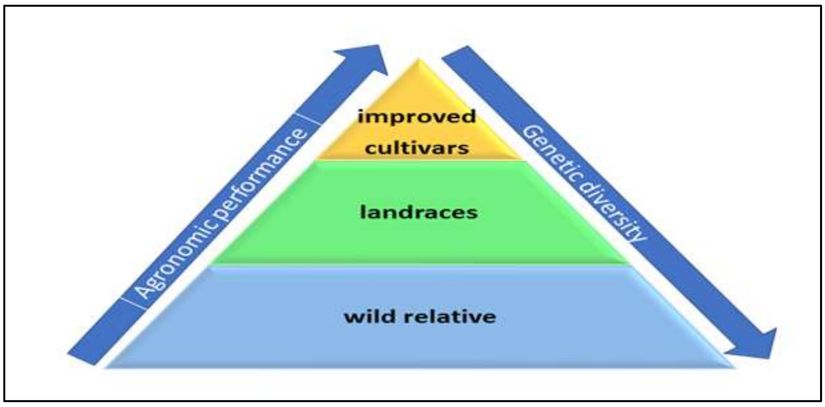

Figure 13.2: Genetic diversity and agronomic performance of germplasm

A. Introduction of Exotic Species into Superior Varieties:

wild species are largely employed to introduced biotic and abiotic stress resistance/tolerance gene in several key crops. This is because most infections can adapt to the climate more quickly than humans, making cultivars susceptible to devastating new diseases[7]. It is common practice to use intergeneric or interspecific hybridization to introduce disease resistance. Making polyploidy crops by hybridization, which mimics natural evolution, this is another method to improve genetic diversity and crop vigour with adaptation to various environmental conditions[8]. Through comparative genome pool sequencing of genes for both biotic and abiotic stress resistance of crop wild relatives can be examined, elucidating the probable genomic regions relevant for adaptation to various ecology. They have been studied in the wild counterparts of numerous crops, such as chickpea, barley, and maize[9-12]. Pan-genomics, based on a complete species' gene repository, can expose the genetic variations, like that the numerous structural variants and single nucleotide polymorphisms present in plants, to address the variety within species. One illustration of structural variants is how differences in the ELR gene's presence or absence between wild and cultivated potatoes affects the plants' susceptibility or resistance to the late blight disease (*phytophthora infestance)*[13]. Larger pan genomes that include both cultivars and their wild relatives might accumulate a surplus of dispensable genes that cause phenotypic variances, making it easier to characterise the trait linked genomic variants. *Aegilops tauschii*, a wild diploid wheat, has many pan-genomic R genes that have been successfully found and cloned in order to combat the rust infections that affect wheat in the reference of a changing climate[14].

B. Introgressiomics Strategies for Adaptation to Climate Change:

As a consequence of linkage drag and numerous breeding challenges with the crops, the CWR's real opportunity for plant breeding is yet mostly unrealized. The introduction of introgression lines from crop wild relatives into the genetic makeup of crops is made possible by the introgressiomics approach[15]. Depending on the goal, this preventive breeding strategy could be concentrated or unfocused. In addition to genetic examination of traits found in crop wild relatives, the establishment of genetically described elite material is made possible by MAS (marker assisted selection) driven generation of chromosome substitution lines and introgression lines, or MAGIC (multiparent advance generation intercross) populations. High throughput genetic markers and other genomic techniques make it easier to characterise and generate Introgressiomics populations, which can be easily introduced into large-scale breeding programmes to address the escalating environmental issues.

C. Several other Methods for CWR use:

After the CWR gene was introgressed into a domesticated background, populations were created to study the introgressed gene, including backcross populations(BC), recombinant inbred lines(RILs), doubled haploids(DH), near isogenic lines(NIL), multiparent advance generation intercross (MAGIC) populations, and nested association mapping (NAM) populations.

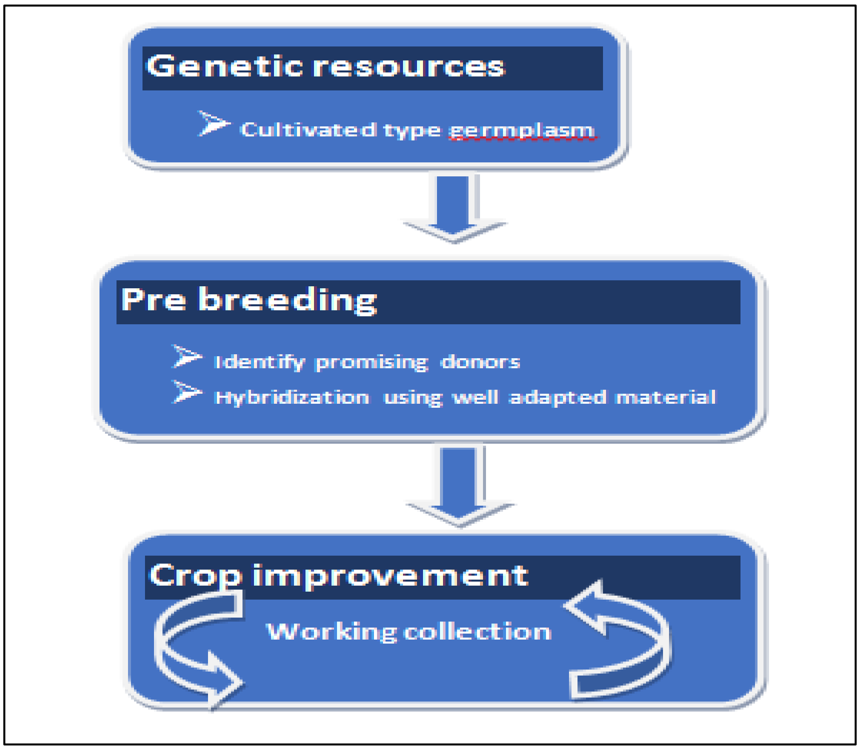

Figure 13.3: Introgression of CWR in breeding programs

13.3 Biotechnology: A Strategy for Climate Resilient Agriculture:

The rapid degradation of arable land and the illogical rainfall patterns, along with the numerous direct as well as indirect effects of climate change on agriculture, all result in a variety of abiotic stresses like drought and heat & biotic stresses like insect, pest and diseases. The advance techniques of biotechnology toolbox has the potential to address these enormous challenges of developing the stress tolerant crops[16].

In order to achieve more sustainable and effective yield increases, it is urgent to switch from conventional breeding practices that rely on fertilizers and pesticides to crop improvement methods supported by genomics. This is because the world's population is expanding quickly under the threat of climate change[17].

A. Marker Assisted Breeding:

Marker-assisted breeding (MAB) is a plant breeding technique that uses molecular markers to identify and select plants with desirable traits, such as tolerance to environmental stresses like drought, heat, and salinity.

This technique can be particularly useful in developing climate-resilient crops that can withstand the effects of climate change, including extreme weather events, changes in temperature and precipitation patterns, and increased pest and disease pressure.

The development of molecular markers like Single Nucleotide Polymorphism (SNP), Rapid Amplified Polymorphic DNA, Kompetitive Allele Specific PCR, Simple Sequence Repeat, Cleaved Amplified Polymorphic Sequence, and others has revolutionised the study of genetics and facilitated molecular crop breeding[18].

The Smart breeding programme places a lot of emphasis on the breeding programmes that have switched from phenotype-based (conventional breeding) to a combination of conventional and genotype-based selection[19].

The process of MAB involves first identifying genetic markers that are associated with the desired trait, such as a gene that confers drought tolerance. Once these markers are identified, plant breeders can use them to screen large populations of plants to identify those with the desired trait, without having to rely solely on time-consuming and expensive phenotypic screening methods.

MAB has already been used to develop climate-resilient crops, such as drought-tolerant maize, rice, and wheat varieties. For example, in Africa, the International Maize and Wheat Improvement Center (CIMMYT) has used MAB to develop maize varieties that are better adapted to drought-prone areas. These varieties have shown increased yields and improved resistance to drought stress.

Overall, MAB can be an important tool for developing climate-resilient agriculture by allowing breeders to more efficiently and accurately select for desirable traits, such as tolerance to environmental stressors.

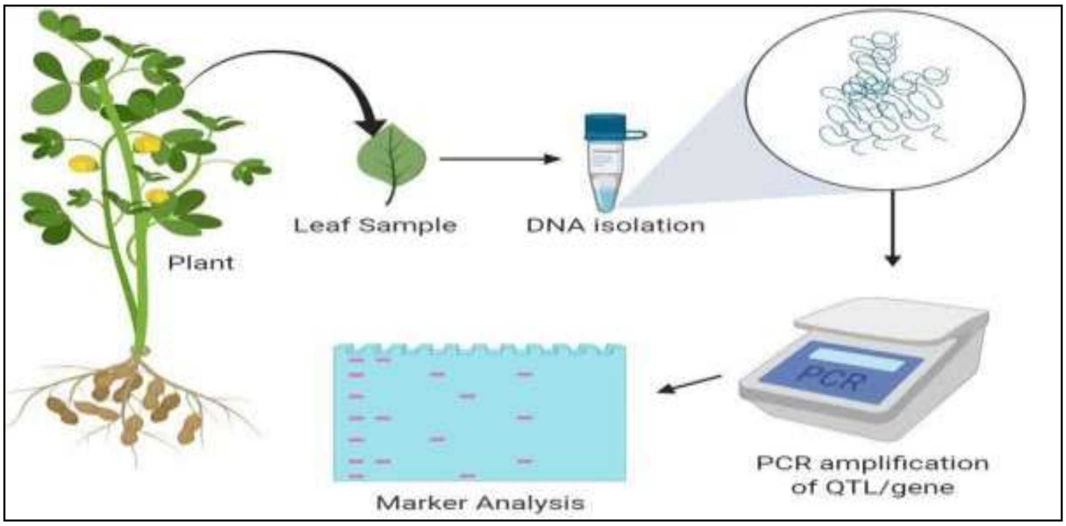

Figure 13.4: Marker Assisted Breeding Selection

B. Dna Sequencing and The Development of Genomics-Aided Breeding:

DNA sequencing is the process of determining the precise order of nucleotides (adenine, thymine, guanine, and cytosine) in a DNA molecule. The sequence of these nucleotides determines the genetic information that is encoded in the DNA.

Using RNA sequencing and the gluten gene families, this method can be used to define genetic diversity in disease resistance gene repositories in Solanaceae and Triticeae plants[20].

There are different methods for sequencing DNA, but the most commonly used method is called "chain termination" or "Sanger sequencing".

In Sanger sequencing, a DNA molecule is first amplified using the polymerase chain reaction (PCR) to produce many copies of the DNA fragment of interest. These fragments are then mixed with a set of DNA primers and DNA polymerase, as well as a mixture of the four nucleotides (A, T, G, and C) and a small amount of modified nucleotides that terminate the chain. As the polymerase synthesizes new DNA strands, occasionally a modified nucleotide is incorporated instead of the regular nucleotides, causing the chain to terminate.

The resulting mixture of DNA fragments of varying lengths is then separated by size using gel electrophoresis. The sequence of the DNA fragment can be determined by reading the order of the terminating nucleotides at the end of each fragment, which is revealed by the positions of the separated bands on the gel.

More recently, new methods of DNA sequencing have been developed, such as next-generation sequencing (NGS) and single-molecule sequencing. These methods can sequence DNA faster and more efficiently than Sanger sequencing, and have enabled the sequencing of entire genomes in a relatively short time.

13.4 Genome Editing: A Revolutionary Tool for Breeders' Toolbox:

Genome editing is the process of making precise changes to the DNA sequence of an organism, typically using a molecular tool such as CRISPR/Cas9. This technology allows scientists to add, delete, or modify specific DNA sequences in a genome, which can have a wide range of applications in areas such as medicine, agriculture, and environmental science[21, 22].

One of the most popular tools for genome editing is CRISPR/Cas9, which is a system that uses a guide RNA to target specific DNA sequences and a nuclease (Cas9) to cut the DNA. This cut triggers the cell's natural DNA repair mechanisms, which can be manipulated to insert or delete specific genetic material[23].

Genome editing may accelerate the domestication of novel crops drawn from their wild relatives or small-scale crops with their ability to adapt to extreme climatic conditions. In order to maximise the use of germplasm adapted to climate change, this will accelerate the spread of currently small gene pools by altering crucial genes for domestication in possible new crops. Additionally, multiplexing CRISPR devices to edit numerous genomic loci simultaneously can greatly speed up and increase effectiveness. Due to the drawbacks of this method, such as off target effects, poor HR efficiency, limited PAM sequences, and regulatory challenges, more complex technologies, such as DNA free genome editing, base editing, and prime editing, have been developed.

A. DNA Free Genome Editing:

DNA-free genome editing (DFGE) refers to a genome editing technique that does not involve the direct modification of DNA. DNA-free genome editing approaches use various methods to deliver editing tools, such as proteins or RNAs, directly into cells without modifying the DNA.

The CRISPR-Cas9 ribonucleoprotein was first effectively used in rice and tobacco with protoplast transfection (RNP)[24]. Moreover, a DFGE method mediated by particle bombardment has been established in wheat and maize[25, 26].

B. Base Editing:

The process of base editing involves the base editor protein being guided to the target DNA sequence by the Cas9 enzyme, where it then binds to the DNA and converts the targeted nucleotide[27]. This process does not involve breaking the DNA, and therefore results in less off-target effects and potentially fewer unintended mutations than traditional genome editing methods.

C. Prime Editing:

With the aid of prime editing guide RNA (pegRNA), a contemporary occurrence in the era of genome engineering, all 12 known base to base conversions as well as mutations like insertions and deletions can be introduced[28].

This promising strategy offers a wide range of opportunities for successfully targeting and changing desirable genome sequences to speed up functional genomics and the inclusion of genes for adaptation to climate change, which will enable breeding for climate resilient crop varieties in the near future[29].

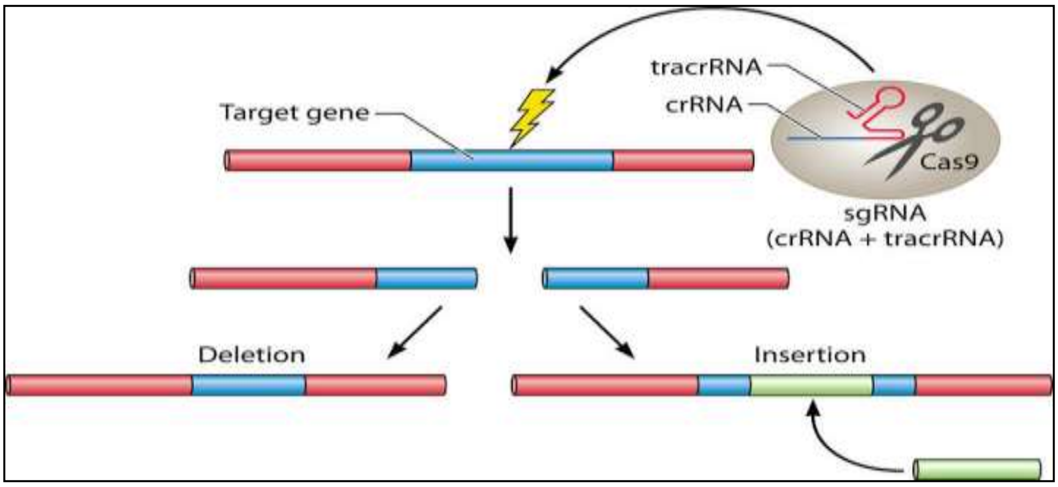

Figure 13.5: Genome editing using Cas9

13.5 Phenomics and Artificial Intelligence:

Phenomics is the study of the physical and biochemical characteristics of an organism, often at a large scale, with the goal of understanding how genes and the environment interact to produce a specific trait. In the context of plant breeding, phenomics can be a powerful tool for identifying and selecting desirable traits in crops.

Phenomics involves the use of high-throughput technologies, such as imaging, sensors, and molecular profiling, to collect large amounts of data on plant traits, such as growth rate, yield, and resistance to pests and diseases. This data can then be analyzed using advanced computational methods, such as machine learning, to identify patterns and correlations between traits and genetic markers.

By using phenomics in plant breeding, researchers can more efficiently and accurately identify and select desirable traits, which can lead to the development of new crop varieties that are more productive, resilient, and adaptable to changing environments[30]. This can be especially important in the face of challenges such as climate change, population growth, and food security.

Overall, phenomics is a powerful tool for advancing plant breeding and improving crop production, and it is likely to become an increasingly important area of research in the coming years. By integrating with phenomics and genomics and utilising big data, artificial intelligence (AI) technologies can accelerate the production of climate resilient varieties with better yield potential, stability, and tolerance to predicted concurrent environmental challenges (abiotic and biotic stresses).

A. Field Phonemics:

High resolution, a large capacity, field level phenotyping that can efficiently screen among higher performing breeding material across bigger populations is crucial for accelerated plant breeding for climate resilience[31]. Over the past ten years, phenomics has raised the collection of more phenotypic data through the creation of novel sensors (such as unmanned aerial vehicles, or UAVs), high resolution imaging, and new platforms for a wide range of features and situations[32,33]. Plant architectural features can be screened for using high throughput phenotyping (HTP), which also enables the early identification of attractive genotypes. It allows for precise, reproducible measurements of physiological parameters as well as agronomical traits (canopy structure, biomass and grain yield seedling vigour, flower counts, flowering duration, height and leaf erectness,) (photosynthesis, disease and stress tolerance). To detect, measure, and keep records of plant diseases, HTP techniques such as fluorescence imaging, RGB imaging, thermal and hyper spectral sensing and 3-D scanning have been effective[34].

B. Next Gen Based GS:

In the past ten years, genomic selection has been widely employed in breeding for climate resilience in agriculture, particularly for complex quantitative traits. It entails developing prediction models by evaluating the simultaneous effects of all current markers on a desired phenotype. By reducing breeding cycles, very accurate prediction can lead to increased levels of yields.

Next-generation sequencing (NGS), also known as high-throughput sequencing, is a method of DNA sequencing that allows the rapid and efficient analysis of large amounts of genetic information. It has revolutionized the field of genomics and has enabled researchers to study genomes at an unprecedented level of detail.

NGS technologies have greatly improved the speed, accuracy, and cost-effectiveness of genome sequencing. These technologies use various methods to generate millions of short DNA sequences in parallel, which are then assembled into a complete genome sequence.

Some examples of next-generation sequencing technologies include Illumina sequencing, Ion Torrent sequencing, PacBio sequencing, and Oxford Nanopore sequencing.

13.6 Speed Breeding: an Acceleration to Crop Improvement:

Speed breeding is a technique that uses controlled environments and optimized growth conditions to accelerate the breeding and development of crop plants. It is a relatively new method that has emerged as a response to the challenges of modern agriculture, including climate change, population growth, and food security.

One common approach to speed breeding is to use LED lighting and other controlled environmental conditions, such as increased carbon dioxide levels, to speed up the growth and development of plants. This technique allows multiple generations of plants to be grown in a single year, significantly accelerating the breeding process[35].

Speed breeding has the potential to revolutionize plant breeding and enable the development of new crop varieties faster and more efficiently. It may also allow for the development of crops that are better acclimatized to changing environmental conditions and more resilient to pests and diseases. Although, more research is needed to evaluate the effectiveness and long-term sustainability of this technique.

Breeders can now able to harvest up to six generations annually by adopting a variety of "speeding breeding" techniques that use longer photoperiods and controlled temperatures.

Speed breeding setup:

Light: PAR region (400-700), ambient lighting with LED.

Photoperiod: 22 hours with 2 hours of darkness.

Humidity: ideally 60-70%

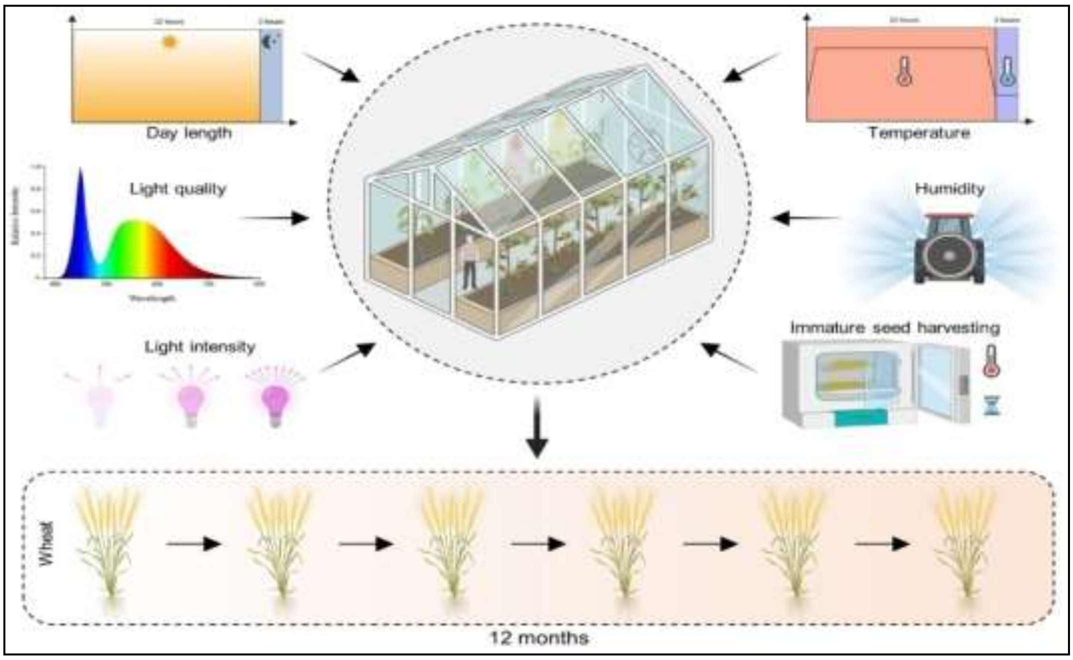

Figure 13.6: Speed breeding

13.7 Conclusion:

Crop plant breeding for greater production and tolerance is critical to ensuring global food security in the face of ongoing and expected climate change, which will result in increasing temperatures and much more unpredictability in the weather throughout a huge part of the world. The goal of climate resilient agriculture can only be achieved in the near future with improved plant varieties which effectively utilise fewer resources, can withstand diseases and pests, and demonstrate consistent yields in stressful situations. Research focus is essential for currently underutilized agricultural species if they are to contribute to climatic resilience. To address crop plants' sensitivity to climate change, smart breeding relies heavily on creating huge breeding populations, effective high throughput phenotyping, large management technologies, and downstream molecular approaches. Climate-smart breeding also requires the effective preservation and protection of plant genetic resources. Using cutting-edge methods like genome editing to introduce new alleles discovered in wild plants into domesticated crop types is one method for acquiring novel diversity. With further knowledge of their fundamental physiological and genetic principles, it will be possible to create crop cultivars that can withstand numerous pressures. The development and use of climate-smart cultivars in future could be facilitated by technological advancements in both phenotypic and genotypic analyses, and also in the biotechnological and digital revolutions.

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