

## New Insights for Plant Genome Optimization, Biotic and Abiotic Stresses and Agricultural Applications

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### Abstract

Plant genomics experienced a revolution as a result of the cheap cost and simplicity of sequencing, which produced numerous assemblies of inferior quality but also a sharp rise in the number of revolutionary genome-enabled discoveries concerning the basic plant biology. Crops physiological, metabolic, and molecular responses to several abiotic challenges appear to be very different from their reactions to single stresses. One of the most crucial fields of plant research is the investigation of the processes underlying plant adaptation to environmental stresses. As biological messengers that control gene expression, ROS and NO work synergistically to activate defense mechanisms in response to biotic and abiotic stresses. It is known that S-nitrosoglutathione reductase (GSNOR), which is thought to be a key regulator of plant stress tolerance due to its effect on protein S-nitrosylation, contributes to *Solanum lycopersicum's* thermotolerance. Vitamin K3, often known as pro-vitamin K, has an addition component called menadione sodium bisulphite (MSB). In contrast, CRISPR/Cas9 can speed up the plant breeding by quickly, precisely, and predictably altering genomes. CRISPR/Cas9 has recently gained popularity as a technique for genome editing and has been extensively utilized in crop resistance breeding because to its effectiveness, simplicity, and adaptability.

**Keywords:** Plant Genome, Transcriptomics, Proteomics, CRISPR/Cas9, Metabolomics.

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## INTRODUCTION

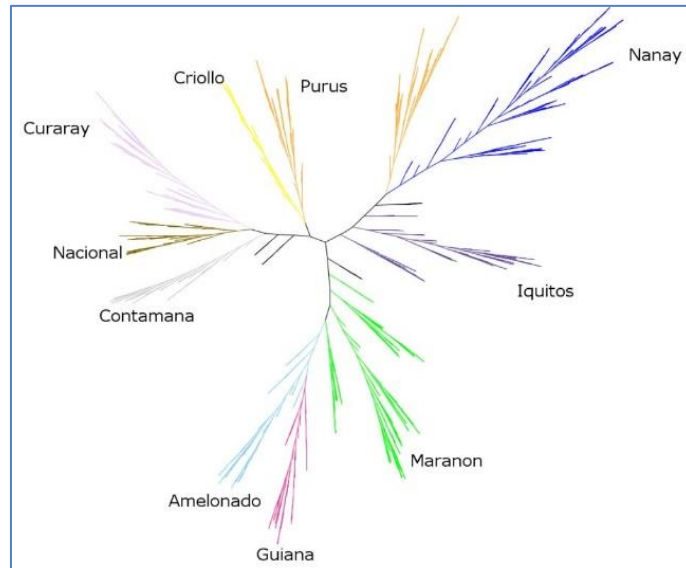
The easiest way to define a plant genome depends its size, gene content, number of repetitive sequences, and polyploidy events. Plants also have genomes in their mitochondria and chloroplasts, but their nuclear genome is the biggest and most complicated. Nuclear genome size varies widely, although there is no evident functional importance to this variation. Many of the initial, high-quality plant reference genomes were put together using BACs that had been Sanger sequenced using a minimal tiling approach [1- 3]. Despite the fact that, these genomes offered excellent chromosomal scale references, they were costly and labor-intensive, typically requiring huge associations. But with the successful genome sequencing of *Drosophila melanogaster*, it was shown that shotgun sequencing combined with an overlap

layout consensus (OLC) technique utilizing the CELERA assembler produced high-quality assemblies at a small fraction of the cost and time. Papaya, soy, and poplar, among other early plant genomes, were assembled using shotgun sequencing and OLC assemblers. De Bruijn graph (DBG) assembly techniques were created in response to the introduction of second generation sequencing technologies like 454 and Illumina, which can handle shorter reads processed at higher depth [4- 5].

Plant genomics experienced a revolution as a result of the cheap cost and simplicity of sequencing, which produced numerous assemblies of inferior quality but also a sharp rise in the number of revolutionary genome-enabled discoveries concerning basic plant biology. Despite the presumed source species for the A and B chromosomal groups being *A. duranensis* and *A.*

*ipaensis*, respectively, there are significant differences across tetraploid peanut species in terms of plant shape and economic traits including oil content, protein content, and disease resistance. The cotyledons of the peanut kernel are pressed to produce peanut oil, which is mostly constituted of triacylglycerol (TAG) and contains nutrients important for human health [6- 8].

The advancement of long read sequencing technology has been the main force behind better plant genome assemblies. Despite advancements in assembly techniques and new physical mapping technologies, read length continues to be a barrier to high-quality plant genome assemblies. Due to their high degrees of heterozygosity, intricate polyploidy, and explosive repetition content, plant genomes are the hardest to assemble [3- 7].



**Fig. 1: Shows the genome-enabled discoveries concerning basic plant biology**

Model organisms such as *Drosophila melanogaster*, *Caenorhabditis elegans*, and *Saccharomyces cerevisiae* that offer genetic and molecular insights share traits like being diploid and suitable for genetic analysis, being responsive to genetic transformation, having a relatively small genome and a short growth cycle, having widely accessible tools and resources, and being the subject of research by a sizable scientific community. Although the use of tobacco and petunia was encouraged by the development of tissue culture techniques, the species today employed as model organisms for mono- and dicotyledonous plants are rice (*Oryza sativa*) and Arabidopsis (*Arabidopsis thaliana*) respectively [8- 12].

**Advances in Plant Genome Optimization, Biotic and Abiotic Stresses**

The initial step in identifying modifications is to characterize the locations of retrotransposon-based sequences using ISTR (Inverse Sequence-Tagged Repeats). Retrotransposons are constantly moving and can provide a gene new regulatory feature. ISTR are oligodeoxynucleotide primers produced from copia-like sequences that are widely distributed across eukaryotic genomes as molecular markers. Crops physiological, metabolic, and molecular responses to several abiotic challenges appear to be very different from their reactions to single stresses [13- 15].

**Table 1: Shows the various factors stresses in plants**

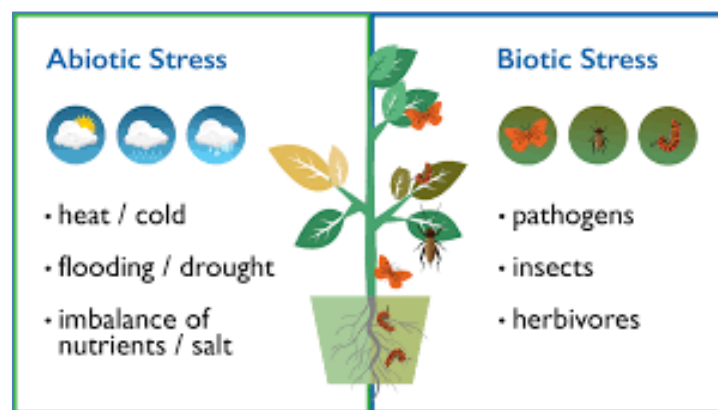
Factors	Effects	Growth influencing	Growth effects
Pathogens	Biotic	Decreases	Lower
Herbivores	Biotic	Decreases	Decreases
Cold	Abiotic	Decreases	Stunt
Heat	Abiotic	Decreases	Weakened
Drought	Abiotic	Decreases	Damaging effects

One of the most crucial fields of plant research is the investigation of the processes underlying plant adaptation to environmental stresses. Although these substances also function as signal molecules at low concentrations, metabolic imbalances brought on by external stimuli like drought, high light intensity,

salinity, flooding, high and low temperatures promote the generation and accumulation of reactive oxygen species (ROS). This may cause oxidative damage to proteins, lipids, and nucleic acids [16- 17].

As biological messengers that control gene expression, ROS and NO work synergistically to activate defense mechanisms in response to biotic and abiotic stresses. have examined how S-nitrosoglutathione reductase (GSNOR), which is thought to be a key regulator of plant stress tolerance due to its effect on protein S-nitrosylation, contributes to *Solanum lycopersicum's* thermotolerance. It is known that GSNOR controls the amount of apoplastic H<sub>2</sub>O<sub>2</sub> that is produced in response to high temperatures and is NADPH oxidase dependent (SIRBOH1) [18- 21].

In fact, one of the most significant factors influencing the occurrence of bacterial diseases cause of bacterial panicle blight in rice , *Acidovorax avenae* (cause of seedling blight and bacterial fruit blotch in cucurbits), and *Ralstonia solanacearum* (cause of wilt in tomato), is temperature. Pathogens' rates of growth and reproduction change as the temperature rises. By influencing the population growth and vector-borne illness transmission, temperature also has an impact on the prevalence of vector-borne diseases. Similar to this, salt stress' influence on plant diseases may result from its modification of the pathogen's virulence, the host's physiology, and soil microbial activity [20- 23].



**Fig. 2:** Shows the different factors affecting the biotic and abiotic stresses

The severity of scabs on the surface of tubers is also influenced by the time of drought occurrence, and it was shown that dryness during the early stages of tuber growth led to more scabs. Drought (water stress), excessive watering (water logging), extreme temperatures (cold, frost, and heat), salt, and mineral toxicity are examples of abiotic stresses that have a detrimental impact on crop and other plant growth, development, yield, and seed quality. Future scientists predict that abiotic stresses will intensify as fresh water becomes more limited [17- 20].

It is critical to develop crop kinds that are resistant to abiotic stresses in order to preserve food security and safety in the approaching years. A plant's first line of defense against abiotic stress is its roots. Historically, producers have handled this problem by choosing naturally existing variations with improved production and quality but lower toxicity. Breeders organize, design, and carry out plant breeding projects that result in varieties improved in specific plant traits, including yield- related traits, defense against pathogens and/or pests, alterations to the structure of plants, and morphological features relating to eatable organs (such as fruits or different vegetative parts such as roots, stems, or leaves [11- 29].

### Agricultural Applications

Domestication has not been a one-way process in this regard; rather, it has been the outcome of numerous, sometimes unexpected admixtures of distinct

genetic origins that have helped to define all currently existent genotypes. Cellular polyamine alterations brought on by stress offer hints about their potential involvement in stress, but they do not show that they play a function in reducing stress [24- 26]. Exogenous polyamines can be administered to raise endogenous polyamine levels. This has been done before or during stressful situations. Exogenous administration of polyamines might maintain the integrity of plant cell membranes, reduce growth inhibition brought on by stress, control the expression of osmotically responsive genes, and boost antioxidant enzyme activities. Another strategy is to address the endogenous polyamine that causes stress sensitivity by using biosynthesis inhibitors to diminish it [21- 25].

However, a significant amount of the agricultural output in the Mediterranean region consists of woody crops, primarily iconic species like grapevine, olive, and citrus, which are significant breeding objectives. Because plants are perennial, the impacts of climate change may have an impact on several plant processes, which may then have a long- and medium-term impact on production and quality [26- 27].

One of these methods is the "Omics" technology. Plant responses to stress and the underlying processes have been disclosed through transcriptomics, proteomics, and metabolomics. These studies also identify possible target genes, proteins, or metabolites for improving plant responses and developing tolerance.

The "Omics" characterization of abiotic and biotic stress combinations is poorly understood, however new papers have addressed this issue [28- 30].

In response to unfavorable environmental conditions, plants activate both particular and non-specific stress responses, enabling them to adapt as effectively as possible to the precise set of conditions faced while preserving resources for development. The exact interaction of each pathway's constituent parts, notably the hormones ABA, SA, and JA, as well as TFs, HSFs, ROS, and short RNAs, results in signal specificity. It is simple to understand how the impact of various pressures on a particular resistance response might be unexpected given the number of interrelated elements. Individual plant stress components have often been investigated as discrete stimuli that initiate linear signaling cascades [31- 32].

Moreover, results obtained with entire plants may be deceptive, as various plant species or even cultivars may react differently. Different technological CRISPR based technologies have wide range of biological and agricultural significance for the plant breeding and genetics. There is need for editing the plant-based genome for biological and physiological properties of the novel varieties. Moreover, results obtained with entire plants may be deceptive, as various plant species or even cultivars may react differently. Plant responses are frequently organ-dependent. Another strategy would include introducing particular genes into agricultural plants through molecular engineering. The resilience of potato to biotic and abiotic stress was enhanced by altering a gene coding for a tiny antimicrobial peptide and introducing it into potato [33- 35].

Vitamin K3, often known as pro-vitamin K, has an addition component called menadione sodium bisulphite (MSB). Menadione has been isolated from fungi and phanerogams, contrary to earlier assumptions that it was synthetic. Additionally, it is a commonly utilized redox-active substance in the investigation of oxidative stress in plants. One electron is immediately reduced by the cell, producing superoxide radicals (O<sup>-2</sup>) and hydrogen peroxide (H<sub>2</sub>O<sub>2</sub>). The redox characteristics of vitamin K are intimately related to its physiological function in plants. Two key chemical characteristics make quinones, benzoquinones, and naphthoquinones like menadione reactive in biological systems [10- 16].

With the advent of industry and the frequent occurrence of harsh weather, the natural environment has progressively changed in a way that makes it unsuitable for the growing of crops. as a result of abiotic stresses like low temperature. The current standard technique for resistance breeding, CRISPR/Cas, may be utilized to develop crops in a specific direction and drastically reduce the breeding

life. This essay examines the use of CRISPR/Cas in crop resistance gene modification and outlines potential issues and difficulties [20- 25].

The prepping an early plant adaption and proline accumulation by soaking Arabidopsis seedlings in 20 mM MSB enhances salt tolerance. Additionally, it was shown that MSB activates the production of important transcription factors including Zat12, one of the important zinc-finger proteins encoded by a multigene family and implicated in a ROS-dependent signaling network against abiotic stress. Zat12 is one of the major transcription factors. It was also shown that MSB causes a hypomethylation condition in the promoter region of genes involved in the production of proline. This finding suggests that an epigenetic mark is one of the mechanisms behind this early adaptation to salt stress [27- 30].

As a result, creating new cultivars using conventional breeding techniques takes time, especially when backcrossing to separate the undesirable traits in the progeny. In contrast, CRISPR/Cas9 can speed up plant breeding by quickly, precisely, and predictably altering genomes. CRISPR/Cas9 has recently gained popularity as a technique for genome editing and has been extensively utilized in crop resistance breeding because to its effectiveness, simplicity, and adaptability. The CRISPR-Cas9 system enables gene knockout, gene insertion, and gene replacement. These techniques produce mutants with loss-of-function, knockdown, or activation, which can result in the development of agricultural plants that are resistant to biotic and abiotic stress. The availability of crop genome sequences, however, enables researchers to precisely design a crop's genome, facilitating the use of CRISPR/Cas9 in resistant breeding. Firstly, it has not yet been possible to identify the main genes governing crucial aspects of crops, which restricts the use of CRISPR/Cas in plant genetic engineering breeding. Second, to overcome the existing resistance created by CRISPR/Cas gene editing, pathogens continue to change their genomes over time. As a result, it is necessary to create fresh versions and incorporate them into the plants every few years. Thirdly, it is challenging to establish a resistant phenotype by knocking out a single gene since many genes are represented by multi-gene families with functional redundancy. To implement multiplex genome editing, strong CRISPR-Cas technologies must be developed [30- 34].

## CONCLUSION

Different technological CRISPR based technologies have wide range of biological and agricultural significance for the plant breeding and genetics. There is need for editing the plant based genome for biological and physiological properties of the novel varieties. Despite advancements in assembly techniques and new physical mapping technologies,



read length continues to be a barrier to high-quality plant genome assemblies.

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