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Applications of Plant Bioinformatics in Crop Improvement and Stress Tolerance

Review Article

Anika Tabassum*

Department of Botany, Jagannath University, Dhaka-1100, Bangladesh

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ABSTRACT

Plant bioinformatics has emerged as a cornerstone of modern plant science by enabling the large-scale analysis and interpretation of genomic and post-genomic data for crop improvement. The rapid advancement of high-throughput sequencing technologies, coupled with powerful computational tools, has transformed traditional breeding approaches into data-driven strategies. Bioinformatics facilitates the identification of genes, quantitative trait loci (QTLs), regulatory networks, and molecular markers associated with agronomically important traits, particularly stress tolerance. Abiotic stresses such as drought, salinity, heat, and cold, as well as biotic stresses caused by pathogens and pests, significantly limit crop productivity worldwide. Integrating bioinformatics with genomics, transcriptomics, proteomics, metabolomics, and phenomics has enabled a deeper understanding of plant stress responses and accelerated the development of resilient crop varieties. This review comprehensively discusses the applications of plant bioinformatics in crop improvement and stress tolerance, highlighting major computational approaches, databases, tools, and emerging trends. The challenges and prospects of bioinformatics-driven plant breeding are also critically examined.

Keywords: Plant Bioinformatics, Crop Improvement, Stress Tolerance, Genomics, Multi-Omics, Computational Biology

1. Introduction

According to the United States Census Bureau's International Database, there will be roughly 9.8 billion people on the planet by 2050 (Javidan, 2024). Additionally, the Global Alliance for Improved Nutrition, which seeks to promote the

availability of healthy and reasonably priced foods for women and infants, reports that 2.6 million children die from malnutrition and that 2 billion people globally are undernourished (<http://www.gainhealth.org/knowledge-centre/fast-facts-malnutrition/>). It is projected that a 70% increase in

* Correspondence: Anika Tabassum
E-mail: anika@bot.jnu.ac.bd

food production is necessary to feed the vast population. This entails increasing meat output from 200 million tonnes to 470 million tonnes and cereal production from 2.1 billion tonnes to 3 billion tonnes. Significant investment and strategies to improve food access, particularly in rural regions, and fight poverty are needed to achieve this expansion (Le Mouél and Forslund 2017). However, the loss of natural resources, population growth, and climate change pose unprecedented challenges for global agriculture (Godfray et al. 2010). Abiotic factors like drought, salinity, extreme temperatures, and nutrient deficiencies, as well as biotic challenges like fungal, bacterial, viral, and insect attacks, significantly limit crop productivity (Atkinson and Urwin 2012). Despite their success, traditional breeding methods are time-consuming and often inadequate for addressing complex, multigenic stress-tolerance traits (Tester and Langridge 2010).

Plant bioinformatics is a specialized branch of bioinformatics that applies computational tools, algorithms, databases, and statistical methods to collect, store, analyze, and interpret large-scale biological data generated from plant research, including genomics, transcriptomics, proteomics, metabolomics, and phenomics (Varshney et al. 2021; Michael 2026). Plant bioinformatics provides a strong foundation for enhancing climate-smart agriculture and maintaining global food security in the face of climate change by hastening the discovery of stress-adaptive mechanisms and promoting data-driven crop innovation (Xiong et al. 2006). Plant research has been transformed by the availability of whole genome sequences for important crops like rice, wheat, maize, soybean, and Arabidopsis. This has allowed for genome-wide studies of gene function and regulation (Xue and

Cui 2025). Researchers can predict protein structures, find candidate genes, examine gene expression patterns, and model regulatory networks linked to stress tolerance using bioinformatics techniques (Cox and Mann 2008). Massive datasets from genomes, transcriptomics, proteomics, and metabolomics research are now being generated using next-generation sequencing (NGS) technology (Metzker 2010). Bioinformatics is critical for managing, integrating, and understanding large information in order to identify biological mechanisms underlying complex features (Satpathy 2025). The purpose of this review is to provide a comprehensive overview of plant bioinformatics applications in crop improvement and stress tolerance, with a focus on modern plant breeding and sustainable agriculture.

Overview of Plant Bioinformatics

Plant bioinformatics refers to a variety of computational methods for storing, retrieving, and analyzing plant-derived biological information. The discipline grew with genomics and computational biology, with the development of databases such as Gramene, Phytozome, and Ensembl Plants, which serve as repositories of plant genome assemblies and annotations (Olson et al. 2026; Marrano et al. 2025).

Key objectives of plant bioinformatics include: Genome sequencing and functional annotation, Gene expression profiling and regulatory network modeling, Identification of molecular markers for breeding, Prediction of plant responses to abiotic and biotic stresses, Integration of multi-omics data to build holistic models of plant metabolism and signaling. Table 1 outlines the key bioinformatics tools employed in plant omics and crop enhancement.

Table 1: Major Bioinformatics Tools Used in Plant Omics and Crop Improvement

Omics area	Tool/Platform	Primary application	Key outputs
Genomics	SOAPdenovo, SPAdes, Canu	Genome assembly and scaffolding	High-quality reference genomes
Gene prediction	AUGUSTUS, MAKER,	Structural gene annotation	Predicted gene

Omics area	Tool/Platform	Primary application	Key outputs
Marker discovery	GeneMark		models
	GATK, SAMtools	SNP and InDel identification	Molecular markers for breeding
Transcriptomics	HISAT2, StringTie, DESeq2	RNA-Seq analysis and DEG detection	Differentially expressed genes
Network analysis	Cytoscape, WGCNA	Gene and protein network construction	Regulatory and co-expression networks
Proteomics	Mascot, MaxQuant	Protein identification and quantification	Stress-responsive proteins
Metabolomics	MetaboAnalyst, XCMS	Metabolite profiling and pathway analysis	Stress-related metabolites
Genome editing	CRISPR-P, Cas-OFFinder	gRNA design and off-target prediction	Optimized genome editing targets
Machine learning	TensorFlow, Scikit-learn	Trait prediction and pattern recognition	Genotype–phenotype models

The growing digitization of plant data has laid the groundwork for *in silico* crop breeding, in which computational analysis comes before field trials, considerably lowering time and expense in varietal creation.

2. Role of Bioinformatics in Plant Genomics

2.1 Genome Sequencing and Assembly

Whole-genome sequencing has emerged as a critical tool in plant biology for studying genome structure, evolution, and function (Michael 2026). Bioinformatics techniques are critical for sequence assembly, error correction, and scaffolding in vast and complex plant genomes, which frequently contain repeated regions and polyploidy (Clavijo et al. 2017). Advanced assemblers such as SOAPdenovo, SPAdes, and Canu have enabled high-quality genome assemblies for a variety of crops (Minhas and Iqbal 2025; Ni et al. 2025). The availability of reference genomes helps comparative genomics and evolutionary investigations, allowing for the identification of conserved and species-specific stress tolerance genes (Pandey 2025). Genome annotation pipelines use transcriptomic and

proteomic data to identify gene models and functional elements, providing information on regulatory mechanisms (Escamilla et al. 2025).

2.2 Gene Prediction and Functional Annotation

Accurate gene prediction is essential for connecting genomic sequences with biological functions (Yandell and Ence 2012). AUGUSTUS, MAKER, and GeneMark are popular bioinformatics tools for *ab initio* and evidence-based gene prediction in plants (Cantarel et al. 2008). Functional annotation assigns biological roles to anticipated genes by homology-based searches against databases such as UniProt, Pfam (<https://www.ebi.ac.uk/interpro/>) and Gene Ontology Resource (Ashburner et al. 2000). Functional annotation enables the identification of stress-responsive genes, transcription factors, and signaling components involved in abiotic and biotic stress responses (Nakashima et al. 2009). Such information is crucial for prioritizing candidate genes for further functional validation and breeding applications.

3. Bioinformatics in Molecular Marker Development and Breeding

3.1 Identification of Molecular Markers

Molecular markers such as simple sequence repeats (SSRs), single-nucleotide polymorphisms (SNPs), and insertion-deletion polymorphisms (InDels) are critical tools in current plant breeding. Bioinformatics pipelines make it easier to identify and validate these markers across the genome using resequencing and comparative genomics data (Varshney et al. 2021). SNP identification using NGS-based techniques has allowed for high-resolution mapping of genomic variation related with stress tolerance features (Rasheed et al. 2017). Marker-assisted selection (MAS) depends largely on bioinformatics to link markers to phenotypic features and speed up breeding operations (Xu and Crouch 2008).

3.2 Quantitative Trait Loci (QTL) Mapping and Genomic Selection

Bioinformatics approaches are critical for QTL mapping, which identifies genomic regions associated with complex traits such as drought tolerance and disease resistance (Collard et al. 2008). Statistical techniques and computational algorithms use genotypic and phenotypic data to accurately identify QTLs (Doerge 2002). Genomic selection (GS) is an advanced breeding strategy that uses genome-wide marker data to predict breeding values (Meuwissen et al. 2001). Bioinformatics-driven GS models improve selection accuracy while decreasing breeding cycles, making them particularly effective for stress tolerance traits influenced by several genes (Crossa et al. 2017).

4. Transcriptomics and Stress Response Analysis

4.1 RNA Sequencing and Differential Gene Expression

Transcriptomic investigations reveal gene expression dynamics under stress circumstances (Wang et al. 2009). RNA sequencing (RNA-Seq) produces huge datasets that require bioinformatics tools for quality control, read alignment, transcript

assembly, and differential expression analysis (Conesa et al. 2016). Transcription factors, signaling molecules, and metabolic enzymes involved in stress adaptation are frequently discovered as differentially expressed genes using transcriptomics (Shinozaki and Yamaguchi-Shinozaki 2007). Bioinformatics analysis allows the creation of co-expression networks that reveal regulatory links between stress-responsive genes (Zhang and Horvath 2005).

5. Proteomics and Metabolomics in Plant Stress Tolerance

5.1 Proteomics Approaches and Bioinformatics Analysis

Proteomics delivers direct insights into the cell's functional molecules by analyzing protein abundance, changes, localization, and interactions under stress circumstances (Pandey and Mann, 2000). Stress responses in plants are frequently regulated at the post-transcriptional and post-translational levels, hence proteome investigations are critical for understanding tolerance mechanisms (Kosová et al. 2019). High-throughput proteomic techniques like two-dimensional gel electrophoresis (2-DE), liquid chromatography-tandem mass spectrometry (LC-MS/MS), and isobaric tagging (iTRAQ, TMT) produce large datasets that necessitate advanced bioinformatics pipelines for protein identification and quantification (Aebersold and Mann 2016). Mascot, MaxQuant, and Proteome Discoverer are popular bioinformatics tools used for peptide-spectrum matching, protein inference, and quantitative analysis (Cox and Mann, 2008). Functional classification and pathway enrichment analyses utilizing Gene Ontology (GO), Kyoto Encyclopedia of Genes and Genomes (KEGG), and MapMan aid in identifying stress-responsive proteins and signaling pathways (Usadel et al. 2009). Heat shock proteins, antioxidant enzymes, and molecular chaperones play roles in plant responses to drought, salinity, and temperature stress, according to proteomic studies (Wang et al. 2016).

5.2 Metabolomics and Computational Interpretation

The focus of metabolomics is on the thorough profile of small molecules, which are the end result of enzyme activity and gene expression (Fiehn 2002). Plant adaptability and survival depend heavily on stress-induced metabolic reprogramming (Obata and Fernie 2012). Complex metabolite datasets produced by methods like nuclear magnetic resonance (NMR) spectroscopy, gas chromatography–mass spectrometry (GC–MS), and liquid chromatography–mass spectrometry (LC–MS) require bioinformatics-driven preprocessing, normalization, and statistical analysis (Dettmer et al. 2007). Metabolite identification, route mapping, and multivariate analysis are made possible by computational tools such as MetaboAnalyst, XCMS, and MZmine (Xia et al. 2015). Osmoprotectants, antioxidants, and stress-related secondary metabolites have been found by metabolomics research to help crops withstand salinity and drought (Arbona et al. 2013). The identification of important metabolic pathways linked to stress tolerance is improved by integrating metabolomic data with transcriptome and genomic information (Fernie and Tohge 2017).

6. Integrative Multi-Omics Approaches

6.1 Systems Biology and Network Analysis

Single-omics techniques frequently offer limited insights into complicated biological processes like stress tolerance, which include several layers of regulation (Liu et al. 2011). Integrative multi-omics techniques use genomes, transcriptomics, proteomics, metabolomics, and epigenomics data to create comprehensive models of plant stress responses (Civelek and Lusis 2014). Bioinformatics tools for data integration and network analysis are essential for systems biology-based crop improvement initiatives (Kitano, 2002). Analysis of the gene regulatory network (GRN) and protein-protein interaction (PPI) networks can assist uncover major regulatory hubs and master regulators involved in stress adaption (Ma et al. 2019). Cytoscape, WGCNA, and STRING are

examples of tools that make complicated biological networks easier to visualize and comprehend (Shannon et al. 2003; Langfelder and Horvath, 2008). These studies have showed that transcription factors, signaling cascades, and metabolic pathways are all coordinated under stress (Nakabayashi et al. 2014).

6.2 Epigenomics and Stress Memory

Epigenetic alterations, such as DNA methylation and histone modifications, play an important role in regulating gene expression in response to environmental stimuli (Chinnusamy and Zhu 2009). Bioinformatics analysis of epigenomic data collected by bisulfite sequencing and chromatin immunoprecipitation sequencing (ChIP-Seq) allows for genome-wide detection of stress-induced epigenetic alterations (Zhang et al. 2018). According to emerging data, plants can store a type of stress memory via epigenetic pathways, which improves tolerance to future stress exposures (Crisp et al. 2016). Integrating epigenomic data with transcriptome and proteomic datasets improves understanding of long-term stress tolerance and resilience in crops (Gallusci et al. 2017).

7. Plant Bioinformatics Databases and Resources

Plant bioinformatics research relies heavily on publicly available databases, which include curated datasets, analytical tools, and visualization platforms. The Arabidopsis Information Resource (TAIR) is a comprehensive resource of gene annotations, functional data, and mutant phenotypes in *Arabidopsis thaliana*, a model plant species (Berardini et al. 2015). Similar crop-specific databases, such as Gramene for grasses and SoyBase for soybeans, facilitate comparative genomics and trait analysis (Tello-Ruiz et al. 2018). Specialized databases focused on stress biology include the Plant Stress Gene Database, PmiREN for plant microRNAs, and PlantPreS for stress-responsive proteins (Gupta et al. 2019; Guo et al. 2020). These resources facilitate data mining, candidate gene identification, and cross-species comparisons of stress response mechanisms.

Bioinformatics platforms integrating expression, regulatory, and interaction data significantly accelerate hypothesis generation and validation in crop improvement studies (Provart et al. 2016). Some important plant bioinformatics databases related to research on stress tolerance are shown in Table 2.

Table 2: Key Plant Bioinformatics Databases Relevant to Stress Tolerance Studies

Database	Focus area	Crop/model coverage	Application in crop improvement
TAIR TAIR - Home	Arabidopsis genomics	<i>Arabidopsis thaliana</i>	Gene function and regulatory studies
Gramene Gramene	Comparative plant genomics	Rice, wheat, maize, grasses	QTL mapping and trait comparison
SoyBase Home–SoyBase	Soybean genomics and breeding	<i>Glycine max</i>	Marker-assisted selection
Plant Stress Gene Database PSGDb database	Stress-responsive genes	Multiple plant species	Candidate gene identification
PmiREN https://pmiren.com/	Plant microRNAs	Multiple crops	Post-transcriptional regulation analysis
STRING STRING: functional protein association networks	Protein–protein interactions	Broad species coverage	Network-based functional prediction

8. Functional Genomics and Genome Editing

Genes implicated in stress tolerance can be identified and validated using bioinformatics-guided functional genomics (Swarbreck et al. 2007). Gene function in model and agricultural plants has been extensively studied using reverse genetics techniques, such as RNA interference and T-DNA insertion mutagenesis (Alonso et al. 2003). Prioritizing targets for experimental validation is aided by computational prediction of gene function and regulatory elements (Mutwil et al. 2010). Plant biotechnology has undergone a revolution with the development of CRISPR/Cas genome editing, which enables precise modification of stress-responsive genes (Jinek et al. 2012). Guide RNA design, off-target prediction, and editing efficiency

evaluation all depend on bioinformatics techniques (Bae et al. 2014). Bioinformatics-informed genome-editing techniques have been successfully used to improve disease, salinity, and drought resistance in many crops (Chen et al. 2019).

9. Machine Learning and Artificial Intelligence in Crop Improvement

Plant bioinformatics is increasingly incorporating machine learning (ML) and artificial intelligence (AI) techniques to forecast complex characteristics and stress responses (Libbrecht and Noble 2015). To find hidden patterns and genotype–phenotype relationships, machine learning models can examine sizable, diverse datasets, such as genomic, phenotypic, and environmental data (Crossa et al. 2017). Genomic selection, stress phenotypic

prediction, and the identification of important regulatory characteristics are some of the applications of machine learning in crop development (Washburn et al. 2025). Deep learning techniques have demonstrated potential for high-throughput stress detection and image-based phenotyping, which will further improve precision breeding techniques (Singh et al. 2016).

10. Applications in Crop Improvement: Case Studies

Bioinformatics-driven approaches have considerably aided the development of stress-tolerant crop varieties (Varshney et al. 2021). In rice, genome-wide association studies (GWAS) and transcriptome analysis have identified critical loci and genes linked to drought and salinity tolerance (Huang et al., 2010). In wheat, genomic selection and marker-assisted breeding rushed the development of heat and disease-resistant cultivars (Bassi et al. 2019). Similarly, using bioinformatics to identify resistance genes and regulatory networks has increased maize and soybean tolerance to biotic stressors (Dodds and Rathjen 2010). These case studies highlight the practical application of plant bioinformatics in improving crop resilience and yield.

11. Climate-smart agriculture

Climate-smart agriculture (CSA) has emerged as a transformative strategy for addressing the growing challenges of climate variability and ensuring sustainable crop production under adverse environmental conditions. It integrates agricultural practices and technological innovations that simultaneously enhance productivity, strengthen resilience to abiotic and biotic stresses, and reduce greenhouse gas emissions to support long-term food security. In the context of modern crop improvement, plant bioinformatics plays a crucial role in advancing CSA by enabling the identification of stress-responsive genes, regulatory networks, and molecular markers associated with drought, salinity, heat, and pathogen resistance through the analysis of large-scale omics datasets.

Computational approaches such as genome-wide association studies, comparative genomics, transcriptome profiling, and predictive modeling facilitate the development of climate-resilient crop varieties with improved adaptive traits. Furthermore, bioinformatics-driven integration of multi-omics data accelerates precision breeding and supports data-informed decision-making, thereby enhancing the efficiency of breeding programs aimed at developing sustainable and climate-resilient agricultural systems (FAO 2013; Lipper et al. 2014; Edwards and Batley 2004; Tan et al. 2022).

12. Challenges and Future Perspectives

Despite substantial gains, there are still various barriers to using plant bioinformatics for crop improvement (Bevan et al. 2017). Data integration across many omics layers, limited computing infrastructure, and the necessity for standardized data formats are significant challenges (Gomez-Cabrero et al. 2014). Furthermore, turning computational predictions into field-level performance necessitates thorough validation and multidisciplinary collaboration (Cooper et al. 2014). Future improvements in bioinformatics, such as enhanced AI algorithms, cloud-based platforms, and the integration of phenomics and environmental data, are projected to improve predictive accuracy and scalability (Tardieu et al. 2017). Strengthening data exchange and skill training in poor nations will broaden the worldwide impact of bioinformatics-based crop improvement.

13. Conclusion

Plant bioinformatics has altered crop development by allowing for extensive study of genomic and post-genomic data to uncover stress tolerance mechanisms. Bioinformatics helps to generate resilient and high-yielding agricultural varieties by combining multi-omics techniques, powerful computational tools, and genome editing technologies. Continued innovation and interdisciplinary collaboration will be required to fully realize the potential of plant bioinformatics for sustainable agriculture and global food security.

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