

New insights for bioinformatics, plant genes, biotic and abiotic stresses, food technology and agricultural applications

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DOI: [10.36348/sjls.2023.v08i09.004](https://doi.org/10.36348/sjls.2023.v08i09.004)

| Received: 02.09.2023 | Accepted: 09.10.2023 | Published: 17.10.2023

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Abstract

The amount of data has grown enormously over the last several decades, because the sciences of molecular biology and genomics are producing ever-larger reservoirs of rich biodata. The plant needs a significant alteration in metabolism to endure unfavorable environmental stress circumstances, such as drought and environmental stresses. This alteration comprises considerable transcriptome reprogramming upon the onset of the stress and transcription and gene expression regulation. Crops including cotton, maize, and potatoes have benefited from the introduction of many genes obtained from *Bacillus thuringiensis*. The genes increase the plants' resistance to insect assaults, which lowers or even eliminates the need for certain pesticide treatments. An increasing amount of research suggests that plants' nutritional status in minerals has a major impact on their ability to adapt to harsh environmental conditions. Being complex creatures, plants may face a variety of biotic and abiotic challenges in their natural habitat. A number of biotic and abiotic pressures coincide as a result of global warming, which lowers agricultural production. Different biometrical analyses, including path coefficient, discriminant function, generation means, line x tester, triple test cross, stability parameters, D2 statistics, metroglyph, diallel, partial diallel, triallel, quadriallel, etc., are performed in plant breeding and genetics. Two kinds of food plants, such as *Oryza sativa* and *Arabidopsis thaliana*, have had their whole genomes sequenced. The production of ABA involves the enzymes zeaxanthin epoxidase (ZEP), 9-cis-epoxycarotenoid dioxygenase (NCED), and ABA-aldehyde oxidase (AAO). Drought tolerance is increased in plants that overexpress these genes.

Keywords: Zeaxanthin epoxidase, ABA-aldehyde oxidase, Drought tolerance, molecular biology.

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INTRODUCTION

The computer-assisted study of genetics and biology is known as bioinformatics. Stated differently, it describes the computer-aided investigation of biological data, including genetics. Bioinformatics is becoming a more and more important branch of life science, particularly in the areas of molecular biology and plant genetic resources [1-2]. Computer simulation assessments of biological inquiries have been performed using statistical, computational, and computer programming methods. These are repurposed "pipelines" for certain analyses, especially in the domain of

genomics, where genes and single nucleotide polymorphisms (SNPs) are identified. By using these pipelines, one may get a deeper understanding of the genetic underpinnings of various diseases, special adaptations, and desirable traits particularly in agricultural animals, and population variations [3-5]. Proteomics, which aims to comprehend the organizing principles inside protein and nucleic acid sequences, is another branch of bioinformatics. Bioinformatics, which has an astounding array of applicability in the current digital environment, leverages the past century of biology study and draws inspiration from the world's species to construct a cleaner and healthier future. The

amount of data has grown enormously over the last several decades, mostly because the sciences of molecular biology and genomics are producing ever-larger reservoirs of rich biodata. "Genome" describes the fundamental group of chromosomes. Every kind of chromosome is only represented once in a genome [6-7]. Genomic science is the study of the structure and function of an organism's whole genome. It is currently being developed as a branch of genetics that focuses on genome mapping, sequencing, and functional analysis. Expanding our knowledge of biological processes is the main objective of bioinformatics. It differs from other methods in that it focuses on creating and using computationally complex methods to do this. Pattern recognition, data mining, machine learning techniques, and visualization are a few examples.

Sequence alignment, gene finding, genome assembly, drug design, drug discovery, protein structure alignment, protein structure prediction, gene expression and protein-protein interaction prediction, genome-wide association studies, and the modeling of evolution and cell division/mitosis are some of the major research areas in this field [1, 6, 7]. The term "genome" refers to an organism's entire genetic makeup in terms of its nuclear deoxyribonucleic acid (DNA) content. It should be remembered, though, that organelles other than the nucleus can store genetic information as well, such as the mitochondrial or chloroplast (plant-only) genomes [4, 6]. Functional Genome Analysis that covers the roles played by each and every protein in a living thing. Proteomics is really a very recent topic in functional genomics. It is the study of proteomes, which are the whole collection of proteins that a genome encodes. Proteomics research employs a range of methodologies. There are now computer-aided programs accessible for proteomics research. The study of every metabolic pathway found in a living thing is known as metabolomics. Stated differently, it is the computer-assisted data on every metabolic pathway found in a living thing [8-9]. Crop improvement is a significant area in which bioinformatics is used. It develops robust, more insect- and drought-resistant crops by using the proteome, metabolome, genetic, and agricultural crop production techniques effectively. Therefore, improving cattle quality and conferring disease resistance. In the modeling of agricultural plants, bioinformatics is crucial. Studies on field pea and a few other field crops have already been conducted with the use of computers. Initially, a variety of plant attributes are used to envision the plant model, and then attempts are made to improve it via proper breeding techniques [9-10].

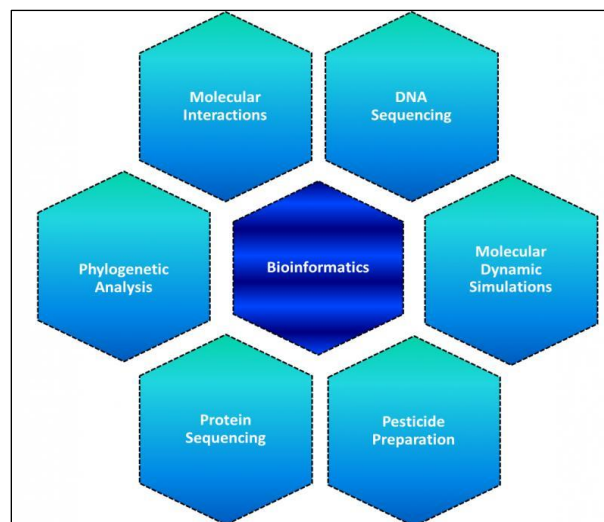


Figure 1: Shows the role of bioinformatics and current applications in agricultural applications

Current advances in agricultural applications

Generally referred to as agri-informatics, some of the various applications of bioinformatics tools and methods in agriculture focus on improving plant resistance against biotic and abiotic stressors as well as enhancing the nutritional quality in depleted soils. Waste clean-up is a significant area in which bioinformatics is used. Here, the main goal is to discover and evaluate the DNA sequencing of microorganisms and bacteria so that they may be used for various purposes such as oil spill cleanup, radioactive waste removal, and sewage cleaning. The bacteria *Deinococcus radiodurans* is regarded as the toughest bacteria. Computer-assisted research is helpful for analyzing the pedigrees of different hybrids and cultivars [11-12]. The computer memory stores information on the lineage of hybrids and cultivars that may be accessed at any moment. It is simple to filter through the list of parents shared by different cultivars and hybrids in the pedigree. It supports pedigree analysis, which is useful for organizing plant breeding initiatives, particularly for choosing parents for hybridization projects. The study of protein structures aids in the analysis of pedigrees. Crops including cotton, maize, and potatoes have benefited from the introduction of many genes obtained from *Bacillus thuringiensis*. These genes increase the plants' resistance to insect assaults, which lowers or even eliminates the need for certain pesticide treatments [13-15]. The comparative study of the microbial genome, which employs metabolic comparison and gene organization at the metabolic reactions level with their operons employing route, reaction, structure, chemicals, and gene orthologs, provides a better knowledge of genome evolution. In this sense, the sequencing of whole genomes from different species facilitates the knowledge of their functioning and allows for the determination of their organization, which supports the practice of human agriculture. Different biometrical analyses, including path coefficient, discriminant function, generation means, line x tester, triple test cross, stability parameters, D2 statistics,

metroglyph, diallel, partial diallel, triallel, quadriallel, etc., are performed in plant breeding and genetics [12-15].

Computer-aided programs are invaluable for doing these kinds of biometric studies. The data gathered from these biometrical analyses is utilized to better organize plant breeding initiatives in order to accomplish certain objectives. A maize model organism database called MaizeGDB makes information on genes, alleles, molecular markers, metabolic pathways, phenotypic photos with descriptions, and other topics relevant to maize study accessible. MaizeDIG is a genotype-phenotype database that enables users to connect the association between genotype and phenotype as expressed by images, while MaizeMine is a data mining resource under MaizeGDB that created to speed up genomics analysis by enabling researchers to better script their own research data in downstream analysis. The association between a gene and its phenotypic traits may be seen inside a picture when accessed using an image search engine. Rapid prioritization of crop phenotypes of interest is made possible by the integration and display of high-quality data using these technologies, which is essential for improving plant breeding [11, 16, 17]. Plants undergo evolutionary changes, yet their genomes do not contain much information since they are conserved. With the advent of bioinformatics technologies, the necessary data may now be extracted from a particular plant's genome. Two kinds of food plants, such as *Oryza sativa* and *Arabidopsis thaliana* have had their whole genomes sequenced. The English names for these two plant species are rice and water cress, respectively. The desirable genes have been incorporated into several plants to make them resistant to insects [11,15,17]. A kind of bacterium called *Bacillus thuringiensis* boosts soil fertility and protects plants from pests. Upon mapping its genome, the scientists were able to exploit its genes to confer insect resistance to the plant. For instance, potatoes, maize, and cotton have all been engineered to withstand insects so far. Because bacteria's genes are present in the genomes of plants, when insects consume the plants, the bacteria enter their circulation, starve the insects, and eventually cause them to die. One kind of food plant that has had bacterial genes inserted into it is bt corn. By creating a resistance to insects, it works well against them. Because Bt genes are incorporated into plant genomes, farmers are now using pesticides sparingly. Consequently, plants will yield more and have more nutritional content, both of which are good for human health [18-21].

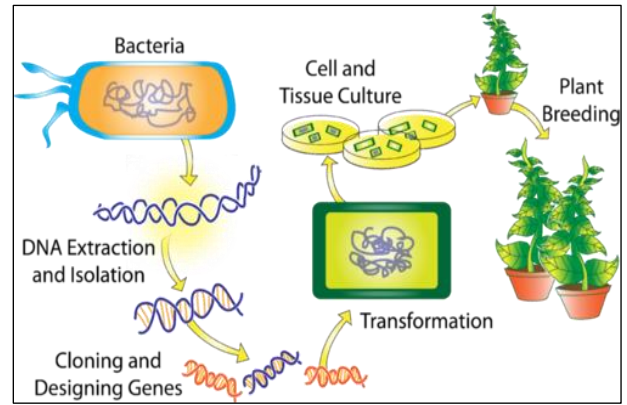


Figure 2: Shows the molecular approaches in the plant genetic sciences

Certain types of cereals are created that can withstand drought and flourish in unfavorable soil conditions. This technique allows for the utilization of locations with less fertile soil. Numerous proteins linked to metabolism have been shown to be involved in the body's reaction to drought. One example are the enzymes involved in the metabolism of ABA. In order to minimize water loss, ABA triggers stomatal closure, which is a crucial component of drought tolerance. The production of ABA involves the enzymes zeaxanthin epoxidase (ZEP), 9-cis-epoxycarotenoid dioxygenase (NCED), and ABA-aldehyde oxidase (AAO). Drought tolerance is increased in plants that overexpress these genes [22, 23]. In order to successfully generate transgenic plants, it is not only necessary to successfully complete the transformation process but also to appropriately integrate stress tolerance. The correct comprehension of the inserted gene's physiological effects and the assessment of transgenic plants under stress represent significant obstacles. The regulatory mechanism of transcription factors has become a new instrument for regulating the expression of numerous stress-responsive genes, after the manipulation and insertion of "single-action" genes. From an agronomic standpoint, DE and early blooming cultivars with quicker life cycles are intriguing because they may enable grain filling before to the beginning of seasonal terminal drought due to an expected changeover to the reproductive stage. On addition, a shorter crop season may make double cropping growing two distinct crops on the same area in the same year possible and lessen the need for agricultural inputs like pesticides and fertilizers. Conversely, crops whose blooming dates are pushed forward would produce less. Although, DE is a relatively new area of study in agricultural science, no biotechnologically enhanced crop currently exists that uses DE as a drought resistant feature. According to some theories, DE may be used to create grain types that develop quickly and blossom early. These kinds of crops would be particularly helpful in temperate places such as the Mediterranean region, where terminal dryness is predicted to have an impact on plants towards the conclusion of the crop season [24-27].

Molecular Factors and stress biology

Significant cross-talk between the drought, high salinity, and ABA response pathways is shown by the fact that over half of these genes that are activated by drought were also induced by high salinity and/or ABA treatments. Conversely, just 10% of the genes that were triggered by dryness were likewise elevated by cold stress. Approximately 8000 distinct Arabidopsis genes were represented by oligonucleotides on the Affimetrix GeneChip array, which was used to identify thousands of stress-inducible genes. Drought is one of the most significant and growing environmental pressures on agricultural productivity. Water intake, plant adaptability, and the long-term development of plant species to climate change are all impacted by drought stress [3]. The plant needs a significant alteration in metabolism to endure unfavorable environmental stress circumstances, such as drought. This alteration comprises considerable transcriptome reprogramming upon the onset of the stress and transcription and gene expression regulation [21, 23, 25]. Consequently, transcriptome research provides valuable understanding of the processes underlying plant stress responses. Hormones are among the tiny plant molecules that are crucial for controlling the intricate physiological and molecular reactions of plants to drought. The primary hormone regulating water loss and maintaining cellular development is abscisic acid. Light is necessary for photosynthesis to occur, which is directly related to the creation of oxygen and carbohydrates. Every plant needs light and sun exposure for growth and development, and these factors are also impacted by their quantity or shortage.

The biostimulant TrichoSym Bio increases a plant's resistance to abiotic stresses including salt, drought, and floods. Plant nutrition is improved and root system growth is facilitated by the solubilization of macro- and micronutrients [27, 27]. It seems that in the next decades, research on plant nutrition will take center stage in efforts to preserve soil fertility and boost agricultural productivity. In order to live and yield, crop plants exposed to environmental stresses need to be able to develop adaption mechanisms that allow them to either endure or escape stress. An increasing amount of research suggests that plants' nutritional status in minerals has a major impact on their ability to adapt to harsh environmental conditions. This review aims to clarify the role that mineral nutrients play in improving agricultural plants' ability to tolerate temperature stress [28-32].

Other environmental stresses

Complex crosstalk controls the course of the responses, with small molecules (like hormones) specifically acting to inhibit or induce key proteins involved in the reception, transmission, and responses to stress signals, including kinases, phosphatases, transcription factors, and defensive responsive genes [6]. Certain important families of transcription factors (TFs),

including bZIPs, WRKY, and MYB, have been seen to have varying degrees of involvement based on the kind of stress. Genetic engineering has been used to enhance the stress tolerance of some TFs in agricultural and model plants [28, 31, 32]. Abiotic stressors alter yield by interfering with regular morpho-biochemical and physiological processes. Based on genetics, different people react differently to various pressures. TFs work in concert with other transcription binding sites to activate the genes found in plants. The TFs connected the cis-acting elements of all gene promoters in upstream regions. Furthermore, TFs are essential for the expression of genes because they either stimulate or inhibit the activity of the DNA polymerase enzyme. TFs improve the response to drought tolerance and activate a large number of genes linked to stress. The essential amino acids have a role in providing plants with resilience to abiotic stress. TFs are beneficial because they shield plants from biotic and abiotic stressors. Being complex creatures, plants may face a variety of biotic and abiotic challenges in their natural habitat. A number of biotic and abiotic pressures coincide as a result of global warming, which lowers agricultural production [1]. Worldwide agricultural production is significantly impacted by abiotic stressors, which lower yields in a variety of crop species. Ion distribution and homeostasis in the cell are disrupted by osmotic stress, which is linked to heat, cold, salt, drought, and toxic metal stressors. The primary cause of this disruption is modifications in a set of genes' expression patterns, which in turn cause reactions that impact productivity and growth rates [33-35].

CONCLUSION

Plants have limitations on their developmental processes, such as germination, flowering, and reproduction, when stress is higher or lasts longer. This eventually leads to the death of the plant. These plants are referred to be sensitive. Plants that are considered stress-escapers often are resistant to stress. Transient or transitory desert plants are examples of this kind of plant. Thanks to recent advances in molecular and genomic studies using transgenic plants and mutants with modified or missing polyamine-producing enzyme activity, our understanding of the biological significance of polyamines in plants has increased.

REFERENCES

1. Kumar, M. (2013). Crop plants and abiotic stresses. *J. Biomol. Res. Ther.*, 3(1).
2. Ashraf, M. Y., & Wu, L. (1994). Breeding for salinity tolerance in plants. *Critical Reviews in Plant Sciences*, 13(1), 17-42.
3. Hurley, J. H., & Misra, S. (2000). Signaling and subcellular targeting by membrane-binding domains. *Annual review of biophysics and biomolecular structure*, 29(1), 49-79.
4. Sutton, R. B., & Sprang, S. R. (1998). Structure of the protein kinase C β phospholipid-binding C2

- domain complexed with Ca²⁺. *Structure*, 6(11), 1395-1405.
5. Cho, W. (2001). Membrane targeting by C1 and C2 domains. *Journal of Biological Chemistry*, 276(35), 32407-32410.
 6. Senthil-Kumar, M., & Mysore, K. S. (2014). Tobacco rattle virus-based virus-induced gene silencing in *Nicotiana benthamiana*. *Nature protocols*, 9(7), 1549-1562.
 7. Shen, Y. G., Zhang, W. K., He, S. J., Zhang, J. S., Liu, Q., & Chen, S. Y. (2003). An EREBP/AP2-type protein in *Triticum aestivum* was a DRE-binding transcription factor induced by cold, dehydration and ABA stress. *Theoretical and Applied Genetics*, 106, 923-930.
 8. Shen, Y. G., Zhang, W. K., He, S. J., Zhang, J. S., Liu, Q., & Chen, S. Y. (2003). An EREBP/AP2-type protein in *Triticum aestivum*
 9. Xu, X. M., Lin, H., Maple, J., Björkblom, B., Alves, G., Larsen, J. P., & Møller, S. G. (2010). The *Arabidopsis* DJ-1a protein confers stress protection through cytosolic SOD activation. *Journal of cell science*, 123(10), 1644-1651.
 10. Yamaguchi-Shinozaki, K., & Shinozaki, K. (2005). Organization of cis-acting regulatory elements in osmotic- and cold-stress-responsive promoters. *Trends in plant science*, 10(2), 88-94.
 11. Zhang, L., Li, T., Wang, Y., Zhang, Y., & Dong, Y. S. (2019). FvC5SD overexpression enhances drought tolerance in soybean by reactive oxygen species scavenging and modulating stress-responsive gene expression. *Plant Cell Reports*, 38, 1039-1051.
 12. Zhao, D., Luan, Y., Shi, W., Zhang, X., Meng, J., & Tao, J. (2021). A *Paeonia ostii* caffeoyl-CoA O-methyltransferase confers drought stress tolerance by promoting lignin synthesis and ROS scavenging. *Plant Science*, 303, 110765.
 13. Shi, H., Ishitani, M., Kim, C., & Zhu, J. K. (2000). The *Arabidopsis thaliana* salt tolerance gene SOS1 encodes a putative Na⁺/H⁺ antiporter. *Proceedings of the national academy of sciences*, 97(12), 6896-6901.
 14. Shinozaki, K., & Yamaguchi-Shinozaki, K. (2000). Molecular responses to dehydration and low temperature: differences and cross-talk between two stress signaling pathways. *Current opinion in plant biology*, 3(3), 217-223.
 15. Du, H., Wang, N., Cui, F., Li, X., Xiao, J., & Xiong, L. (2010). Characterization of the β -carotene hydroxylase gene DSM2 conferring drought and oxidative stress resistance by increasing xanthophylls and abscisic acid synthesis in rice. *Plant physiology*, 154(3), 1304-1318.
 16. Kuppu, S., Mishra, N., Hu, R., Sun, L., Zhu, X., Shen, G., ... & Zhang, H. (2013). Water-deficit inducible expression of a cytokinin biosynthetic gene IPT improves drought tolerance in cotton. *PLoS One*, 8(5), e64190.
 17. Way, H., Chapman, S., McIntyre, L., Casu, R., Xue, G. P., Manners, J., & Shorter, R. (2005). Identification of differentially expressed genes in wheat undergoing gradual water deficit stress using a subtractive hybridisation approach. *Plant Science*, 168(3), 661-670.
 18. Weber, M., Trampczynska, A., & Clemens, S. (2006). Comparative transcriptome analysis of toxic metal responses in *Arabidopsis thaliana* and the Cd²⁺-hypertolerant facultative metallophyte *Arabidopsis halleri*. *Plant, Cell & Environment*, 29(5), 950-963.
 19. Fernández, V., Guzmán-Delgado, P., Graça, J., Santos, S., & Gil, L. (2016). Cuticle structure in relation to chemical composition: re-assessing the prevailing model. *Frontiers in plant science*, 7, 427.
 20. Fita, A., Rodríguez-Burruezo, A., Boscaiu, M., Prohens, J., & Vicente, O. (2015). Breeding and domesticating crops adapted to drought and salinity: a new paradigm for increasing food production. *Frontiers in Plant Science*, 6, 978.
 21. Gupta, A., Singh, M., & Laxmi, A. (2015). Multiple interactions between glucose and brassinosteroid signal transduction pathways in *Arabidopsis* are uncovered by whole-genome transcriptional profiling. *Plant physiology*, 168(3), 1091-1105.
 22. Hörtensteiner, S. (2009). Stay-green regulates chlorophyll and chlorophyll-binding protein degradation during senescence. *Trends in plant science*, 14(3), 155-162.
 23. Abe, H., Yamaguchi-Shinozaki, K., Urao, T., Iwasaki, T., Hosokawa, D., & Shinozaki, K. (1997). Role of *Arabidopsis* MYC and MYB homologs in drought- and abscisic acid-regulated gene expression. *The Plant Cell*, 9(10), 1859-1868.
 24. Bartels, D., & Sunkar, R. (2005). Drought and salt tolerance in plants. *Critical reviews in plant sciences*, 24(1), 23-58.
 25. Maruyama, K., Sakuma, Y., Kasuga, M., Ito, Y., Seki, M., Goda, H., ... & Yamaguchi-Shinozaki, K. (2004). Identification of cold-inducible downstream genes of the *Arabidopsis* DREB1A/CBF3 transcriptional factor using two microarray systems. *The Plant Journal*, 38(6), 982-993.
 26. Balan, B., Caruso, T., & Martinelli, F. (2017). Gaining insight into exclusive and common transcriptomic features linked with biotic stress responses in *Malus*. *Frontiers in plant science*, 8, 1569.
 27. Kim, D., Langmead, B., & Salzberg, S. L. (2015). HISAT: a fast spliced aligner with low memory requirements. *Nature methods*, 12(4), 357-360.
 28. Benjamini, Y., & Hochberg, Y. (1995). Controlling the false discovery rate: a practical and powerful approach to multiple testing. *Journal of the Royal statistical society: series B (Methodological)*, 57(1), 289-300.
 29. Bent, A. F. (1996). Plant disease resistance genes: function meets structure. *The Plant Cell*, 8(10), 1757.

30. Tanksley, S. D., & Orton, T. J. (2012). *Isozymes in plant genetics and breeding*. Elsevier.
31. Gilmartin, P. M., Sarokin, L., Memelink, J., & Chua, N. H. (1990). Molecular light switches for plant genes. *The Plant Cell*, 2(5), 369.
32. Heidecker, G., & Messing, J. (1986). Structural analysis of plant genes. *Annual Review of Plant Physiology*, 37(1), 439-466.
33. Sharma, H. C., Crouch, J. H., Sharma, K. K., Seetharama, N., & Hash, C. T. (2002). Applications of biotechnology for crop improvement: prospects and constraints. *Plant Science*, 163(3), 381-395.
34. Taylor, N. J., & Fauquet, C. M. (2002). Microparticle bombardment as a tool in plant science and agricultural biotechnology. *DNA and cell biology*, 21(12), 963-977.
35. Christou, P., & Klee, H. (Eds.). (2004). *Handbook of plant biotechnology* (Vol. 1). Chichester: John Wiley & Sons.