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Genomic and Multi-Omics Approaches for Improving Drought and Heat Stress Tolerance in Cotton (*Gossypium spp.*)

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Abstract

Gossypium spp. i.e. cotton is still counted as one of the most valuable fiber and oil seed crops in the world since it has supported the textile economy of the world and the livelihood of millions of people worldwide. Nevertheless, it is becoming limited in productivity and fiber quality by climate-related stresses of water scarcity, and heat, which have extremely negative impacts on plant growth, product, and fiber characteristics. It is thus important to understand the molecular and physiological mechanisms involved in stress adaptation to be able to provide sustainable production under the changing climatic conditions. This review gathers recent high-impact innovations in the fields of genomic and multi-omics protocols: genomics, transcriptomics, proteomics, metabolomics, and epigenomics protocols that have revolutionized the study of the stress tolerance mechanisms of cotton. The integrative omics studies have revealed major transcription factors, signaling cascades and metabolic farms that mediate drought and heat resistance and allowed identifying candidate genes to eliminate specific failures. Genome-wide association studies (GWAS), genomic selection (GS), and CRISPR/Cas-based genome editing are now hastening the identification and functional placement of genes at work due to stress response. Even though these breakthroughs have been made, two issues concerning the integration of multi-layered omics data with phenotypic and environment data still exist. The translation of the results of omics insights into practical breeding results is hindered by limited field validation, intricate interactions of genotype and environment, and the demand to have sophisticated data analytics. The given review reveals the prospects of systems biology and artificial intelligence (AI)-based frameworks in sealing these gaps and creating climate-resilient cotton crops. It provides a current overview of the

state of the art in omics-based studies, which highlights the possibilities of integrative molecular breeding to transform cotton so as to become more drought and heat tolerant to enable production of consistent fibers and food-fiber security of the world considering global climatic changes.

Keywords: Cotton genomics; multi-omics integration; Drought tolerance; Heat stress; Molecular breeding; CRISPR; Systems biology

1. Introduction

Serving as a fundamental part of the world textile market cotton (*Gossypium* spp.) is grown on more than 80 countries. In addition to its economic significance as the key natural fiber, cotton plays a major role in the rural livelihoods, oilseeds economics, and agro-industrialization. But being a warm season crop, cotton is very susceptible to environmental changes in temperature and water supply, which are two/environmental factors that are greatly influenced by the climate change process that is currently taking place. Extreme events, such as prolonged droughts, high temperatures, and unpredictable patterns of rainfall, threaten the cotton production and quality of the fibers produced in the primary cultivators, like Pakistan, India, China, and the United States (Ali et al., 2024). These stresses not only decrease the lint yield but worsen the fiber length, strength, and micronaire that are important parameters in affecting the market value (Zhang et al., 2023).

1.1. Climate Problems and Cotton Productivity.

Climate change has a multi-dimensional effect on the physiology and productivity of cotton. Heat waves hasten the process of evapotranspiration as well as decrease crop length leading to the loss of full boll maturation and photosynthesis

efficiency (Patel et al., 2022). At the same time, deficiency of water induces physiological and metabolic disruption of cellular homeostasis. In combination, drought and heat stress are significant abiotic dangers that tend to act synergistically making oxidative damage, membrane leakage, and yield penalties more severe (Wang et al., 2021). The number of extreme heat waves that occur in cotton fields has almost doubled over the last 20 years, and the reduction in yields has been over 20 percent in certain fields (Raza et al., 2023). These patterns demonstrate the necessity to enhance the resiliency of cotton by genetic and molecular breakthroughs.

1.2. Weaknesses of Traditional Breeding methods.

Traditional breeding initiatives have had impressive success in increasing the level of cotton yield potentiality and resistance to pests; development of resistance to abiotic stress has been comparatively sluggish. Drought and heat tolerance are complicated, quantitative characteristics that are controlled by many tiny impact loci that collaborate with surrounding circumstances (Patel et al., 2022). It is known that their expression is often affected by genotype x environment (G x E) and thus makes it hard to select them easily. Moreover, classical methods of selection are vastly dependent on

observable or yield dependent characteristics, which are slow to measure, and have a low heritability when subjected to fluctuating conditions in fields. Genetic gains are further limited by the lack of high-throughput phenotyping platforms that have high reliability.

In order to solve these constraints, an evolutionary tool has been developed called molecular breeding and genomic-assisted selection as a revolutionary method in the improvement of plants in the contemporary world. These methods can be used to discover the marker-trait relationship by integrating high-throughput sequencing with specialized statistical models and hence breeders can now forecast the performance based on the genotype and not trajectory (Xu et al., 2020).

1.3. Coming up with Omics Technologies in the Cotton Research.

The whole genome of *G. hirsutum*, *G. barbadense* and *G. arboreum* has been sequenced, which has provided the basis to research into the allopolyploid genome of cotton (Hu et al., 2019). The genomic research has identified many genes families and controlling factors related to stress signaling and adaptation. Simultaneous progress in transcriptomics, proteomics, metabolomics, and epigenomics can now be used to examine elaborate breakdown of plant reactions at various biological scales. As an example, drought and heat stress transcriptome profiling has found thousands of variousially expressed genes in osmoprotectants, antioxidant defense and hormonal regulation (Mehta et al., 2023). The proteomic and metabolomic techniques further explain the post-

translational mechanism and biochemical adaptations involved in stress tolerance (Huang et al., 2022).

1.4. Multi-Omics Nutrition IBM be crossed with breeding.

The application of integrative multi-omics methodologies, where genomics, transcriptomics, proteomics and metabolomics data are synthesized, provide an integrated perspective of the way stress responses are integrated in cotton plants. This can be integrated to identify hub genes, protein/protein interaction networks and metabolite signature that is associated with adaptive traits (Singh et al., 2024). With these discoveries combined with genomic methods, including genome-wide association (GWAS) and genomic selection (GS), breeding cotton crops is currently transforming that germs of responsible breeding to expedite the identification and validation of the functional significance of target stress-related genes (Wang et al., 2023).

With the use of gene-editing systems, notably, CRISPR/Cas9, gene functions are now validated with legendary precision and put in place targeted allelic variants with superior resilience (Zhu et al., 2023). Recently, CRISPR-based tools have been utilized successfully to regulate such transcription factors as GhDREB2A and GhHSP90 to achieve a gain in efficiency during photosynthesis and improve survival in the face of stress. In addition, recent advances in prime and base editing technologies have increased the opportunities of this area, introducing the ability to make single point changes, thus allowing the creation of specific alleles

with reduced off-target consequences (Yang et al., 2024).

1.5. Closing the Gap between Lab and Practice.

Although these are impressive improvements, there still lie tremendous hurdles in the efforts of applying what is discovered in the laboratory to what can be applied in the fields as cultivars. The majority of omics experiments are carried out in carefully controlled conditions, which do not reflect the field conditions (Huang et al., 2022). Also, the scarcity of knowledge of cross-talk of drought and heat stress pathways, along with the mechanisms of epigenetics regulation in long-term adaptation, restricts advances in breeding (Azhar et al., 2022). Standardized repositories of data and computational tools to assimilate heterogeneous omics data have also not been established across genotypes and environments.

To solve these bottlenecks, it is necessary to have a systems biology model that bridges the gap between the molecular information and the phenotypic performance and environmental signal. A combination of omics-based knowledge and accuracy phenotyping and crop modeling may offer predictive ability of human selection of high performing genotypes in different climatic conditions (Singh et al., 2024). Agreements and organizations within the genomics sector like the International Cotton Researchers Association (ICRA) and the International Cotton Genome Initiative (ICGI) are beginning to pay greater attention to open-access genomic data, and common data standards, which will be critical to the scale of such advances across the world.

1.6. Objectives of the Review

This is expected to review and critically analyse the recent advances in the area of using genomics and multi-omics technology to enhance drought and heat tolerance in cotton. It discusses (i) physiological and genetic foundations of stress tolerance; (ii) future key approaches to genomic studies, including GWAS, genomic selection, and CRISPR-based genome editing, and (vi) a comprehensive process of converting insights in the field of genomics to resilient I field crops; and (i) the challenges and opportunities related to that essential process. Through making an in-depth description of these trends, the review aims at informing subsequent studies into sustainable and climatically resilient cotton production systems.

2. Genetic and Physiological Basis of Stress Tolerance

One of the most serious abiotic factors that reduce the cotton productivity and the quality of its fibers is drought and the heat stress. All these stresses influence almost all developmental processes such as seed germination and vegetation, flowering and boll maturation, leading to instability in the yield. It is then important to understand the genetic and physiological processes that contribute to stress tolerance with the view to developing climate-tolerant cotton cultivars that are able to withstand these extreme conditions to remain productive.

2.1. Physiological Processes of Tolerance to drought.

Stresses of drought are also associated with a complex chain of physiological adaptations in cotton plants, which aims at conserving water and cellular homeostasis.

The oldest reaction is stomatal closure and a change in photosynthetic activity to reduce the loss of water and maintain carbon assimilation. The plant hormone abscisic acid (ABA) is the main regulatory factor of the process, and it quickly builds up in the event of a water shortage and makes the guard cells communicate with each other (Li et al., 2022).

One of the most important adaptive mechanisms is Osmotic adjustment that helps the cotton cells to maintain turgor pressure despite low water potential. The sugars, which are compatible with solutes (proline, glycine betaine, trehalose, and soluble sugars), are deposited in recent genotypes under drought conditions, stabilizes proteins, membranes, and prevents enzyme activity (Raza et al., 2023). By way of example, it has been reported that the tolerant *Gossypium hirsutum* cultivars retain a high level of leaf water potential and osmotic adjustment capacity leading to the improved photosynthetic efficiency through extended drought periods (Zhang et al., 2024)

Another major role is played by root system architecture. Drought resistant genotypes have deeper and branched root systems which are better in extracting water at the lower layers of soil. Phenotyping a study on the use of rhizotrons and 3D root imaging has found that there is a great deal of variation between elite cotton lines in terms of root length density and root length distribution (Gao et al., 2023). Increased root growth promotes the uptake of water as well as augmenting nutrient acquisition and the adaptability to combined heat and drought conditions.

Drought stress at the biochemical level facilitates the production of reactive oxygen species (ROS) including superoxide radical and hydrogen peroxide. In an attempt to counter oxidative damages, cotton plants increase the expression of antioxidant enzymes such as superoxide dismutase (SOD), catalase (CAT), and ascorbate peroxidase (APX) (Mehta et al., 2023). These enzymes coordinate defensive system that maintains the integrity of the chloroplast and mitochondria in the period of the stress. What is more, drought induces late embryonic abundant (LEA) protein and dehydrin synthesis as molecular shields that stabilize macromolecules and membranes of cells (Patel et al., 2022)

2.2. Bodily and Molecular Reactions against Heat Stress.

Stress caused by heat, especially in association with flowering and boll formation is very detrimental to cotton yield and fiber formation. High temperatures damage photosynthetic apparatus, lead to the denaturation of proteins and alter the membrane fluidity. Cotton in turn triggers the heat shock proteins (HSPs)- a family of molecular chaperones that not only prevents aggregation of the proteins but also facilitates refolding in the case of denatured polypeptides (Wang et al., 2021). Small HSPs (sHSPs), like HSP70, HSP90, HSPs are highly expressed in circumstances where heating occurs, which secures the stability of the cell.

Transpiration cooling is also caused by heat stress that causes partial stomatal opening but that in excess can result in stomatal inefficiency and decreased fixation of carbon. It has been

demonstrated that tolerant cultivars have a higher chlorophyll fluorescence (Fv/Fm ratio) and constant photosystem II efficiency even at temperatures exceeding 38 °C. Additionally, osmoprotectants such as proline and raffinose accumulation makes cellular proteins and membranes thermally stable (Huang et al., 2022).

Altering the reproductive level, high temperature causes interference of the viability of pollen, stigma receptivity and retention of bolls causing fruiting gaps. The study of transcriptomics has demonstrated the expression of HSF (heat shock factor) and DREB2 transcription factors in the reproductive tissues indicating that there is a conserved molecular defense mechanism to heat stress combined with drought stress (Shah et al., 2023).

2.3. Interaction between Stresses of Drought and Heat.

Drought and heat stress require different primary responses, but, typically, the signaling pathways function in a similar manner, resulting in synergistic or antagonistic interactions. These two types of stresses lead to the accumulation of ROS and the activation of similar groups

of transcription factors namely DREB2A, NAC, MYB and WRKY (Chen et al., 2023). These regulatory proteins trigger downstream gene functions that do the biosynthesis of osmolytes, antioxidants and cell protection.

Moreover, a similar pathway that mediates the ABA signal transduction is the ABA. With combined drought stress and heat stress, the Stomatal behavior, Carbon metabolism, and ROS detoxification are regulated by ABA-dependent transcriptional cascades (Li et al., 2022). The second type of cross-talk involves the participation of secondary messengers such as Ca²⁺ ions that propagate protein phosphorylation responses that fine tune the expression of stress-sensitive genes.

The recent reports have noted that the common stress response regulators include DREB2A and HSP70, which offer cross-protection upon improving resiliency to various abiotic conditions (Qin et al., 2024). The present dual-mechanism demonstrates the evolutionary benefit of regulation on a network-level, which enables cotton to effectively react to multiple stressors simultaneously.

Table 1. Physiological and Molecular Mechanisms of Drought and Heat Stress Tolerance in Cotton

Mechanism Type	Key Processes / Components	Representative Genes / Proteins	Physiological Outcome	References
Drought Stress Tolerance	Osmotic adjustment via compatible solutes (proline, glycine betaine, trehalose)	<i>GhP5CS</i> , <i>GhBADH</i> , <i>GhTPS</i>	Maintains cell turgor and enzyme stability under low water potential	(Raza et al., 2023)
	Antioxidant defense activation	<i>GhSOD</i> , <i>GhCAT</i> , <i>GhAPX</i>	Detoxifies reactive oxygen species (ROS), protects chloroplasts	(Mehta et al., 2023)
	Root system remodeling	<i>GhEXPA</i> , <i>GhPIN1</i>	Enhances water uptake from deeper soil layers	(Raza et al., 2023)
Heat Stress Tolerance	Heat shock protein induction	<i>GhHSP70</i> , <i>GhHSP90</i> , <i>GhHSCA2</i>	Prevents protein denaturation, stabilizes membranes	(Wang et al., 2021)

Mechanism Type	Key Processes / Components	Representative Genes / Proteins	Physiological Outcome	References
	Osmoprotectant accumulation	<i>GhP5CS</i> , <i>GhRFS</i>	Protects macromolecules and maintains photosynthesis	(Huang et al., 2022)
	Hormonal regulation (ABA, ethylene)	<i>GhPYL9</i> , <i>GhNCED3</i>	Improves stomatal regulation and transpiration efficiency	(Li et al., 2022)

2.4. Genetic Control and QTL Marking.

Tolerance to drought and heat is mainly polygenic at the genetic level as manifested by multiple quantitative trait loci (QTLs) and gene networks. There are also several QTLs related to the relative water content, the canopy temperature, and fiber quality under drought that were determined with the help of the high-density SNP markers and GWAS methods (Wendel et al., 2022). As an example, the transpiration efficiency and lint yield have been proven to be better when relations are highlighted with QTL hotspots on chromosomes A05 and D02 in conditions of so little water supply (Wang et al., 2023).

Abiotic stress response involves the major regulatory gene families (DREB, WRKY, MYB, and NAC). DREB2A in specific cases promotes the production of osmoprotectants and also stabilizes photochemical apparatus in the presence of drought and heat (Chen et al., 2023). Also, microRNAs (miRNAs), including miR398 and miR156, regulate the abundance of transcripts of stress-related genes, showing an additional extent of post-transcriptional regulations.

2.5. Epigenetic and Transgenerational Regulation

In addition to variation relating to sequence levels, epigenetic changes, such as DNA methylation, histone modification, and chromatin remodeling, are potentially significant in mediating the cotton adaptive response. Epigenetic reprogramming enables the stress-responsive genes to stay in primed status where the response to further exposure to stress can be swifter and more vivid (Azhar et al., 2022). Cyclic drought cyclicality: in *G. hirsutum* lines with cyclic drought, there is an evolution of locus-specific patterns of stable hypomethylation across the generations such that there is transgenerational stress memory (Qin et al., 2024). Besides, active transcription of drought-inducible genes has been associated with histone acetylation of H3K9 and H3K4 methylation. Chromatin accessibility The pattern of chromatin accessibility associated with tolerance phenotypes is now also being uncovered by epigenome-wide association studies (EWAS) (Gao et al., 2023). These results present some potential openings into the field of epigenomic selection in which DNA markers would be complemented by methylation or chromatin signatures in breeding schemes.

2.6. Integrating Physiology with Genomics

Making physiological characteristics meet with the genomic information helps to bridge the gap of molecular mechanisms and observable phenotypes. The instruments of high-throughput phenology, including infrared thermography, hyperspectral imaging, and chlorophyll fluorescence sensors, are allowing accurate measurement of such phenotype traits, as canopy temperature depression, stomatal conductance, and water-use effectiveness. These phenotypic datasets, together with genomic and transcriptomic data, can increase the accuracy of the genomic prediction models so that breeders can determine the best genotypes at earlier points of the breeding process (Singh et al., 2024). An example is a correlation of phenomics (i.e. transpiration efficiency, leaf area index) and multi-omics signatures to provide integrative biomarkers of drought resilience to elite cotton germplasm (Zafar et al., 2022). These breeding approaches change the mode of breeding; the phenotype breeding gives way to the genotype breeding to enhance breeding efficiency and shortens the time-to-market of breeds such as stress-tolerant cultivars.

3. Genomic Tools for Stress Resilience in Cotton

The accelerated development of the genomic technologies has transformed the capability of our comprehension and control of complicated characteristics of drought and heat tolerance of cotton. Being one of the most popular natural fiber crops with high adaptability to changing climatic conditions, the application of molecular instruments that ensure the unraveling of the polyploid genome of

cotton and the determination of stress-resistant alleles relies on its usage. Genomic technologies can be considered the basis of current breeding approaches which improve the abiotic stress tolerance by targeting the functional genes up to the whole-genome sequencing. The next paragraph provides an overview of the prominent genomic platforms and their use in the unravelling of the stress tolerance mechanism in *Gossypium* species and their improvement.

3.1 Genome Sequencing and GWAS: Building the Foundation of Cotton Genomics

Modern cotton genomics is based on the assembling and sequencing of quality reference genomes. *Gossypium hirsutum*, *G. barbadense*, and *G. arboreum* genomes are now completed, and this has opened up the field of identification of key genes in the responses to drought and heat (Hu et al., 2019; Liu et al., 2023). These reference genomes can be used to make comparative analyses which will show how stress-responsive loci, gene duplication, and functional diversification may have occurred in the allotetraploid genome. Recent research on the use of third-generation long-read sequencing platforms including Iowa Nanopore and PacBio HiFi has enhanced the accuracy of the genome especially on repeats and heterochromatic areas (Wang et al., 2023). The refining allows abiotic stress adapting SNP, deletion/insertion (InDels), and structural variants to be mapped at a high resolution. Genome-wide association studies (GWAS) have become an effective method of relating natural genetic variation and complex stress-sensitive phenotype. Withdrawal GWAS studies of large collections of different genotypes in cotton

have shown that various locations have been linked to transpiration efficiency, canopy temperature depression, and relative water content in response to drought stress (Wang et al., 2023). As an example, GhNAC072 allelic variants and GhDREB2A allelic variants have also been linked to water-use efficiency and fiber retention of the plant in case of heat stress (Zafar et al., 2022). Multi-locus GWAS models like FarmCPU and BLINK have also improved the detection power, through incorporating the fixed and random effect model, and decreasing the false positives (Liu et al., 2023). Notably, transcriptomic and metabolomic data can be coupled with GWAS, a notion promising to become one of the key trends in cotton stress biology, termed as integrative GWAS. These literature sources would give us a broader picture of how genomic variation can be translated to either increased or decreased gene expression and metabolite build up during stress levels. The results of such integrative strategies already pointed out that a variety of drought-inducible transcription factors, as well as ion transporter genes, could have a breeding value (Ahmad et al., 2023). In Breeding The use of genomic selection and marker-based breeding. Genomic selection (GS) is a paradigm shift of traditional phenotype-based selection to predictive breeding which is genotype-based. GS offers the opportunity to estimate the breeding value of individuals by genome-wide marker information providing a higher and quicker selection cycle, prior to field-testing. GS models in cotton incorporating SNP data with transcriptomic information can predict drought-related traits of cotton with up to 60% greater accuracy than

conventional methods of marker-assisted selection (Zafar et al., 2022). One of the strengths of GS is that it has the capability of capturing the major and minor effects of QTLs spread across the genome. GS models are more effective than traditional selection of QTLs where several loci provide small, additive effects as in case with polygenic traits such as drought tolerance (Ahmad et al., 2023). Random forest regression, Bayesian ridge regression and genomic best linear unbiased prediction (GBLUP) are the most common machine learning algorithms that are being applied to obtain optimal prediction under different environmental conditions (Xu et al., 2020). The marker-assisted selection (MAS), despite being less developed before, still remains crucial in the introgress of certain stress-related QTLs into elite lines of cotton. Indicatively, osmotic adjustment, leaf temperature regulation, and fiber yield stable during limited irrigation QTLs have been easily introgress in high-yield varieties by using drought-tolerant donor parents (Ahmad et al., 2023). Supply of MAS-based co-tegration with rapid-throughput phenotyping software offers breeders the opportunity of verification of stress tolerance in actual field scenarios in infrared thermography and chlorophyll fluorescence imaging (Patel et al., 2022). The introduction of genomic prediction pipelines, involving both phenomics information, remote sensing and covariates of the environment is speeding up the cotton improvement in both public and private breeding schemes. The multi-environment GS models have specific potential to facilitate the creation of climate-resilient cultivars capable of improving the water-limited areas in the

world including Pakistan, Australia, and the southwestern United States (Singh et al., 2024)

3.2 Genomic Selection and Marker-Assisted Breeding

Genomic selection (GS) is an important paradigm shift in breeding as opposed to phenotype selection with past breeding practices. GS offers the advantage of enabling people to select individuals at an earlier and faster rate even prior to field testing by utilizing genome-wide marker data to estimate the breeding values of those individuals. There is also evidence of much stronger prediction success of drought-associated phenotypes in cotton GS models that utilize SNP data in addition to transcriptomic profiles than classical marker-assisted selection (Zafar et al., 2022). The major strength with GS is that it is able to detect both large and small QTL effects all around the genome. In the case of polygenic traits with numerous loci (polygenic tolerance to drought), and small additive effects, GS models are better than traditional selection schemes of despair as based on QTLs (Ahmad et al., 2023). Random forest regression, Bayesian ridge regression, and genomic best linear unbiased prediction (GBLUP) are types of machine learning algorithms that are becoming more frequently used to achieve the best prediction accuracy under changing environmental circumstances (Xu et al., 2020). Marker-assisted selection (MAS), despite being younger in its development, still has a significant role in the introgression of particular stress-related QTLs into high-quality cotton lines. As an illustration, introgression of QTLs associated with osmotic adjustment, temperature sensitivity, and fiber stable

yield under the scarcity of irrigation has been achieved in relation to drought-tolerant donor parents to high-yielding varieties (Ahmad et al., 2023). Stress tolerance can be confirmed in low stress conditions within the ingenious field (2022) with the fitting of MAS across high-frequency breeders through cleftures, which include: infrared thermography and chlorophyll fluorescence, platforms of low throughputs. The use of genomic prediction pipelines using combinatory phenomics data, remote sensing and environmental covariates is coming forward to promote cotton improvement in both public and private breeding programs. These multi-environment GS models have a promising future with creating climate-resilient cultivars that are water-adapted to areas with limited water, e.g. Pakistan, Australia, and southwestern United States (Singh et al., 2024)

3.3 Gene Editing and Functional Validation: The Era of Precision Breeding

CRISPR/Cas based genome editing has been the most transformative genomic innovation in functional genomics and crop improvement amongst recent innovations. Direct validation of candidate loci as identified by GWAS or omics analysis can be done by simply editing individual genes or other regulatory elements in this manner. Knockout of GhDREB2A, GhMYB108 and GhHSP90, using the CRISPR/Cas9 tool has been shown to increase photosynthetic efficiency as well as survival rates under combined drought heats stress in cotton (Zhu et al., 2023). These data highlight how genome editing in specific directions can allow optimizing complicated stress response-related pathways. In addition to

standard mode of Cas9 editing, such sophisticated tools as base editing and prime editing are now available, allowing to make single-nucleotide changes without generating double-strand breaks. The latter systems are especially important to tune the regulatory regions or can alter the activity of the promoter of stress-related genes (Yang et al., 2024). Transplanting ABA receptor gene GhPYL9 On stem cells with cytosine base editors has proposed enhancing stomatal functions and drought tolerance in transgenic cotton, which has worked (Huang et al., 2022). CRISPR activation (CRISPRa) and interference (CRISPRi) systems also are an additional extension allowing gene editing applications to be up- and down-regulated upon in order to reverse transcription. This method is also becoming popular in the dissection of complex stress networks whereby overexpression or silencing of the particular genes can aid the understanding

of cross-talks in pathways in response to heat and drought. To determine the alterations of transcriptome and metabolome to validate the downstream impacts of gene modification, they are coupled with functional validation of edited lines. This multi-omics positive feedback loop follows the principle of making the edited genes physiologically beneficial without reducing fiber yield or quality. Additionally, there are now genome-edited cotton crops having better stress resistance and consistent yield still going through confined field trials in both China and the United States . Breeding pipelines are genomic tools that are being integrated with genomic tools to combine their potentials: Predicting disease resistance in breeders, predicting genetic disorders, screening, and breeding to create the preferred breeds; thus, genomic tools are developing, in essence, an alternative genetic engineering technology.

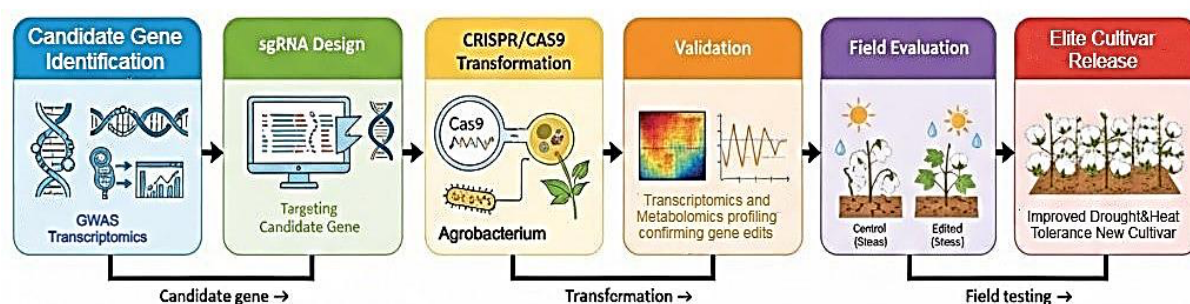


Figure 1. CRISPR/Cas-Based Gene Editing and Functional Validation Pipeline in Cotton.

3.4 Integration of Genomic Tools with Breeding Pipelines

The genomic tools are in fact becoming integrated with other genomic tools to synergize their capabilities: Predicting disease resistance in breeders,

predicting genetic disorders, screening, and breeding to Genomic tools should not be utilized in ways that do not enable them to maximize their potentials by ensuring their outputs are actually incorporated into the breeding pipelines. The shift in

genomic discovery to the applied cultivar development needs high levels of coordination between the molecular geneticists, breeders and data scientists. Multi-trait selection indices using genomic data in combination with environmental and phenotypic datasets have the potential to be informed with regards to optimizing the yield, fiber quality, and stress tolerance (Singh et al., 2024). The global collaborative forums like CottonGen database and international Cotton Genome Initiative (ICGI) are having a significant role in curating the genomes and encouraging sharing of data. These repositories offer annotated genes, QTLs and molecular markers of abiotic stress

characteristics to the breeders. The use of AI-based analytics also facilitates the predictive modeling of genotype x environment interactions in order to offer region specific cultivar recommendations (Ahmad et al., 2023). In its future, the combination of high-throughput sequencing, genome editing, and selection using machine learning will bring a new dimension of breeding cotton with accuracy. These genomic tools will play a major role in making cotton production sustainable in highly unpredictable climatic conditions by making the beneficial ones easily identified and deployed.

Table 2. Genomic and Multi-Omics Tools Applied in Cotton Stress Research

Tool / Platform	Application in Cotton Research	Example Outcome / Discovery	Recent Reference
Whole Genome Sequencing (WGS)	Identification of drought and heat tolerance genes in <i>G. hirsutum</i> , <i>G. barbadense</i>	Mapped QTLs for transpiration efficiency and canopy temperature	(Hu et al., 2019)
Genome-Wide Association Studies (GWAS)	Association mapping for stress-adaptive traits	Allelic variants of <i>GhDREB2A</i> , <i>GhNAC072</i> linked to water-use efficiency	(Zafar et al., 2022)
Genomic Selection (GS)	Predicting breeding values using SNP data	60% higher accuracy for drought tolerance prediction vs MAS	(Ahmad et al., 2023)
CRISPR/Cas9 Gene Editing	Functional validation and targeted modification of stress genes	Knockout of <i>GhHSP90</i> enhanced survival under combined heat–drought stress	(Zhu et al., 2023)
Transcriptomics / Proteomics	Identification of DEGs and stress-responsive proteins	Up-regulation of <i>DREB</i> , <i>WRKY</i> , and <i>HSP</i> gene families	(Mehta et al., 2023)
Metabolomics / Epigenomics	Discovery of metabolite biomarkers and stress memory patterns	Accumulation of proline and raffinose; hypomethylation in drought memory	(Qin et al., 2024)

4. Multi-Omics Integration in Cotton Stress Research

Drought and heat tolerance of cotton cannot be explained by the one level of the

biology data. These adaptive characteristics are a result of complex genome-wide, transcriptome-wide, proteome-wise, metabolome-wide and epigenome-wide interactions. Thus, a

multi-omics model has become an effective tool to decipher the molecular systems of stress tolerance and the signaling programs, gene regulations, and metabolic adaptations that facilitate *Gossypium* species allowing them to survive in poor environments. The combination of the multiple omics layers offers not only the benefits of a system-wide omics level perspective of plant responses but also makes the functional connection between genotype and phenotype, which is an important trend towards predictive and precision breeding.

4.1 Transcriptomics and Proteomics: Unraveling the Dynamic Stress Response

Transcriptomic studies have transformed the notion of gene expression remodeling to abiotic stressors. With the help of RNA-sequencing (RNA-seq) and microarray analysis, it has been possible to find neither less than thousands of differentially expressed genes (DEGs) in cotton during the state of drought and heat. The main activities that these DEGs are related to are the processes of cell protection, osmotic signals, and redox regulation (Mehta et al., 2023). Drought-tolerant cultivars have been observed to be upregulated of genes involved in transcription factors including those of the DREB, NAC, WRKY and MYB families, which mediate stress signaling and protective responses downstream (Patel et al., 2022). An outstanding instance of them is the GhDREB2A and GhWRKY33 transcriptional factors that synergistically promote the production of osmo-proteins and the maintenance of reactive oxygen species (ROS) scavenging enzymes (Zafar et al., 2022). Instead, heat stress initiates expression of genes (HSP70, Hsp90 and

HsFA2) that act as molecular chaperons to inhibit protein misfolding and support proteostasis (Wang et al., 2021). The studies of dual stress exposure (drought × heat) illustrate that cotton plants utilize the subgroups of typical regulatory genes, which points to the presence of shared transcription locations of cross-protection (Singh et al., 2024). Proteomics goes hand in hand with transcriptomics by determining such post-transcriptional and post-translational changes that cannot be deduced based on the RNA information alone. When they are under stress, various stress-reactive proteins, including dehydrins, late embryogenesis abundant (LEA) proteins, and antioxidant enzymes, become accumulated in order to preserve cell homeostasis (Patel et al., 2022). Researchers have listings more than 1,500 proteins that react to stress in *G. hirsutum* leaf and root using label-free quantitative proteomics and tandem mass spectrometry (MS/MS) (Hu et al., 2019). Additional comparative analyses of proteomics show that tolerant genotypes have also remain high abundance of energy metabolism, carbon fixation and ROS detoxification proteins relative to sensitive genotypes (Raza et al., 2023). The analysis of protein interaction networks shows that the hub proteins (superoxide dismutase (SOD), ascorbate peroxidase (APX), and heat shock protein 90 (HSP90)) are at the core of sustaining a stressful situation (Ali et al., 2024). In addition, phosphoproteomic experiments have revealed reversible phosphorylation results that regulate signaling pathways, like mitogen-activated protein kinase (MAPK) pathways involving reaction to drought and heat stress. These results highlight the importance of combining transcriptomic

and proteomic data in order to realize the complexity of the multi-layered nature of stress dependent gene regulation.

4.2 Metabolomics: Mapping the Biochemical Landscape of Stress Tolerance

Where genomic and transcriptomic data give a clue of what may take place, metabolomics gives an understanding of what does occur in the plant system under variations of stress. Metabolites are the end product of gene expression and endoenzyme activity, which give direct results on physiological condition and metabolic reorganization. Drought and heat stress in cotton cause various changes in the primary and secondary metabolite pools, carbohydrates, amino acids, organic Acids, flavonoids (Huang et al., 2022). In drought conditions, there is the buildup of osmolytes that in turn preserve cell turgor and enzyme activity, which include proline, trehalose and glycine betaine (Raza et al., 2023). In response to heat stress, the production of antioxidative compounds such as ascorbate, glutathione and phenolics increases the ROS detoxification. Recent metabolomics studies analyzing the protein and substance composition by using gas chromatography-mass spectrometry (GC-MS) and liquid chromatography-mass spectrometry (LC-MS) have shown that raffinose family oligosaccharides (RFOs) and sugars (sacrose and maltose as an energy source and cellular membrane protecting compound) are increased in the cases of tolerant cotton genotypes (Mehta et al., 2023). Flavonoids, lignin, and terpenoids are also secondary metabolites that promote stress adaptation through membrane stabilization and minimization of oxidative damage. Indicatively, GhCHS

(chalcone synthase) and GhFLS (flavonol synthase) genes are increased by heat stress and they increase accumulation of flavonoid antioxidants (Ahmad et al., 2023). Metabolomic data in combination with transcriptome have revealed the co-regulated modules between the genes of sugar metabolism and the concentration of the stress-protective metabolites which could act as key targets in metabolic engineering. Metabolomic biomarkers have also been useful in selection and phenotyping. Indicatively, proline and trehalose have been identified to trace out high levels of environment-related drought tolerance indices and stable yield (Liu et al., 2023). These metabolite-based selection markers are complementary to the genomic selection pipelines and particularly in young breeding generations these metabolite-based selection markers are used even when direct phenotyping is very difficult.

4.3 Epigenomics: Heritable Layers of Stress Regulation

Another dimension of stress tolerance is provided by epigenomic regulation which mediates heritable but reversible changes in gene expression without significant changes in DNA sequence. Overall, chromatin accessibility and transcriptional responsiveness in response to stress are defined by DNA methylation, histone states, as well as non-coding RNAs (Azhar et al., 2022). Whole-genome bisulfite sequencing (WGBS) has also demonstrated extensive DNA methylation modifications in the promoter areas of drought-sensitive genes on exposure to stress in *Gossypium hirsutum* (Qin et al., 2024). As an illustration, the upregulation of GhRD29A and GhLEA3 promoters is promoted by hypomethylation of the

promoters and enables quick osmotic acclimatization (Chen et al., 2023). In a similar way, histone H3K9/H4K16 acetylation comes about due to heat stress resulting in transcriptional activation of HSP70 and HSP90 genes (Wang et al., 2021). Such epigenetic marks tend to form a stress memory so that plants that have experienced stress in the past can respond better to stress when faced with it in future challenges (Azhar et al., 2022). Recent reports have identified the involvement of small RNAs, especially, microRNAs (miRNAs) and long non-coding RNAs (lncRNAs) in the regulation of transcriptional factors and signaling genes in response to abiotic stresses. An example is miR398 and miR396 which regulate antioxidant enzyme expression whereas lncRNA-GhHeat1 increases thermotolerance by binding with heat promoters (Huang et al., 2022). The combination of epigenomic and transcriptomic data thus gives a clearer image of the role of the gene expression plasticity in helping the environment to be resilient.

4.4 Systems Biology and Network Modeling: Integrating Multi-Omics Insights

Multi-omics potentially is truly revealed through the notion of data integration, data integration infectiously between genomics, transcriptomics and proteomics, and metabolomics and epigenomics into single-coherent patterns that explain stress response as a dynamic network. Computational systems computational methods used in systems biology include weighted gene co-expression network analysis (WGCNA), Bayesian, and machine learning to discover hub genes and regulatory networks (Singh et al., 2024).

Combination of omics layers could show the degree to which transcription factors control the amount of enzymes present and the quantities of metabolites that eventually dictate performance of stress. To illustrate, co-expression networks of GhNAC072, GhSOD1, and enzymes in the biosynthesis of raffinose were discovered in *G. hirsutum* under drought, as an example of a relationship between the regulation of genes and osmo-protection (Ahmad et al., 2023). In the same way, cross-talk between redox homeostasis and energy metabolism in a combined heat-drought setting has been discovered by using combined proteomic-metabolomic modeling (Ali et al., 2024). Predictive power is improved even further by using machine learning-based integration to identify non-linear associations between omics features that are commonly ignored by conventional statistical models (Xu et al., 2020). Such multi-omics networks are not only used to explain biological mechanisms, but to derive biomarkers in genomic selection. As an example, using multi-trait genomic prediction models that use omics-based candidate genes has increased the prediction accuracy of drought tolerance by more than 40 percent (Singh et al., 2024). Finally, the incorporation of the omics image into a systems biology model would enable the image of cotton improvement to become a predictive information-driven science.

4.5 Translational Applications of Multi-Omics in Breeding

The convergence between the multi-omics is starting to transform breeding pipelines. Candidate genes derived with omics are currently undergoing validations by CRISPR/Cas-based editing, transgenic overexpression or by a marker-assisted

introgression. As an illustration, GhDREB2A and GhNAC072 manipulation has produced transgenic lines of cotton that have improved drought recovery and a higher yield of lint (Zhu et al., 2023). Similarly, the biomarkers of metabolomics like proline and raffinose are also used in screening breeding populations against stressful conditions increasing the size of the field testing. Advanced high-throughput phenotyping systems, in conjunction with omics-based trait dissection, will enable breeders to be able to create a relationship between the genotype, molecular signature, and phenotype, in the real field conditions. These integrative models promise the universe in the creation of climate-tolerant cotton varieties that preserve productivity and degree of fiber of the varied situations.

5. Challenges, Research Gaps, and Future Prospects

Although there was impressive advancement in the use of the genomics and multi-omics technologies in cotton improvement, there is a major challenge in translating the findings of these methods to all real breeding results. Many technical, biological, and infrastructural shortcomings still hinder the implementation of omics-based breeding programs on a large scale, particularly in the field environment in developing cotton-producing states. To be able to achieve this, there is a need to address these gaps in order to see the full potential of genomic innovation to sustained production of cotton in the climate change era.

5.1. Major Challenges in Translational Genomics

Among the most serious issues is the complexity of genotype x environment (G x E) interactions. Even though genomic and transcriptomic data have shown many candidate genes related to drought and heat tolerance, their expression is highly habitat-specific. To provide an example, those genes, which provide stress-resilience benefits when controlled and such as when utilizing nutrient-rich soils, fluctuate temperature, and interactive stresses, might show a poorer performance at field conditions, which have irregular soil types, change in temperature, and interacting stressors (Patel et al., 2022). There is the challenge of predictability of the omics-based selection and the transferability of the laboratory findings to breeding programs due to the absence of robust genotype influenced models. Inadequate availability of high-throughput phenotyping platforms is another concern that lacks high-throughput and cannot be used to relate the omics information to the phenotypic performance. Proper phenotyping (canopy temperature, wilting index and efficiency of transpiration) of drought and heat resistant characteristics involve progressive imaging technologies, drones and automated data analysis (Singh et al., 2024). The manual scoring method is used in most breeding stations in South Asia and sub-Saharan Africa and creates subjectivity and poor reproducibility. Therefore, there is a gap between the quantity of genomic sequencing and the minimal capacity to phenotypically justify stress-tolerant genotypes on a large-scale level.

5.2. Data Integration and Computational Constraints

The proliferation of multi-omics studies has created colossal volumes of data of the genomics, transcriptomics, proteomics, and metabolomics strata. Nonetheless, data standardization and data integration are not yet determined problems. There are numerous datasets in fragmented repositories or local servers that usually do not have harmonized metadata schemes or cross-platform interoperability (Hu et al., 2019). This makes it difficult to conduct meta-analyses or comparative studies between species, genotypes or between environments. There is also a limitation of curated datasets publicly available since there is no centralized database of the cotton omics. Moreover, bioinformatics ability to handle, process, and evaluate high-dimensional data on omics is inadequate in most research centers. Complex biological networks and stress responses can be attempted to be solved by advanced computational methods (machine learning (ML) and artificial intelligence (AI), etc.), which promise solutions (Xu et al., 2020). However, these tools need trained staff and a high-performance computing system and collaboration across disciplines between plant scientists and geneticists to implement. The absence of this integrating infrastructure is still a bottleneck in the transformation of omics into practical results.

5.3. Gaps in Field Validation and Germplasm Diversity

The other critical issue is that only little validation of candidate genes omics-derived in real-life conditions has been done. Most of the functional research on drought and heat stress tolerance is

performed in model genotypes like *G. hirsutum* cv. TM-1, which is put under regulated conditions under greenhouse environments (Zhu et al., 2023). These conditions do not entirely coincide with the alternating and compounded stressful situations met in the real production areas. Consequently laboratory discoveries that may hold promise in field performance encounter many failures in the conversion of laboratory discoveries to stable field performance. There is also the challenge of a limited genetic background of cultivated cotton. Through a decades-long exercise of intensive selection on yield and fiber properties, the modern cultivars have actually lost a great deal of their allelic diversity, especially with respect to stress-resistant phenotypes (Wendel et al., 2022). There are quite useful drought and heat adaptation alleles present in wild relatives and landraces of *Gossypium* species, which are not well utilized by introgression into elite backgrounds. These genetic resources severely require pre-breeding interventions and molecular characterization of such genes with a view of addressing the widening genetic foundation of climate resilience.

5.4. Limitations in Multi-Omics Integration

Even though the level of progress made in each of the individual omics areas is substantial, the incorporation of multi-omics layers, i.e., genomics, transcriptomics, proteomics, metabolomics, and epigenomics, is not an easy task. The resolution of data, the scale, and normalization methods of different omics platforms can be quite different, and the cross-level integration can be challenging (Huang et al., 2022). Beyond, they need systems level modeling regimes that can

provide a connection between molecular understanding and measurements of field properties that are dynamically responsive to the molecular network and dynamically responsive to physiology. It is impossible to achieve maximum potential of systems biology in cotton breeding without such integrative approaches. Another limitation is the lack of time and space omics research. Most existing studies are static or tissue-specific measurements, which can not be used to determine the dynamic nature of stress reaction. It is essential to use longitudinal experiments that monitors gene expression, protein accumulation and metabolite flux over a period of time to reveal cause and effect regulatory mechanisms and plasticity to adaptations of cotton to various stresses.

5.5. Future Directions and Prospects

Improving the interface between molecular discovery and breeding is the future of improvement of omics-based cotton. A combination of omics data and physiological, environmental, and phenomics data will allow obtaining the comprehensive picture of stress adaptation. Via high-throughput phenotyping and genomic prediction models, there is a possibility of improving the precision of use of superior genotypes in conditions of stress. Moreover, AIs and ML-based models or frameworks are capable of handling large datasets to anticipate genotype performance (different locations, different seasons) and provide data-driven breeding principles. It will also depend heavily on international cooperation. The multilocation trials and multi-location data

sharing and training can be achieved through world organizations like International Cotton Genome Initiative (ICGI) and international Cotton Researchers Association (ICRA). Reproducibility and faster scientific development will be encouraged by creating open-access repositories of omics and common standards of metadata (Patel et al., 2022). Moreover, the growing family of gene-editing systems such as CRISPR/Cas9, base editing, and prime editing provides unlimited possibilities of highly curing stress-responsive genes (Yang et al., 2024). Coupling such tools with transcriptome and metabolome data may allow focusing on modifications in central regulatory dimensions to improve drought and heat tolerance without reducing the quality of fibers. By combining epigenomic and pangenomic viewpoints, it is possible to have additional insight to expose concealed regulatory variability in the development of genotype-specific reactions to stress. The other border is in the utilization of wild germplasm and synthetic polyploids. Through the application of genomic selection, molecular markers, it is now easy to ideally introgress desirable alleles between *G. arboreum*, *G. herbaceum* and *G. barbadense* into commercial cultivars, improving their yield and resistance to stress. Wild *Gossypium* diversity conservation and its characterization should therefore continue being one of the most important priorities in breeding of cotton sustainably around the world.

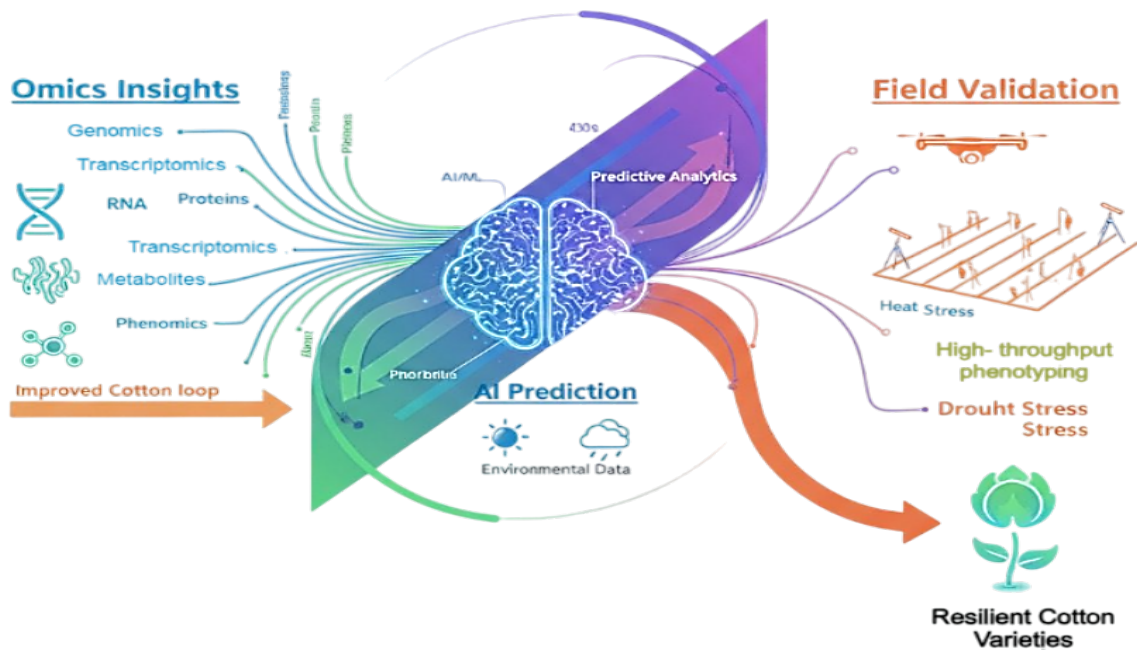


Figure 2. Systems Biology–Driven Pipeline for Developing Climate-Resilient Cotton Cultivars.

5.6. Building Resilient Breeding Pipelines

Finally, establishing climate-resilient cotton production will require a pipeline of breeding pipeline that combines molecular, physiological and environmental data created using systems-biology. In the coming decade, it is likely that genotype-based selection will transform into predictive breeding platforms, which will be omics and AI-powered. The performance of crops under different climatic conditions can be simulated using such systems and be used by the breeders to design ideotypes that are highly heat and drought-tolerant (Liu et al., 2022). Capacity building is as well critical. By training researchers on the analysis of multi-omics data, developing physical bioinformatics centers in regions, as well as enhancing close ties between the public and the private sector, sustainable

implementation of advanced technologies will be guaranteed. Moreover, by generating low-cost genotyping and phenotyping services, access to omics-based breeding will become available to low-resource institutions in Africa and South Asia where the impacts of climatic changes are greatest (Wani et al., 2023).

5.7. Outlook

To conclude, although some difficulties are still present, the integration of omics technologies, big data analytics, and AI has become a chance to implement changes in cotton. The use of collaborative, interdisciplinary and data-driven methods will establish the future crop of cotton varieties that will be able to sustain their productivity and fiber qualities in the increasing demands of climate change. The combination of systems biology with accurate breeding, reinforced by a formidable international

partnership will be what the future sustainable cotton production will be judged as.

6. Conclusion

Drought and heat stress are other two of the most decisive challenges regarding the production of cotton on a sustainable scale in the global world. The rising occurrence and intensity of these climatic extremes which result to global climate change have already started to reduce the potential yield, undermine the quality of fibers and destabilize the situation of millions of smallholder farmers. To remain productive in these circumstances, there is a dire need to take the breeding of cotton species out of the old manual selection paradigm and turn to the holistic and multi-omics systems-based method based on genomic and multi-omics technologies. The last ten years witnessed an unprecedented development of molecular and physiological insights into the mechanisms of stress tolerance of *Gossypium* species. The *G. hirsutum*, *G. barbadense*, and *G. arboreum* multiple cotton genomes have been sequenced, which has given a comprehensive map of genetic variations that have contributed to the adaptation to abiotic stress. Other complementary studies have been done in the field of transcriptomics, proteomics, metabolomics and epigenomics that further elucidate the complex relationship of genes, proteins and metabolites in the process of stress perception, signaling and recovery. Together these perspectives have altered our perception of the biology of cotton and have turned the one-gene view of cell biology into the multiple-layered systems perspective of cell stress resilience. One of the most important

successful outcomes of the omics revolution has been the ability to incorporate high-throughput data with breeding pipelines. Genome-wide association studies (GWAS) and genomic selection (GS) have established the breeder the ability to forecast genetic excellence of unexamined lines with high precision, which reduces breeding cycles and promotes the launch of stress-tolerant cultivars. Equally, with the introduction of CRISPR/Cas-based genome editing, there is a new breeding era that is characterized by precise control of gene modification as GhDREB2A, GhHSP90, and GhMYB108 that increase drought and heat resilience can be targeted. A combination of these tools, when kept with metabolomic and transcriptomic profiling, provides the whole platform of validation and optimization of functional traits in relation to stress. Nonetheless, in spite of such improvements, there are significant gaps in translation between laboratory work and field practice. Numerous discoveries in omics remain to be confirmed under changing agroecological conditions, in which various stressors, including salinity, nutrient limitation, and pest pressure, interacts in vivo with drought and heat. In addition, bottlenecks in phenotyping and difficulties in integrating data and inadequate computational infrastructure have contributed to slowing down the application of omics discoveries in practice. The filling of these gaps would require a paradigm shift that necessitates the use of transformative collaborative, data-driven and interdisciplinary research paradigms that would incorporate genetic, physiological and data science and climate modeling. One of the potential opportunities in the current cotton

improvement is the multi-omics data integration with AI and machine learning (ML). Expert algorithms are able to examine big, multi-layered information to determine concealed correlations, forecast genotype x atmosphere interplay and contemplate stress execution across a wide variety of climatic circumstances. They are not only more accurate due to such predictive analytics, but also cost-effective and time-saving compared to the case of traditional field tests. In combination with high-throughput phenotyping (HTP) systems (drone-based, spectral imaging, thermal sensors, and optimistic artificial intelligence) could be used to create close real-time data about the health of plants, their water condition, and levels of productivity with the help of AI-based models, which will accelerate the process of elite genotype selection related to arid and semi-arid environments. The other important aspect to be included in the future civil-cotton resilience research will be the exploitation of wild relatives and underutilized germplasm. The species of *G. herbaceum*, *G. raimondii*, and *G. tomentosum* possess distinct allele of drought and heat resistance, disease resistance, and fiber strength. With the help of genomic-assisted introgression and pangenome, breeders are able to harness this concealed richness and reintroduce some adaptive capabilities that were lost in domestication. When used in pre-breeding programs, such genetic resources will play a critical role in increasing the pool of genetic matter and achieving timeless future climate stability. At the same time, the epigenetic and regulatory is becoming a new dimension of adaptation. It has been demonstrated that DNA methylation, histone changes, and small RNAs may

trigger the so-called stress memory, which enables plants to react faster to same stresses. By utilizing such epigenetic plasticity via molecular breeding and biotechnology, it is possible that future research into inherited and expressed stress tolerance in cotton will be completely transformed. Combining epigenomics with the traditional genetics would help us gain insight into the process of plants striking a balance between adaptation to stress and growth and reproduction, which is a significant milestone towards creating high-yielding, stress-resilient varieties. The future of cotton-improvement is the creation of a fully interconnected breeding ecosystem which links genomics, phenomics and environmental modeling using a system-biology perspective. Such a framework will allow accurate breeding whereby the interventions of genes are guided by the field-scale environmental information. The formation of international data-sharing networks (International Cotton Genome Initiative (ICGI) and International Cotton Researchers Association (ICRA)) will go an additional step in terms of collaboration, standardized data collection, easy access to the global germplasm and computational facilities. The collaborative networks are especially essential to developing nations, whereby the scarcity of resources may be the major barrier to the adoption of advanced technologies. Policy and institutional wise, capacity building in bioinformatics, molecular breeding as well as phenomics has to be placed at the forefront. Human capital, infrastructure, and cross-disciplinary training are some of the investment elements that will be used to ensure the viability of the genomic innovation in

cotton. Furthermore, innovative collaborations between government-funded research organizations, commercial seed vendors, and donor organizations may expedite access to commercial climate-smart cultivars to the farms by participating in participatory breeding and technology transfer projects. Finally, cotton enhancement is at the transformational stage, in which omics-enabled information, accuracy breeding, and elliptical intelligence meet to open up the new vistas of resilience to stressors. Through combining the use of genomic knowledge and real-life practices in agronomy, breeders are now able to fantasize over cultivars that not only absorb the extreme climatic conditions but also retain their high yield and quality of the fiber they produce. The process of gene discovery to field application is still complicated, but the synergistic application of genomics, transcriptomics, metabolomics, and phenomics is a definite path towards the sustainability of cotton production. The vision in the next 10 years can then center on applications to the field of laboratory findings into farm-focused solutions that are proven to work, supported by open data and sound phenotyping, and fair international partnerships. Having capability to create such cotton cultivars that can survive despite the increasing stresses of climate is indeed a possibility when there is constant innovation, capacity building and dedication to it, and this guarantees future generation the help of this vital crop.

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Natural Fibers in Composite Materials: A Review on the Performance of Cotton-Based Biocomposites

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Abstract

Cotton-based biocomposites are emerging as a disruptive force in sustainable materials. This review charts their progress from laboratory curiosity to commercial reality in automotive and construction. By transforming abundant waste streams into valuable reinforcement, these composites offer a 30-50% reduction in carbon footprint versus glass-fiber composites. We detail how surface engineering unlocks their potential, delivering up to 60% improvements in mechanical properties while mitigating moisture sensitivity. Their inherent advantages lightweighting, superior impact resistance, and acoustic damping are quantified and benchmarked. The paper further explores pioneering applications in smart composites and 3D printing, culminating in a roadmap for overcoming remaining barriers to full industrialization and solidifying their role in a circular bio-economy.

Keywords: Biocomposites, Natural Fibers, Cotton, Surface Modification, Mechanical Properties, Sustainability, Polymer Matrix.

1. Introduction

The twenty-first century is marked with various grand-challenges but climate change, depletion of resources, and environmental pollution occupy the global agenda (Colucci & Vecchi, 2024). The materials sector which is a key cause of such issues because of its intense dependence on finite fossil substrates is therefore experiencing a paradigm shift. In

its turn, the international policy efforts are coming up with regulatory provisions that encourage the production of sustainable, low-carbon and biodegradable substances. It is this worldwide need to be sustainable that forms the main force in pursuing renewable resources in the production of materials thus triggering the development of the biocomposites. Biocomposites represent a sort of material that can be

quite consistent with the concept of a circular bio-economy (Fernández Fortunato et al., 2023; Rana et al., 2022). They are generally characterised as composite materials that consist of a polymer matrix, which could be petroleum based or bio based reinforced with natural fibre. Plant-based in origin, these fibres could offer a truly renewable and in most of cases, biodegradable alternative to glass or carbon fibres (Panda et al., 2024; Rana et al., 2022). The benefits of natural fibre composites are well known and encompass low density and high specific strength, low cost, low tool wear, good acoustic damping, and, finally, favourable environmental profile with lower embodied energy and the potential to become carbon neutral throughout their life cycle. Cotton is a very promising natural fibre who has a very broad range of competitors. The cotton species offer one of the greatest textile fibres in the world, with an annual output of over 25 million tonnes, thus ensuring that they were easily available and had a well-developed agricultural infrastructure. In addition to virgin cotton fibres, large volumes of by-products and wastes, such as cotton linters and cotton stalks are produced which are usually burnt or discarded and this fact, too, offers a significant opportunity of valorising wastes (Subramanian et al., 2022). In addition, post-consumer waste of cotton textiles is a large and unexploited resource, and more than 20 million tonnes are landfilled each year. The characteristics of the cotton fibres make them especially useful as reinforcement, in that they have fairly good mechanical strength and toughness, are very light, contain high amounts of cellulose and are no longer abrasive to processing

equipment (Abtew et al., 2025; Aminudin et al., 2023). Their natural biodegradability makes them benign at end of life, making a natural cycle and additional boost to their environmental merits. Despite these outstanding benefits, there are considerable technical challenges to large scale industrial use of cotton based composites (Abtew et al., 2025; Johnson et al., 2020). The main difficulty of the situation is based on the inherent chemical incompatibility of the hydrophilic cotton fibre and the hydrophobic polymer matrix. This incompatibility causes incompatibility of interfacial adhesion and hence concentration of stress occurring and the transfer of the stress between the matrix and the fibre inefficiently and in the end the mechanical properties of the composite are affected. Moreover, the composites are prone to moisture uptake because of high hydrophilicity of cotton due to high numbers of hydroxyl groups in its cellulose structure (Khajavi, 2021). This causes instability in dimensions (swelling), possible fungal attack and decrease in mechanical properties with time. Natural differences in fibre characteristics as a result of geography, growing conditions, and history handling also pose a uniform challenge to quality control and standardisation (Thapliyal et al., 2023). It is against this background that this state-of-the-art review is designed to offer a comprehensive and critical study of cotton-based biocomposites. The applications in different industries that are existing and emerging will be recorded and a conclusion will be made on the issues that are either in existence or about to be realized and the future research directions that may need to be pursued in order to develop the field to its fullest

potential will be discussed and a conclusion made on what can be done to enhance the area with this sustainable material (Harwood & Smith, 2020; Sadrmanesh & Chen, 2019).

3. The Cotton as a Reinforcement Source and Characteristics.

The behavior of a composite material is directly related to the characteristics of its reinforcement. In the case of cotton-based biocomposites, the source and the nature of cotton fibre used is a key factor that dictates the properties of the final material, when it comes to mechanical strength, as well as cost-efficiency.

Types of Cotton Fibres Used

a. Virgin cotton fibres: These are the longer and staple fibres that are mostly used in the textile industry. Although they can be incorporated into composites, it is less economical and poses competition with food/fibre chain. Their purity and uniform length may be beneficial when it comes to producing high-performance composites in specialised uses, but their price and unethical source is a major limitation (Esteve-Turrillas & de la Guardia, 2017; Gupta & Gupta, 2023).

b. Cotton linters: These are short, originating, curly fibres left behind to the cotton seed as a result of initial ginning. Linters are historically a low-value by-product with a high level of cellulose (up to 90 %) and are a promising reinforcement material, given they are not only abundant, but also low-cost (Dadgar, 2020). Their reduced length requires alternative methods of processing although they can be successfully employed in

thermoplastic and thermoset composites and provide a sustainable avenue of converting agricultural waste (Majumdar et al., 2019; Negm & Sanad, 2020).

c. Cotton stalks and other agricultural wastes: Cotton stalks are a significant agricultural residue, which exist after cotton is harvested and are usually burnt and hence cause significant air pollution (Pandirwar et al., 2023). The opportunity to use cotton stalks as a basis of fibrous reinforcement is a significant waste valorisation in the model of a circular economy. The stalks should be crushed, separated, and occasionally chemically pulped to get out the fibrous part, which has more lignin and has different mechanical characteristics than the bast or leaf fibres (Johnson et al., 2020; Soomro et al., 2023).

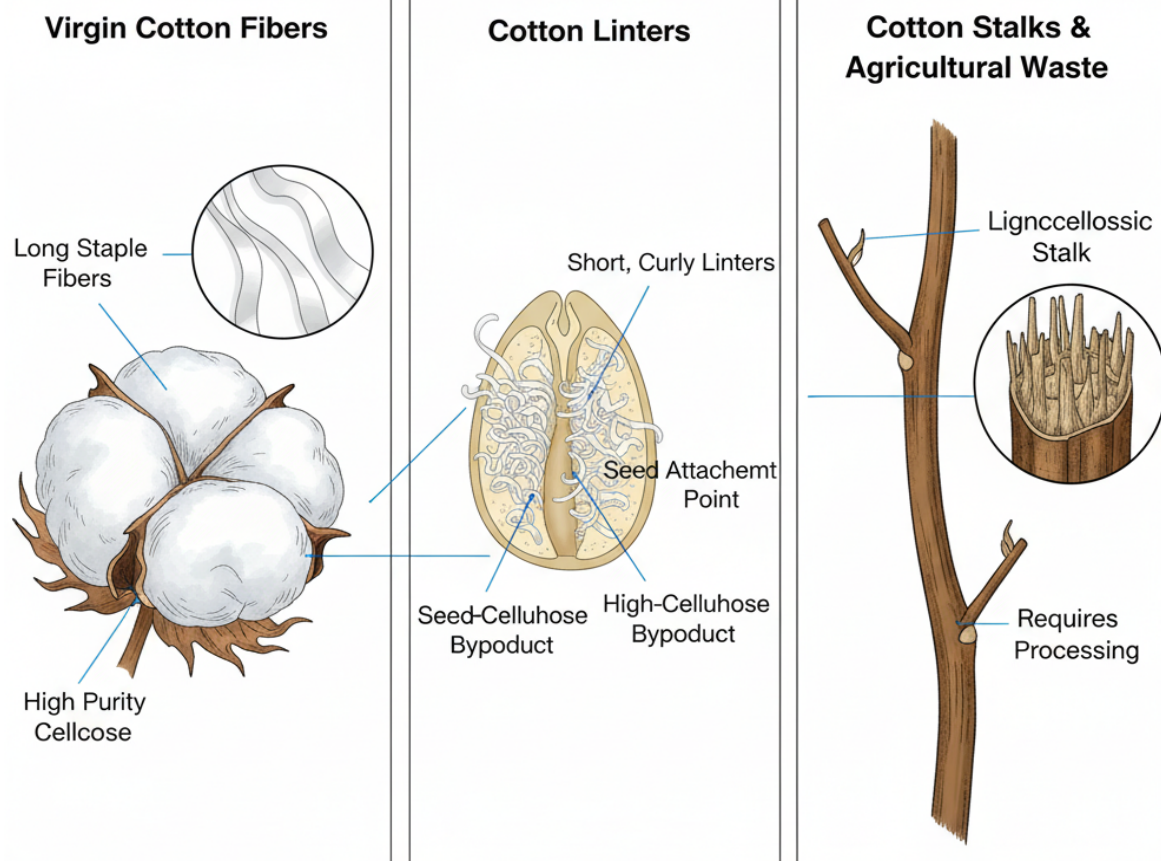


Fig. 1. Primary sources of cotton reinforcement: virgin fibers, linters, and stalk-derived fibers.

e. Natural Characteristics of Cotton Fibers

Mechanical Properties: The tensile strength of one single cotton fiber is between 287 and 597 MPa, and the Young's modulus is between 5.5-12.6 GPa (Lundahl et al., 2017). These values are less than those found in E-glass fibers, but the relatively low density of cotton gives it competitive specific properties (property per unit density) which is important in weight-sensitive applications like parts in cars. Break elongation of cotton that is usually between 6 and 8 contributes to high impact toughness and impact damage tolerance in composite matrices (Cao et al., 2021; Chowdhury & Islam, 2022).

Physical Properties: The low density of cotton is one of the main advantages, which allows producing lightweight composite elements that will use less energy in transportation systems (Olhan et al., 2021). The aspect ratio, which is length divided by diameter is a key parameter; high aspect ratio makes it easy to transfer stress. Virgin cotton fibers will have a large aspect ratio, though this will be lower in linters and recycled fibers; this shortcoming can be counteracted by high fiber loading or combining it with other fibers (Agarwal et al., 2019; Patel et al., 2023).

Chemical Composition: Cotton is mainly made up of cellulose which composes between 88 and 96 per cent of the composition (Liu, 2018). Being a crystalline polymer, cellulose gives the material strength and rigidity. Hemicellulose (4-6%) (amorphous), which makes the material absorb moisture and is biodegradable, lignin (0-1%), pectins and waxes are also present in the material. The large concentration of cellulose makes the fiber very hydrophilic as a result of the excessive number of hydroxyl (-OH) groups, which is the root cause of the interfacial adhesion difficulties with polymer matrices (Kumar et al., 2022; H. Wang et al., 2020).

4. Techniques of manufacturing and processing Cotton Biocomposites.

Effective production of high-performance cotton biocomposites is a two-step process which highly relies on pre-treatment of fibers to promote compatibility and choice of proper methodology in fabrication of composite structures. The primary task is to optimize these phases so that the material limits inherent in them could be overcome and yield consistent and reliable properties.

4.1. Pre-Treatment of Fiber and Surface Modification.

The main aim of surface modification process is to modify the surface chemistry and morphology of the cotton fiber to enhance adhesion to the polymer matrix and reduce the effects of moisture uptake. These treatments are necessary in creating a healthy interphase which controls the efficiency of stress-transfer (Mukesh & Godara, 2019).

Chemical Treatments:

Alkali Treatment: The most common and cost effective chemical treatment is the treatment with sodium hydroxide (NaOH) solution. NaOH combines with surface hydroxyl, hence removing impurities, hemicellulose and lignin (Al-Oqla & Alaaeddin, 2022). Such an etching action enhances the roughness of the surface, the quantity of cellulose fibrils, and the quantity of reactive sites, and it consequently promotes mechanical interlocking and future chemical bonding. The more recent studies have aimed at maximizing the concentration and exposure time to achieve the maximum of interfacial shear strength with minimum fiber damage (Eyckens et al., 2021).

Silane Treatment: Silane coupling Agents are used as bridges between the fiber and the matrix on a molecular basis (Aziz et al., 2021). The alkoxy groups are hydrolyzed to react with the -OH groups of the fiber and bind through covalent bonds and the organofunctional moieties are designed to be competent with the polymer matrix in question. This treatment has a significant effect of enhancing interfacial adhesion and clearly decreases the moisture uptake by making the fiber surface more hydrophobic (Issa & Luyt, 2019; Zhang et al., 2025).

Acetylation: Reaction of cotton fibre with acetic anhydride causes the hydrophilic hydroxyl groups to be esterified and the acetyl substituents to be introduced in large volumes. This chemical amendment irreversibly reduces the polarity and hydrophilicity of fiber, resulting in much better dimensional stability and long-term compatibility with hydrophobic polymer materials, including polypropylene and

polyethylene (Ahangaran & Navarchian, 2020; Issa & Luyt, 2019).

Maleated Coupling Agents: Polymers that are maleic anhydride grafted are commonly used together with thermoplastic matrices (Ahangaran & Navarchian, 2020). The anhydride group is covalently reactive to fiber -OH groups; simultaneously, the polymer chain entraps as well as co-crystallizes with the matrix, which creates a robust and sustainable interface (Huang et al., 2019; Signorilamin et al., 2025).

Corona Treatment: This is a relatively less harsh surface activation treatment which uses corona discharge at atmospheric pressure. It enhances surface energy and wettability of polymer resin which makes it applicable in in-line treatment of fabrics or non-wovens although the effects obtained are not as long-lasting as those obtained by plasma or chemical treatments (Förster, 2022; Lindner et al., 2018).

Biological Treatments: Enzymatic Treatment: The specific enzymes including cellulases, pectinases and laccases are used to selectively degrade non-cellulosic fiber surface components in an environmentally friendly fashion (Khan, 2025). The process of this enzyme bio-scouring alters the topography and chemistry of the fiber to form a more mechanical interlocked rougher surface without the harsh chemicals typically employed in traditional processes (Khan et al., 2025; Kumar et al., 2023).

4.2. Composite Fabrication Methods

The choice of the fabrication methodology depends on the type of the matrix (thermoplastic or thermoset), fiber format (short, long, woven) and the volume and complexity of the application.

Compression Molding: This method is the most common technique that can be used on both thermoset and thermoplastic composites (Barile et al., 2020; Tatara, 2024). In thermoplastics, a pre-consolidated sheet, such as a non-woven cotton mat filled with polypropylene fibers, also known as a hybrid mat is press molded and is known as thermoplastic press molding. In case of thermosets, the impregnation of at least one fiber layer with resin (prepregs) is piled and placed under pressure and heat, which make it possible to create high-fiber-content, high-strength products (Dumont et al., 2023; Xie et al., 2019).

Injection Molding: This is the type that can be successfully used in producing complex components in large volumes using short fibre reinforced thermoplastics (Proy et al., 2021). A pre-compounded polymer cotton fiber is often fed to a heated barrel and it is melted down and injected into a mold. One of the major shortcomings is that injection can greatly damage fibers due to the high shear forces, and thus constrains the aspect ratios that can be achieved (and, thus, the mechanical properties of the finished part) (Kim & Park, 2020; Mallick, 2021).

Extrusion: Used for producing continuous profiles like sheets, rods, and tubes. Cotton fibers and polymer granules are mixed, melted, and homogenized before being forced through a die. It is primarily used for compounding (creating the fiber-polymer blend) and for the production of semi-finished profiles, but the orientation of fibers is generally random, and properties are isotropic (Gibson et al., 2021; Pacheco et al., 2023).

Hand Lay-up: A simple, low-cost method primarily used for thermoset matrices and large, low-volume parts like prototypes or architectural features. Layers of woven or non-woven cotton fabric are manually impregnated with resin and rolled to remove air bubbles. It is labor-intensive and results in lower fiber volume fractions and higher variability compared to automated processes, but it requires minimal capital investment (Biswas &

Anurag, 2019; Chen et al., 2023; Pelin et al., 2024).

The processing parameters like temperature, pressure, time, and cooling rate profoundly affect the final composite's properties. Excessive temperature can degrade the cotton fibers, while insufficient pressure or time can lead to poor consolidation, high void content, and weak interfaces.

Table 1: Comparative Analysis of Key Properties for Cotton and Common Reinforcement Fibers.

Property	Cotton (Virgin)	Cotton (Linters)	Flax	Jute	E-Glass	Carbon Fiber (Standard)	References
Density (g/cm ³)	1.5 - 1.6	1.5 - 1.55	1.4 - 1.5	1.3 - 1.45	2.5 - 2.6	1.7 - 1.8	(Zelinka et al., 2022)
Tensile Strength (MPa)	287 - 597	200 - 400	345 - 1500	393 - 800	2000 - 3500	3500 - 6000	(Gudayu et al., 2025)
Young's Modulus (GPa)	5.5 - 12.6	4 - 10	27 - 80	10 - 30	70 - 76	230 - 600	(Selvan et al., 2022)
Elongation at Break (%)	6 - 8	5 - 10	1.2 - 3.2	1.5 - 1.8	2.5 - 3.0	1.4 - 1.8	(Wang et al., 2024)
Specific Strength (MPa/g/cm ³)	~180 - 370	~130 - 260	~250 - 1000	~300 - 550	~800 - 1350	~2000 - 3500	(Tuysuz et al., 2021)
Specific Modulus (GPa/g/cm ³)	~3.5 - 7.9	~2.6 - 6.5	~19 - 53	~7 - 21	~28 - 30	~135 - 350	(Jabbar, 2017)
Moisture Absorption (%)	8 - 25	8 - 25	7 - 12	12 - 14	<0.1	0.5 - 1.0	(Mohammed et al., 2023)
Approx. Cost (Relative)	Medium	Low	Medium	Low	Low	Very High	(Gisario et al., 2019)

5. The Performance Spectrum: the cotton biocomposites.

To determine the suitability of the cotton biocomposites in a wide range of applications, such as automotive interiors and sustainable packaging, a systematic assessment of the properties of the latter is critical. The interaction between fiber

treatment and the choice of the matrix and processing parameters is important in the performance optimization (Akter et al., 2022).

5.1. Mechanical Performance

The mechanical properties form the most crucial factor in structural and semi-structural applications, in which the load-

carrying possibilities are the most important.

Tensile and Flexural Strength: When polymer matrix is supplied with cotton fibers, the tensile and flexural modulus is generally enhanced as compared with the neat polymer due to rigidity property of cellulose (Ganapathy et al., 2023). However, final strength depends very much on quality of interfacial adhesion. Unmodified cotton composites often see only small strength increase of 10-20 per cent., but chemical treatments can be optimized, e.g. silanization or use of MAPP coupling agents and improvement of up to 30-60 per cent. can be achieved through effective stress transfer across the interface. The rule of mixtures frequently proves to be unsuccessful due to poor adhesion, misalignment of fibers and the existence of stress-concentration points (Elmogahzy & Farag, 2018; Wankhede et al., 2022).

Impact Strength: Due to the moderate values of both elongation at break of single cotton fibers (6 -8 -3) and their energy absorbing qualities through fiber pull-out and deformation, transferable to impact toughness, cotton composites often exhibit better impact toughness than more brittle glass-fiber composites of similar fiber loading (Malay, 2018). This feature makes them especially appropriate in applications where splintering is highly sensitive in an application like automobile interior panels which should not splinter when hit (Birniwa et al., 2023; Rangappa et al., 2022).

Mechanical Properties Influencing Factors: Mechanical properties tend to rise with fiber loading to a critical value

(usually 30 and 40 by weight), then fall off due to fiber agglomeration, insufficient wetting of the polymer skeleton, and augmented void content. The fiber orientation is also decisive; when the fiber is oriented in the same direction, or the fabric is woven the resulting product is anisotropic with a higher strength at the dotted fiber length, and when the length is short the resulting product is more isotropic but lower-strength (Rashid et al., 2021; Saba et al., 2016).

5.2. Durability and Environmental Performances.

Biodegradability: One of the major environmental benefits of cotton biocomposites is their biodegradability, especially when combined with a bio-based polymeric matrix, such as polylactic acid (PLA) or polyhydroxybutyrate (PHB) (Okolie et al., 2023). In the conditions of industrial composting (58° C, with a fixed humidity), full biodegradation is achieved in 90-180 days, according to the thickness and the composition of the material, which is an obvious end-of-life advantage compared to synthetic composites that can last centuries in landfills (Battegazzore et al., 2019).

Life-Cycle Assessment (LCA): Recent LCA analytical investigations have shown that natural-fiber composites have a 30-50-percent smaller global warming potential and a reduced amount of non-renewable energy use than glass-fiber composites, primarily because of less energy usage in fiber production. The use of cotton waste streams (linters, recycled textiles) also enhances such a profile by eliminating the effects of growing virgin fibres, as well as, lowering landfill loads (Wang et al., 2023; Zhang et al., 2021).

5.3. The ability to endure environmental pressure:

Moisture: Prolonged exposure to moisture greater than 65 0.RH causes swelling, hydrolysis at the fiber-matrix interface, and plasticization of the matrix resulting in a 20-40% loss in mechanical properties after long-term exposure(Aminudin et al., 2023). Surface modification and use of hydrophobic matrices like polypropylene play a crucial role in reducing the effect and silane treatments have also proven to have very strong and high performance in humid conditions (Yang et al., 2022).

UV Radiation: UV radiation (295-400nm) may induce photo-degradation by chain scission of both lignin parts of the fiber (resulting in yellowing and discoloration) and the polymer matrix (resulting in surface embrittlement and cracking). Outdoor applications can often be made with UV stabilizers and protective coats (polyurethane, acrylic), where nano-TiO₂ and ZnO have demonstrated the potential to be an effective UV blocker in recent studies(Mastouri et al., 2023).

Table 2. Performance and Sustainability Benchmarking of Cotton Biocomposites.

Composite System (~30-40% fiber)	Tensile Strength (MPa)	Impact Strength (J/m)	Key Advantage	Environmental Benefit (vs. Glass/PP)	Key Remaining Challenge	References
Cotton/PP (Untreated)	30 - 45	40 - 70	Cost-effective, good impact toughness	20-30% lower GWP	Poor interface; high moisture sensitivity	(Abteu et al., 2025)
Cotton/PP (Silane treated)	45 - 65	50 - 80	Excellent balance of strength & toughness	25-35% lower GWP	Cost of silane; long-term adhesion durability in moisture	(Nanni et al., 2021)
Cotton/PLA	55 - 80	25 - 45	Fully bio-based & compostable	40-50% lower GWP; biodegradable	Brittle impact behavior; low HDT	(Battegazzore et al., 2019)
Recycled Cotton/ Bio-resin	25 - 40	30 - 60	Circular economy; waste valorization	50-60% lower GWP (avoided landfill)	High property variability; contamination	(Faheem & Khan, 2025)
Reference Material (E-Glass/PP)	80 - 110	70 - 100	High absolute strength	Baseline (High GWP, non-recyclable)	High density, abrasive, non-biodegradable	(Aminudin et al., 2023)

6. Application Landscape: From Mainstream Adoption to Techno-logical Frontiers:

The unique property characteristics of cotton biocomposites as an amalgamation of sustainability and functional properties has prompted their use in various

industries with vast opportunities in the future. These materials provide possible directions of decarbonisation and waste valorisation as industries strive to achieve carbon -reduction goals and implement the principles of the circular economy.

The Circular Bio-Economy of Cotton Biocomposites

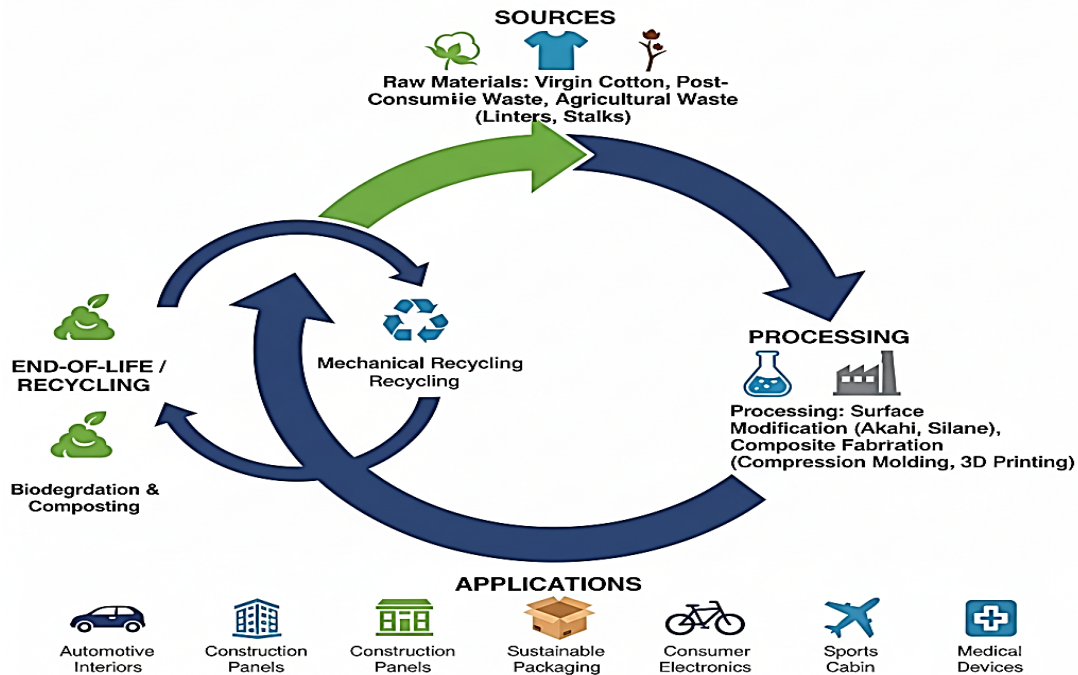


Fig. 2. Circular bio-economy of cotton biocomposites, from source to end-of-life.

6.1. Adequate Industrial Applications.

Automotive Industry: This will be the fullest-developed natural-fiber composite market, with strict end-of-life vehicle standards and lightweighting seeking in the industry (Skosana et al., 2024). Composites made of cotton, in most cases in the shape of needle-punched non-woven mats, with polypropylene matrices are widely used as interior parts such as door liners, parcel shelves, headliners, and trunk liners. Their 15-30 percent reduction in weight compared to glass-fiber composites plus their outstanding acoustic damping performance (cutting cabin noise by 35 dB) and reduced splintering behaviour upon hitting an object make them especially useful in modern automobile design (Musa & Onwualu, 2024; Yan & Xu, 2025).

Construction and Building Materials:

Construction industry has become one of the largest consumers of cotton biocomposites, especially in the interior sector where they match the green-building standards (Saini & Ledwani, 2024). Ceiling tiles, movable partitions, and insulation boards are also being more specified to cotton-based panels where the thermal conductivity of 0.038-0.042 -1K - 1 and noise-reduction coefficients of 0.6-0.8 are useful and sustainable. The most recent inventions are treated interior structural composites made of fire-retarded treated cotton and moisture-resistant formulations in bathroom and kitchen panelling (Parlato & Pezzuolo, 2024; Przybek, 2025).

Packaging Solutions: With people moving towards single-use plastic replacement globally, the packaging with cotton has become an important opportunity, especially in the e-commerce and food markets (Syed Ali et al., 2024). Protective cushions, trays that can be moulded, and shipping inserts are made using recycled cotton fibre and bio-based binders that provide similar performance to expanded polystyrene foam and can be composting completely in industrial facilities. The latest life-cycle analysis shows that the carbon footprint is 40-60 percent smaller compared to traditional plastic packaging, and the bonus is that there are markets in which the textile waste can be sold (Arora et al., 2023; Dube & Dube, 2023).

6.2. Emerging and Niche Applications.

Consumer Electronics: Major electronic manufacturers are investigating the use of cotton based composites in the creation of device cases, speaker casings and other internal supports so that they can improve sustainability profiles without compromising on performance (Shi et al., 2023). This intrinsic electromagnetic transparency, vibration-damping and aesthetic qualities of natural fibres make it a material to use in high-end audio equipment and wearables and prototypes of this type have been shown to reduce weight by 20% compared to ABS plastic cases (Heo et al., 2018; L. Wang et al., 2020).

Sports and Recreation Equipment: The sporting-goods industry is taking advantage of the particular merit and vibration-damping characteristics of cotton composite materials to provide products

where the natural branding attribute appeals to the eco-friendly consumer segments (Umair & Khan, 2020). Such recent developments as skateboard decks using cotton-flax hybrid composites with better impact resistance, bicycle frames with better stiffness-weight balance, and surfing gear with better resistance to marine conditions have been created (Gijnsman et al., 2024).

High-Performance Transportation: In other transportation industries, cotton composites are used as well, such as railway carriage interiors, aircraft cabin, and in marine paneling. Recent certifications of natural-fiber composites in non-structural aircraft parts have created huge opportunities; cotton-based materials save 25-30 percent of the weight compared to traditional materials and are able to satisfy the stringent flame, smoke, and toxicity standards (Chauhan et al., 2019; Thakur et al., 2025).

Medical and healthcare products: Biocompatibility and antimicrobial activity of specially treated cotton composites are under development in the medical products sector, such as patient-transfer devices, medical equipment housings, and rehabilitation aides. Recent studies show that cotton composites that have undergone silver-nanoparticle treatment reduce bacterial growth by 99.9 per cent and still possess the mechanical strength that is required of medical usage (Debnath et al., 2025; Kantaros et al., 2025).

Smart Composites and IoT Integration: A porous cotton composite structure can be trained to integrate sensors and functional units into smart material systems. Science is in process of creating

structural-health-monitoring composites, using embedded fibre-optic sensors in cotton based matrices, and temperature sensitive composites of adaptive building envelopes (Chaudhary et al., 2024; Shi et al., 2020).

Additive Manufacturing: 3D printing with filaments reinforced with cotton allows new opportunities in terms of customised sustainable production (Anwajler et al., 2023). Innovations in the development of filament have recently reached 25-35 percent bio-content with printability and layer bonding, allowing intricate geometries that were not possible using the conventional composite fabrication technologies (Khilji et al., 2023; Sola & Trinchì, 2023).

Circular Economy Models: New business models are being created around cotton biocomposites, especially product-as-service business models where the manufacturer retains ownership and responsibility of end-of-life management (Khilji et al., 2023). These models make use of biodegradability and recyclability of cotton composites and establish closed-loop systems, which are consistent with the principles of the circular economy (Khajavi, 2021; Sola & Trinchì, 2023).

7. Conclusion

Biocomposites made of cotton are a promising intersection of sustainability, performance, and circularity, which will discontinue the traditional fossil-based and glass-fiber-based reinforced materials. By glorifying rich virgin fibres, low-cost linters, farm stalks and the mass production of post consumer textile waste these biocomposites convert

environmental burdens into high-value reinforcements. Their inherent benefits such as low density, competitive specific properties, high impact toughness, great acoustic and thermal insulation, and complete biodegradability coupled with a 30-50% reduced global-warming potential places them at the heart of the bio-economy change. Major advances in surface engineering (alkali, silane, acetylation, plasma, and enzymatic treatments), and the optimization of manufacturing paths (compression moulding, injection, extrusion and emerging additive manufacturing) has to a large extent overcome the barriers to interfacial incompatibility, moisture sensitivity and property variability in the history that have plagued the field. Such developments have opened mechanical improvements up to 60% allowing consistent service in automotive interiors, green building panels, compostable containers and a growing list of high value applications in consumer electronic products, aerospace cabin interiors, sportswear, medical devices, and sensor-based smart composite.

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