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Climate Smart Cotton: Integrative Genomics, Breeding and Biotechnological Strategies for Sustainable Fiber Production

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Abstract

Cotton (*Gossypium spp.*) is a significant fiber crop in the world but its productivity, as well as sustainability is being limited by climate-related pressure such as drought, salinity, heat, and increased pest population. Although traditional breeding has enhanced yield and fiber quality, the breeding process is not always precise and efficient to provide the ability to respond to complex and multigenic stress-adaptive traits. This review brings together recent innovations on cotton improvement by combining the use of genomic tools molecular breeding and the contemporary biotechnological tools. We present progress in the research of the physiological and molecular mechanisms underlying abiotic stress tolerance, such as osmotic regulation, ion homeostasis, and heat-shock reactions. Genome-wide association studies, quantitative trait locus mapping and multi-omics platforms have enabled the discovery of traits and identification of functional alleles at a faster rate. Further, there are novel technologies, including CRISPR/Cas-based genome editing, RNA interference, genotype-independent systems of transformation, and genomic selection, alleviating the breeding pipelines, i.e. allowing the rapid and specific generation of multi-stress-tolerant cultivars. The review focuses on integrative and data-driven breeding models with successful help of seed systems and international cooperation to deploy genomic innovation into climate-sensitive cotton varieties. Taken together, these developments make cotton improvement a systems science with the potential to maintain the productivity of fibers and financial sustainability amidst fluctuating climatic conditions.

Keywords: Climate-smart agriculture, Abiotic stress, Tolerance, Genomic selection, Molecular breeding.

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Introduction

Cotton (*Gossypium spp.*) is one of the most significant natural fiber crops in the world, the basis of the world-wide textile industry, and a significant factor in the economy of numerous developing and developed nations (1). Over the decades, breeding goals in cotton have shifted beyond the production and quality of fiber to encompass the ability to cope with the climatic stress factors (drought, salinity, heat, and evolving pest pressures) (2,3). Climate change, a decrease in arable land, and increased production costs have served as a manifestation of this, highlighting the weaknesses of traditional phenotypic selection in selecting complex, polygenic traits with high environmental interactions (4). This is why the programs of cotton improvements are shifting to genomics-aided and data-based breeding approaches that can be used to dissect traits accurately and in a very short period of time (5). Several significant innovations in cotton genomics have occurred in the past decade with the publication of high-quality reference genomes (6). The sequencing of allotetraploid *Gossypium hirsutum* (TM-1) genome offered initial information in the arrangement of polyploid genomes, evolution of fiber, and domestication of fiber sources, with consequent assemblies of *G. barbadense* led to genetic dissection of extra-long staple fibers (7). However, more recently, phenotypic presence-absence variation, structural variation, and non-reference genes pertaining to domestication, yield, and fiber quality have been found in the development of cotton pangenomes, using a variety of germplasm collections (8). These experiments show that single reference genomes only reflect a part of the genetic diversity of cotton, and it is necessary to use pangenome resources to expand the breeding pool (9). Simultaneously, genome-wide association studies, quantitative trait locus mapping, and functional haplotype studies and analyses have also been extended extensively with transcriptomic, metabolomic, and epigenomic data to discover traits in cotton (10). Thousand accessions scale GWAS have made it possible to identify quantitative trait genes that regulate yield and fiber quality and ensure the functional utility of key alleles, including FAH1, is experimentally validated (11). High-density SNP-based QTL analyses have further narrowed down the genetic aspect of complex traits (12-15). Collectively, these solutions have enhanced the connection between phenotypic performance and genomic variation, establishing new possibilities of accurate breeding (16). More genetic resources in cotton have been enhanced through the establishment of high populations of mutants generated by chemical mutagenesis and genome editing with the use of CRISPR-Cas (17). These resources along with the high-throughput sequencing and time, tissue-specific transcriptomics have facilitated the functional validation of the candidate genes in the association with fiber development and abiotic stress tolerance (18). In spite of this, the practical uses of genomic findings in terms of breeding advantages are constrained by a multitude of factors, including a strong linkage disequilibrium based on bottlenecks in the domestication process, a functional redundancy between homoeologous pairs of genomes, and a large ratio of genotype-environment interactions that could lead to a challenging phenotypic selection under varying conditions (19).

To break these challenges, the trend of cotton optimization is increasingly becoming a combination of molecular markers, genetic selection, genome editing, and predictive analytics to accelerate the rate of genetic gain and breeding performance (20,21,22). Systems-level solutions that will keep up with genomics, phenomics, and data science are a reminder of such strategic plans as Cotton 2035 which will create climate-smart cultivars that would still remain productive against the environmental pressure (23).

In contrast to previous reviews that focus on individual components of cotton improvement separately, this review presents an integrative synthesis that establishes clear connections among pangenome diversity, functional haplotypes, molecular breeding, and biotechnological innovations within a climate-smart breeding framework. It is a critical review of the manner in which genomic and multi-omics findings can be applied to breeding pipelines. Moreover, it considers the problem of polyploidy, linkage disequilibrium, and environmental complexity. It is through such a combination that this review is intended to fill in the gap between scientific uncovering and practical application in contemporary cotton improvement schemes (Figure 1).

Cotton Genomic Resources

Genomic resources are the biological information, equipment, and infrastructures that characterize the composition, operation, diversification and control of the genome of an organism (24). These are the resources that aid in discovering genes, diversity and breeding by the use of molecules (25). They give the basis of translating genomic information into viable crop enhancing measures (26). One of the major genomic resources is reference genome sequences, which offer a full blueprint of DNA of a species (27). Pangenomes capture the cumulative gene content across multiple cultivars and wild relatives, revealing structural variations and non-reference genes absent in single reference genomes (28).

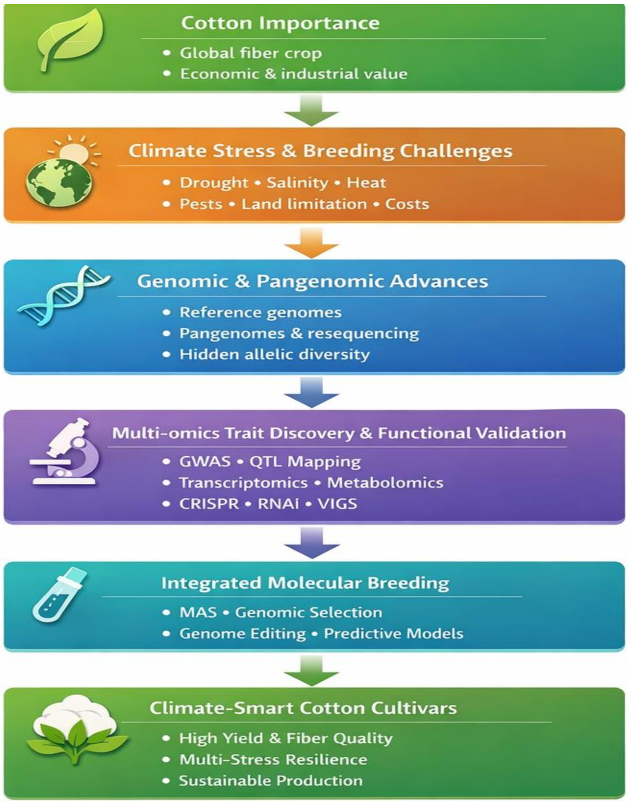

Figure 1: Integrative framework for climate-smart cotton improvement

The positions of genes and quantitative trait loci (QTLs) can be discovered using genetic and physical maps and subsequently used to dissect traits (26). SSRs and SNPs are molecular markers that facilitate the use of markers in breeding and genomic breeding (29). The datasets of population resequencing display the genetic diversity, haplotypes, and the signature of selection (25). The resources of transcriptomics provide a description of gene expression patterns in tissues and development stages, especially those involved in fiber development and how the body responds to stress (30). Epigenomic and multi-omics datasets further clarify gene regulation and environmental adaptation (6). Public databases and bioinformatics platforms allow efficient storage, retrieval, and analysis of genomic variation for breeding applications (31).

In cotton, recent advances in long-read sequencing technologies and chromosome-scale scaffolding approaches, particularly Hi-C based assemblies, have enabled the development of high-quality reference and cultivar genomes for diploid and tetraploid Gossypium species (24). These improved assemblies have enhanced understanding of structural variation, gene content diversity, and genome organization associated with fiber development and environmental adaptation (28). Updated versions of the TM-

1 reference genome of *Gossypium hirsutum*, along with newly assembled elite cultivars, have captured breeding-relevant variation and resolved gaps present in earlier drafts (32). This has increased their value for comparative genomics, QTL mapping, and map-based cloning (33).

High-quality A- and D-genome diploid progenitor assemblies of high quality have enhanced subgenome annotation and homoeologous family genes identification (1,32). They have a powerful framework where functional and evolutionary studies in polyploid cotton can be performed (34). The combination of population-scale resequencing and genomic studies has been very powerful in strengthening candidate gene discovery and marker development (35). Genomic variation and diversity of cotton are available in public databases that assist in the exploration of genetic variation and its application in the marker-assisted selection (36).

Comparative studies on diversity always indicate a narrow genetic base in modern cultivars when compared to the landraces and wild relatives. It underscores the necessity to use exotic germplasm in order to increase adaptive potential and climate resilience (37). Abiotic stress tolerance, fiber traits, and seed characteristics have also been characterized on the basis of favorable alleles as a result of resequencing and haplotype analyses (38). The results can be useful in the context of pre-breeding, as well as introgression programs (39).

This has been allowed through refined gene models that are supported by high-resolution transcriptomic profiling which have advanced the understanding of regulatory networks in the regulation of fiber initiation, fiber elongation, and biosynthesis of secondary cell walls (40). Combined, integrated genomic and transcriptomic tools constitute a robust basis of the precision and climate-smart cotton breeding (24).

In the past, phenotypic selection and low-density markers have been used in cotton improvement. Initial genomic mapping on SSR based linkage mapping and rough draft genome assemblies. Recent advances encompass chromosome scale recombination's, pangenome assembly, genome-wide association, genome selection modeling and genome editing. The developments have made the process between the discovery of genes and practical use on the field faster. The same genomic advancement has been witnessed in other high crops. Oryza sativa has high quality reference genomes, pangenomes that have facilitated breeding of resistant rice to stresses. Developed genomic selection systems are commonly used in hybrid programs of Zea mays. Assemblies of chromosomes in the polyploid crop Triticum aestivum have enhanced trait dissection. Glycine max has enormous SNP resources that have boosted quality and the increase in yield. Such illustrations show that the overall genomic tools are at the core of breeding and climate-adaptation plans of crops.

Molecular Breeding Approaches

The physical breeding has transformed cotton breeding through the application of high throughput genotyping with decisive phenotyping and breeding to identify complex traits such as fiber quality, yield stability and stress tolerance (41). As traditional breeding has provided substantial returns, its effectiveness is limited by the lengthy breeding cycle and limited polygenic trait resolution by environmental variation (42). Allele discovery, allele tracking, and allele deployment via the usage of molecular tools have also enabled the dissection of trait architecture and prediction of breeding values to be more reliable (43).

In cotton breeding programs, three molecular techniques marker-assisted selection (MAS), quantitative trait locus (QTL) mapping, and genomic selection (GS) are popular and are becoming more and more combined to achieve maximal genetic gain as demonstrated in Figure 2. These methods are not independent of each other, but instead, they constitute a continuum to assist in both short term development of the cultivars and long-term population enhancement. In cotton, marker-assisted selection and QTL mapping are used to identify QTL that explain genetic variation in metabolism levels, seed traits, and drought resistance.

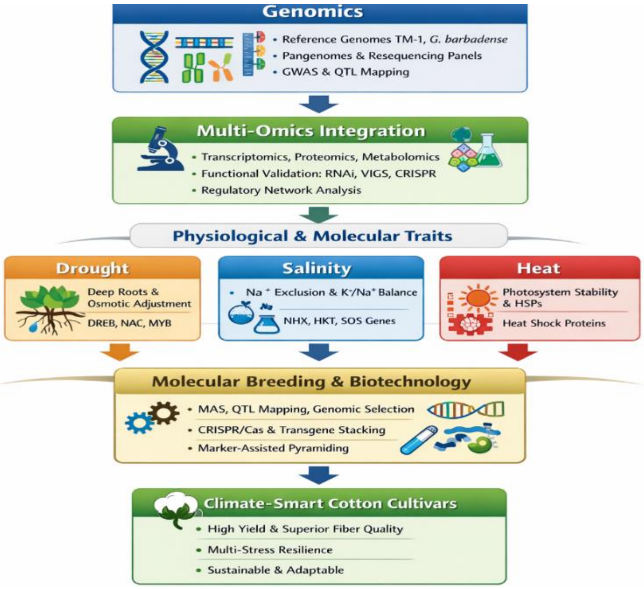

Figure 2: Integrative framework for developing climate-smart cotton cultivars, showing the flow from genomic resources and multi-omics integration through physiological and molecular traits to molecular breeding and climate-resilient cotton varieties.

Marker-Assisted Selection (MAS) and QTL Mapping in Cotton

Marker-assisted selection and QTL mapping are applied in cotton to identify QTL to explain genetic variability in the levels of metabolism, seed characteristics and drought-resistance (44). Introgression and pyramiding of major-effect loci that control fiber quality, disease resistance, and other important agronomic factors have been successfully used in cotton via MAS (45). The key strength of it is the diagnostic marker use, which allows selecting it at an early age and independent of the environment, especially in phenotypes with challenging phenotyping (46). Cotton breeding programs have been able to use MAS to transfer QTLs related to fiber length, strength, and resistance to biotic stresses using both marker-assisted backcrossing and pre-breeding methods (47). MAS is based on QTL mapping which is a method used to determine the genomic regions that regulate complex traits (48). SNP-based linkage maps produced on a high density by using recombinant inbred lines, lines of chromosome segments substitution, and population of introgression have identified many QTLs related to fiber quality, yield components, and stress tolerance (49). The meta-QTL analyses have also found significant stable environment QTL clusters that enhance their breeding use. Combination of QTL mapping and transcriptomics and fine-mapping methods have allowed reducing the interval size of candidates and simplified downstream functional validation (50). Although useful, MAS and QTL-based methods are not as useful with traits that are regulated by numerous and highly small-impact loci, which complementary approaches are required to capture genome-wide variation (51). The major QTLs and candidate genes identified in previous cotton studies, along with their associated traits and chromosomal locations, are summarized in Table 1.

Table 1: Important QTLs and Candidate Genes Identified for Fiber Quality, Yield Components, and Stress Tolerance in Cotton through QTL Mapping and Marker-Assisted Selection (MAS).

Trait Category	QTL-Gene	Chromosome	Associated Trait	Findings	Citations
Fiber Length	qFL-Chr7	Chr07 (At)	Fiber length	Stable QTL detected across environments; used in MAS programs	Rajan *et al.*, 2025 (17)
Fiber Strength	qFS-Chr25	Chr25 (Dt)	Fiber strength	Major-effect QTL introgressed through backcrossing	Hugie, 2015 (43)
Fiber Quality	GhEXP1	At subgenome	Fiber elongation	Expansion gene associated with cell wall loosening during elongation	Fang *et al.*, 2014 (49)
Fiber Development	GhMYB25	At/Dt	Fiber initiation	Regulates early fiber differentiation	Fang *et al.*, 2014 (49)
Yield Components	qBN-Chr16	Chr16	Boll number	Stable QTL cluster identified through SNP mapping	Rajan *et al.*, 2025 (17)
Drought Tolerance	qDT-Chr3	Chr03	Drought resistance	Linked with physiological stress-response traits	Rehman *et al.*, 2018 (44)
Disease Resistance	qDR-Chr11	Chr11	Verticillium wilt resistance	Used in marker-assisted backcrossing	Kushanov *et al.*, 2021 (41)
Multiple Traits (Meta-QTL)	MQTL-Fiber Cluster	Chr5/Chr21	Fiber length & strength	Environmentally stable QTL cluster	Rajan *et al.*, 2025 (17)
Complex Traits (Limitation)	Polygenic small-effect loci	Genome-wide	Yield & stress tolerance	Low efficiency of MAS alone; requires genome-wide approaches	Zhang *et al.*, 2019 (48)

Genomic Selection for Complex Traits

This is used to solve biological problems in organismal studies. Genomic selection (GS) can overcome the weaknesses of MAS by estimating breeding values based on genome-wide marker data without the need to detect a single QTL (52). GS has demonstrated specific opportunities to enhance the quality and low-heritability characteristics in cotton like lint yield, fiber stability, and stress-resilience (35). The model predictions based on extensive training populations consisting of both high-density genotyping and multi-environment phenotyping have shown better selection accuracy and time saved on breeding cycle (53). Recurrent genomic selection Pilot GS experiments in cotton suggest that genetic gain can be significantly increased when recurrent genomic selection is combined with standardized phenotyping and powerful statistical models. With the decreasing genotyping and increasing phenomic platforms, GS will become more and more central in cotton improvement programs.

Complementarity and Integrated Molecular Breeding Frameworks

Currently, MAS, QTL mapping, and GS are not competing techniques in the breeding of cotton, but rather complementary methods (54). The major-effect loci are accurately manipulated with MAS and QTL mapping, and the cumulative effect of the genome-wide small-effect alleles that are key to complex traits can be captured with GS (55). Combining GWAS, QTL discovery, functional validation, and genomic prediction enable the breeders to optimize target characteristics and genetic background merit at the same time (56).

Additionally, the genome editing tools like CRISPR-Cas can bring even more confidence to that framework as they have allowed modifying candidate genes that have been discovered after QTL or GWAS results (57). Collectively, these combined molecular breeding approaches present a potent avenue of accelerating the breeding of cotton cultivars with improved fiber quality and yield potential and adaptability to biotic and abiotic stresses in changing climatic conditions (58).

Biotechnological Advances in Cotton Improvement

The emergence of biotechnological innovations has enhanced the area of cotton improvement significantly by allowing micro-targeting of complex traits with even more specificity and efficacy than the traditional breeding methods (59). The traditional selection is frequently limited by the length of the generation cycle, the complexity of their polyploid genome, and their very high environmental impact, but modern biotechnological methods enable direct editing of genes and regulatory circuits, which facilitates the rapid validation of their functions and the production of cultivar (60). Transgenic cotton has been one of the most successful biotechnology applications, especially in pest and herbicides treatment, and extensive use has been shown as a measure of its agronomic and economic utility (61).

The recent work has focused on the opportunity of piling up of numerous genes to increase the period of trait and expand agronomic advantages (62). The use of pyramided cotton cultivars containing Bacillus thuringiensis (Bt) toxins in combination with RNA interference (RNAi) construct, abiotic stress responsive gene and fiber-quality related locus have been shown to enhance pest resistance and environmental adaptability (63). The in-field tests indicate that stacked traits with them may be implemented with minimal consequences on non-target organisms in case properly designed and controlled (64). Simultaneously, improvements to genotype-independent transformation systems such as Agrobacterium-mediated systems improved with morphogenic regulators have minimized genotype effects and made the development of elite cultivar-engaging genes-to-elite cultivar-development interval shorter (54).

Genome editing with the use of CRISPR-Cas has become especially strong to study functional genomics and to enhance traits in cotton (65). Mb2Cas12a, a high-efficiency platform, has been demonstrated to have been highly mutagenic in T0 plants, making it easy to test the hypothesis in the context of rapid gene discovery in the plant architecture and chloroplast development (66). The multi editing techniques have been especially useful in polyploid cotton because they enable simultaneous editing of homoeologous loci in A and D-sub genomes (33). In more recent versions, the base editing and prime editing technologies have made it possible to make precise nucleotide-level edits without the introduction of, and with the introduction of, double-strand breaks, offer novel opportunities to enhance the quality of fibers, seed oil composition and stress responses in elite germplasm (67).

Recent genome editing methods, such as RNAi and virus-induced gene silencing (VIGS), can also be used to supplement genome editing, allowing the functional validation of candidate genes (68). The possible prospects of tissue-specific gene regulation are exemplified by RNAi-based silencing of delta-cadinene synthase genes to produce ultra-low-gossypol cottonseed with no adverse effect on the plant defense capabilities (69). VIGS is a fast, temporary system of validating genes which have been observed with GWAS or transcriptomic studies without any stable transformation (70).

In spite of this pledge, biotechnology methods on cotton improvement are not free of significant limitations (28). The availability of regulatory frameworks of genetically modified and genome-edited crops also differs by region and has the potential to slow down implementation. The off-target effects especially during multiplex genome editing need strict validation to ascertain the integrity of genome. Moreover, the adoption is still affected by the audience and market perceptions, which is why it is important to provide a clear risk evaluation and consultation (51). However, these biotechnological tools can be leveraged with high throughput genomic and phenomic resources to provide a potent supplement to molecular breeding strategies and develop more climate resilient and cotton with high quality as the environmental and economic pressures continue to rise (71).

Agronomic and Fiber Quality Traits Genetics

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Table 2: Key physiological and molecular mechanisms underlying drought, salinity and heat tolerance in cotton

Stress	Physiological Traits	Molecular Regulators	Breeding Relevance	Citations
Drought	Deep root systems, stomatal regulation, osmotic adjustment (proline, sugars, glycine betaine), enhanced antioxidant activity	DREB, NAC, MYB transcription factors; ABA signaling; ROS-scavenging enzymes (SOD, CAT, POD)	MAS for drought-tolerant alleles, genomic selection (GS) for polygenic drought resilience, introgression from wild/exotic germplasm	Huang *et al.*, 2020 (26)
Salinity	Ion homeostasis (Na+ exclusion, K+ retention), osmotic adjustment, chlorophyll retention, antioxidant activity	NHX antiporters, HKT transporters, SOS pathway genes, compatible solute synthesis genes, ABA signaling	MAS for salt-tolerance QTLs, GWAS to identify alleles for ion regulation, multi-environment phenotyping for salt stress adaptation	Kumar *et al.*, 2024 (10)
Heat	Canopy cooling, maintenance of photosynthetic activity, membrane stability, pollen and ovule protection	Heat shock proteins (HSPs), antioxidant enzymes, transcription factors regulating thermotolerance, ROS detoxification pathways	Introgression of heat-tolerance alleles, genome editing for HSPs and protective regulators, selection of reproductive resilience traits	Dong *et al.*, 2019 (36)

Abiotic Stress Tolerance in Cotton

Cotton is also very sensitive to drought, salinity, and heat stress, especially flowering, boll development, and fiber elongation cycles (64). These stresses interfere with photosynthesis, water relations and cellular metabolism leading to oxidative damage, disrupting nutrient balance and decreased reproductive success (86). These stresses are becoming more common and increasingly overlapping due to climate change, which requires a combination of breeding strategies that are based on physiological knowledge and are of molecular and genomically avenues (87). Abiotic stresses do not usually exist alone. Integrated drought, salinity, and heat stress increases physiological perturbation by causing an over-accumulation of reactive oxygen species (ROS), hormonal disproportion, and broken stomatal control (76). Germplasm adapted to stress enables valuable alleles to be used in the breeding programs to address these complex stress environments with the help of their wild relatives (65).

Drought, Salinity and Heat Tolerance

Co-ordinated Processes. During drought, salinity, and heat stress, cotton has overlapped morphological, physiological, and molecular adaptive responses (Figure 3) (71). Cellular protection and metabolic stability during stress are achieved by the involvement of root system architecture, osmotic adjustment through compatible solutes (proline, sugars, glycine betaine) and the increase in antioxidant capacity (81). At physiological level, photosynthetic efficiency, membrane stability and ion homeostasis are essential to maintain (47). Salinity-tolerant genotypes can control Na + exclusion and vacuolar uptake and maintain desirable K +/Na + ratios, but the heat tolerance depends on membrane lipid rearrangements and temperature control of canopy (48). Heat stress on reproductive organs can be mitigated through site-specific heat shock proteins (HSPs) expression and part of carbohydrates as necessitated (50).

Downstream pathways regulated by molecularly by transcription factors like DREB, NAC, MYB and bZIP family can be used to regulate Osmo protection, antioxidant and stress-responsive gene expression across a range of stresses (88). These combined regulatory centers are useful in breeding multi-stress-tolerance and reduce the trade-offs (74).

Shared and Stress-Specific Signaling Pathways

Common abscisic acid (ABA) and Ca 2-mediated signaling networks, which interact in the control of stomatology, antioxidant systems, and transcriptional responses, are met at the intersection of drought, salinity, and heat stress (51). Although these common pathways are the foundation of stress adaptation, there are more layers of specialization like ion transport in response to salinity and HSP in response to heat (89). This balance is very important to understand in order to design effective breeding strategies that are based on multi-stress.

Integration and Translational Breeding of Omics

As it is depicted in Figure 3, the application of multi-omics technologies that combine transcriptomics, proteomics, and metabolomics with stage-specific phenotyping has allowed identifying regulators and biomarkers of stress resilience (49). These data sets can be used to carry out functional validation by RNAi or VIGS or CRISPR-based genome editing and speed up translating these datasets into breeding pipelines (90). Genomic selection models with genotype × environment interaction, such as GWAS, QTL mapping, and genomic selection model will allow the simultaneous enhancement of stress tolerance and yield-related traits (91). Acknowledging physiological trait stacking, genome editing, and predictive modeling, translational breeding approaches are also gaining preeminence in efforts to overcome combined abiotic stress effects to maintain yield and fiber quality in climate-smart cotton cultivars (75).

Integrative Breeding Strategies

It is necessary to involve a combination of genomics, biotechnology and conventional breeding to develop climate-smart cotton varieties that can yield high-quality fibers, maintain their stability under stress, and be highly yielding (92). High-quality reference genomes, pangenomes and GWAS datasets increase the pool of alleles and candidate loci for fiber quality, stress tolerance and yield stability (47). Genomic selection (GS) works in a hurry to gain polygenic trait and precision breeding with CRISPR-Cas and new genome editors allow to make specific gene, promoter, and regulatory element amendments, which takes into consideration that the genome of cotton is tetraploid (93). Other methods such as allele mining of wild relatives, speed breeding and doubled-haploid pipelines have been used to complement each other and also shorten breeding cycles and mix complex traits. Predictive models fed with high-throughput phenotyping provided by imaging, remote sensing, and root platforms rank genotypes to test multi-locations and deal with genotype x environment interactions (94).

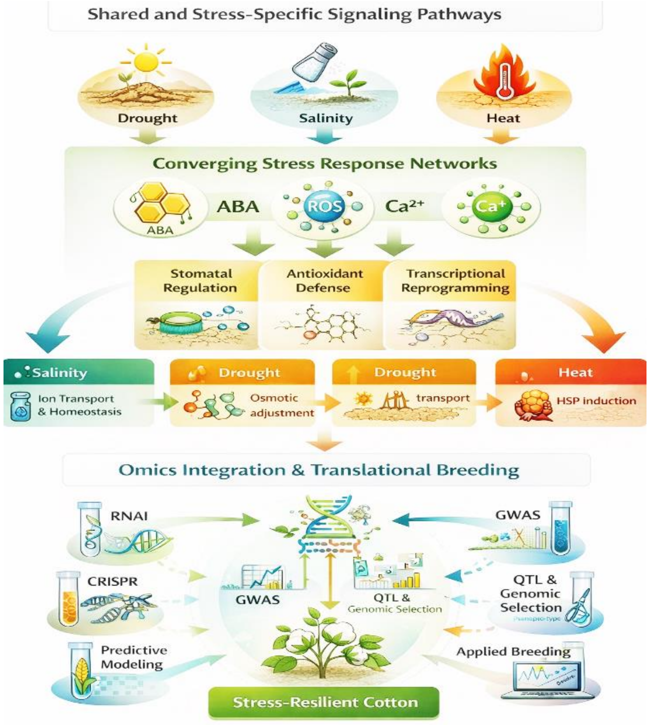

Figure 3: Shared and Stress-Specific Signaling Pathways and Omics-Driven Translational Breeding for Developing Stress-Resilient Cotton.

Bioinformatics services assist in the calling of variations, the discovery of haplotype, genomic forecasting, and the integration of multi-omics (85). Effective pipelines integrate germplasm diversity, high quality phenotyping, statistical genomics, and precision deployment (through editing or marker assisted backcrossing), and are coordinated by multi-disciplinary teams (95). Guidance on the application of scientific knowledge to the field can be ensured through field validation, interplay of seed systems, and regulatory stewardship to ensure the on-farm impact of scientific knowledge is achieved (Table 2) (96).

Prospects and Challenges in Future Cotton Breeding

The future of cotton breeding has its exciting prospects and great challenges. Advances in genomics, precision breeding, and climate-smart agriculture provide tools to accelerate genetic gains. However, achieving sustainable, resilient, and high-performing cultivars requires careful integration of biological, technical, and socio-economic aspects.

Breeding Sustainability

Breeding must move beyond single-trait improvement toward sustainable multi-trait approaches (39). Efficient resource use, soil health, and resilient agro-ecosystems are key priorities. Selection of functional traits such as root depth, nutrient efficiency, and rhizosphere microbiome interactions, combined with genomic selection, accelerates genetic gain while reducing input intensity (65). Rapid breeding cycles and speed breeding platforms allow faster introgression of desirable alleles, enabling the timely release of cultivars that are both high-performing and sustainable (74).

Climate-Smart Cotton Varieties

Developing climate-smart cotton requires stacking multiple stress-tolerance alleles to maintain fiber quality under drought, heat, and salinity (51). Multi-omics approaches including transcriptomics, proteomics, and metabolomics help identify regulatory hubs and stress adaptation biomarkers (81). Genome editing tools, such as base and prime editors, offer precise control over regulatory elements, improving stress response (42). Introgression of adaptive alleles from wild Gossypium relatives further enhances tolerance to combined stresses (47).

International Collaboration and Policy Support

Global collaboration accelerates cotton improvement through shared genomic resources, standardized phenotyping, and multi-location trials, as exemplified by initiatives like the International Cotton Genome Initiative (ICGI) (63). Policy frameworks should promote gene-edited crops, seed certification, and climate-linked incentives (93). Adoption of sustainable cotton varieties, particularly in developing countries, is critical to translate scientific progress into agricultural impact (74).

Challenges and Research Priorities

Despite remarkable progress, significant challenges remain. Accurately modeling genotype × environment × management (G×E×M) interactions across agro-climatic zones is essential to predict trait stability and performance (24). At the molecular level, assembling optimal homoeologous gene combinations in allotetraploid cotton remains complex and prone to unintended outcomes (89). Equitable access to high-quality seeds for smallholder farmers is necessary to convert scientific advances into sustainable productivity (97). Overcoming these challenges requires investment in advanced breeding facilities, open-access genomic and phenotypic databases, and international collaboration for knowledge exchange, capacity building, and coordinated research agendas (66).

Conclusion

The breeding of cotton is experiencing a transformational phase that has been necessitated by the use of advanced genomics, precision breeding and integrated production management. Conventional applications where individual traits were applied like yield or fiber length have now developed into holistic pipelines that operate using genetics, physiology, agronomy, and bioinformatics. The quality of genome assemblies, pangenomes, and functional gene annotations enable breeders to be able to find major genes, alleles and regulatory networks. These instruments are combined with high-throughput phenotyping to assist in the correlation of genotype to performance in a variety of field conditions. The new generation of cotton needs to be climate adaptable, productive and sustainable to heat, drought, salinity, and pests. This can only be attained through a combination of adaptive features such as root architecture, reproductive stability, water and nutrient efficiency, rhizosphere interactions and antioxidant mechanisms in a unified genetic background. Increasing adaptive potential is further enhanced by increasing the genetic base by using landraces and wild Gossypium species. New technologies such as genome editing, base editing, speed breeding and genomic prediction are used to expedite the construction of these multi-factorial trait packages. But scientific invention can do no good. Better varieties should be incorporated in effective seed systems, regulation systems and in market systems. The adoption can be improved with the help of clear certification; incentives related to climatic aspects and farmer-focused allocation. The international cooperation of research centers, markets, groups of farmers, and multinational organizations will be essential. This will be facilitated by open-access germplasm, standardized phenotyping as well as multi-environment trials. Cotton can become a skill model of climate-smart production of fibers when used to predict breeding, deploy more precisely, enable policies, and combine multi-omics information, to guarantee the livelihood of farmers, conservation of resources, and competitiveness of global textiles in a changing climate.

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