

CURRENT SITUATION AND PROSPECTS OF COTTON PRODUCTION IN PAKISTAN

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Abstract: Pakistan is the world's fifth-largest cotton producer. It is grown largely for fibre, and its oil is used as a vegetable oil and contributes significantly to the local oil industry. Cottonseed oil meets 18.1% of Pakistan's edible oil needs. In 2030, there will be 5.5 million tonnes of total demand for this purpose, with 2 million tonnes of local supply. Bt cotton, which was introduced in 2010 to remove three harmful lepidopteran insects, currently accounts for more than 90% of all cotton grown in Pakistan. Pakistan offers a lot of potential for organic cotton cultivation, particularly in unconventional cotton-growing locations with low insect burdens. Climate change-induced high temperatures and water scarcity are a big worry because contemporary agriculture is practiced in areas that already experience very high temperatures. Phenotypic selection in breeding is ineffective in creating stress-tolerant cotton. Marker-assisted selection technologies have considerably increased the effectiveness of traditional breeding. Modern breeding techniques contributed to the development of novel cotton breeding strategies. Furthermore, CRISPR/Cas9 and genome editing can establish a good foundation for improving resistance against biotic and abiotic stresses.

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Introduction

Cotton is the primary significant cash crop in Pakistan. In the agricultural sector, it is commonly referred to as "white gold" due to its potential to generate profits for farmers. Cotton is essential to Pakistan's economy since it is the principal foreign exchange earnings source that directly supports the country's gross domestic product (Shahzad et al., 2022). The discovery and dissemination of novel germplasm and Bt cotton cultivars have recently increased seed cotton yield. In addition, technological advances in cotton breeding and production have benefited the entire industry. In addition to the historical increase in production, various factors have led to the plateauing of cotton production (Masood et al., 2022; Shuli et al., 2018). A number of factors influences Pakistan's cotton production. Cotton's susceptibility to insects makes insect pests the most severe global constraint on cotton productivity, which is managed mostly by applying pesticides. Insect pests, a scarcity of high-quality seeds, cotton diseases such as cotton leaf curl disease, heat and drought stress, labor-intensive harvesting, fluctuating cotton prices, and shifting cropping patterns are the most significant problems in the cotton zone. This review examines the current condition of production, cotton-based breeding techniques, germplasm development, mechanization, and significant

production limits (Aslam et al., 2022; Fatima et al., 2022ab; Malik & Ahsan, 2016).

Phenotype-based cotton breeding's restrictions

In Pakistan, acceptable genotypes are often developed by traditional breeding techniques. Many screening techniques are utilized to pick the best potential parents for crossing, as shown in figure 1. Multiple crossings are performed to produce a useful variation. Sometimes a small number of mutagenesis has employed to acquire the desired mutation. Backcrossing, recurrent selection, pure line selection, pedigree, and mass selection are routinely used to select and fix desired traits. One of the most important selection factors is the phenotypic expression of the progeny's desired characteristics under different environmental settings (RAZZAQ et al., 2021). In addition to its outstanding efficacy, the phenotype-based method of cotton breeding has significant drawbacks. Phenotype-based selection often yields the greatest outcomes for qualitative traits influenced by various environmental factors. Due to the low heritability index, the phenotype-based selection is typically ineffectual for quantitative factors such as cotton yield (Aslam, 2016). In addition, phenotypic evaluation of the vast majority of cotton cultivars subjected to environmental factors is unreliable. Due to the influence of recessive genes or environmental

influences, some recessive traits may not be detectable at the phenotypic level, making recessive trait selection even harder (Abbas, 2020). The lack of selection tools during the early segregation generations is a significant impediment to phenotype-based cotton breeding. As a result, more resources are gradually allocated to enabling many cycles of propagation advancement and selection. Six to ten years will pass before cotton recovers its homozygous properties. These effects have a detrimental impact on the genetic makeup of improved cultivars, hence diminishing the breeding effectiveness (Shabbir & Yaqoob, 2019). To produce top genotypes, -breeding parents must be genetically and physiologically exceptional. Identifying superior parental material remains challenging in phenotype-based cotton breeding programs. Parental selection includes general and specific combining ability tests administered in various situations, necessitating additional screening cycles, resources, and time. In contrast, using genetic markers to evaluate the genetic diversity of inbred parents is an effective method for selecting superior inbred lines (Kouser et al., 2019).

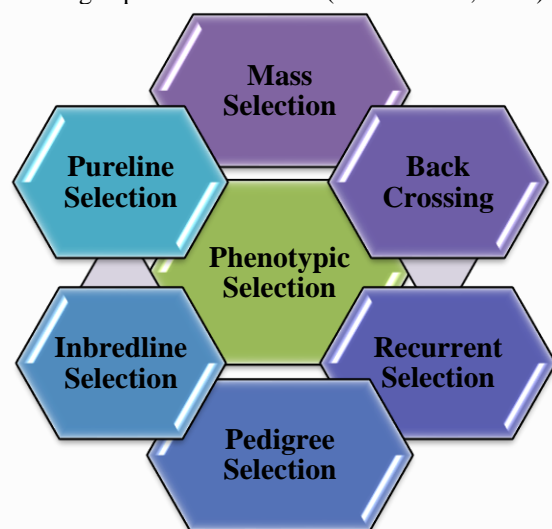


Figure 1: Different breeding and selection methods based on phenotype
Insufficient germplasm

All breeding programs are dependent on the genetic diversity of their breeding stock. It differentiates

genetic differences and similarities among genotype, strain, and germplasm groups (Bakhsh et al., 2016). Consequently, plant breeding materials can be identified based on an estimate of genetic diversity. Previous research has shown that the *Gossypium* genus contains a wide range of genetic diversity in plant structures, leaf pubescence, leaf morphology, flower colour, pollen colour, boll size, yield, fibre quality, early maturity, and stress resistance. Most cotton breeders in Pakistan performed crosses with legally recognized, locally suited cultivars to produce new cultivars. Diverse breeders combined cultivars that were closely related to develop the desired cultivars. These breeding strategies resulted in genetic similarity among cultivars, hindering cotton breeding progress (Shahbaz et al., 2019). On the other hand, hybridization between parents with various genetic makeup permits the formation of usually acceptable and stable mutations. Previous research has showed that the genetic diversity of Pakistan's cotton farmers is limited. Due to a lack of genetic variety, cotton leaf curl virus was able to spread (Karar et al., 2020) rapidly. High genetic similarity in breeding led to decreased cotton output and susceptibility to diseases, pest insects, and environmental variations (Spielman et al., 2015). Researchers are compelled by these limits to analyze and characterize novel cotton germplasm resources. Cotton germplasm resources are indispensable for creating novel genetic fusions for agronomic, yield, fibre quality, and tolerance to biotic and abiotic stresses (Wei et al., 2020). Like other major cotton-producing nations, Pakistan has a long history of acquiring, preserving, and maintaining cotton germplasm. Some genetic resources of cotton in Pakistan National Agricultural Research Centre (NARC), Cotton Research Station (CRS) and Central Cotton Research Institute (CCRI) shown in figure 2. Adoption of genetic variants from core germplasm is necessary for the long-term viability of cotton production. Cotton has difficulty utilizing germplasm using conventional breeding techniques. High-throughput genetic diversity mapping can support the identification of important cotton germplasm resources in Pakistan (Saleem et al., 2016).



Figure 2: Major germplasm resources of cotton in Pakistan

Marker-based breeding

In genome fingerprinting and marker-assisted selection (MAS), molecular markers enable molecular characterization and genetic diversity

detection (Noureen et al., 2016). Because molecular markers are not always related to an organism's phenotypic manifestation, they are essential to genomics research (Khan et al., 2015). The most

significant molecular markers in cotton genomes include Inter Simple Sequence Repeats (ISSRs), Amplified fragment length polymorphism (AFLP), Single Sequence Repeats (SSRs), Random Amplified Polymorphic DNA (RAPD) and Restriction Fragment Length Polymorphism (RFLP), as shown in figure 3.

These markers have been utilized to build linkage maps in numerous mapping populations. According to the study, DNA markers have been related to over 29 essential features, including fibre yield and quality, leaf and flower morphology, trichome density and disease resistance (Ali et al., 2019).



Figure 3: Various molecular marker used in cotton breeding program

Genomic-based breeding

Crop improvement increasingly makes use of high throughput sequencing technology. The developments in molecular genetics, bioinformatics, genetic engineering, whole genome sequencing, and re-sequencing have considerably benefitted plant breeding. The complete cotton genome was recently sequenced and made available to scientists worldwide (Rehman et al., 2015). Knowing how genes affect phenotypes makes it simpler to modify a single attribute than a combination of traits (Khan et al., 2020). Due to its low cost and speed, next-generation sequencing has been utilized to analyze plant genomic and transcript changes. DNA microarrays are less effective than RNA sequencing for detecting variations in gene expression (Bakhsh et al., 2017). Recent studies on short RNAs, DNA methylation, transcriptomics, proteomics, and metabolomics indicate that molecular markers and differentially expressed genes (DEG) are associated with varied cotton quality traits (Imran et al., 2018). Several crucial approaches to improve the efficiency of cotton breeding in Pakistan have already been analysed. Massive genomic database accessibility improves the application of molecular techniques. Due to genome-wide association studies, cotton breeding and genomics research has advanced substantially (GWAS). Using this technique, many SNPs highly related to the important traits are found effectively (Kouser & Qaim, 2015). Due to the genetic definition of breeding qualities, breeders are now better

equipped to pick genotypes with superior characteristics. GWAS and genomic selection use genotyping-by-sequencing (GBS) methods because they are straightforward and affordable (Arshad et al., 2021). Utilizing genome-wide association analysis has assisted in identifying candidate SNPs in Pakistan that are significantly linked with cotton yield, fibre quality, and stress tolerance. Breeders were able to establish how desired traits are controlled genetically, allowing them to circumvent screening limitations. Thanks to functional genomics research, it is now possible to discover the precise role of candidate genes. Genome editing effectively uses clustered regularly interspaced short palindromic repeats (CRISPR/Cas), RNAi, Transcription activator-like effector nucleases (TALENs), and Zinc-finger nucleases (ZFNs) (figure 4). Agrobacterium-mediated genetic transformation is Pakistan's most common method of creating transgenic cotton lines. A secondary objective of the breeding program was to generate trustworthy triple transgenic cultivars. It is anticipated that these cutting-edge cotton cultivars would generate risk-free cotton crops. Given the method's success in other nations, it has been suggested that the CRISPR/Cas system be utilized in Pakistan's cotton agriculture alongside other breeding techniques to combat the multiple strains of cotton leaf curl virus (Farooq et al., 2015). To generate exact target genotypes in cotton, modern genome editing technologies are required.



Figure 4: Different gene editing tools which are widely used in breeding programs

Hybrid cotton

It can boost crop output and quality by introducing fixed heterosis into hybrid breeding. Typically, during heterosis, hybrid offspring surpass their inbred parents in terms of growth, biomass, yield, quality, and resistance (Abdelhameed & Emam, 2022). Significant heterosis in cotton productivity and fibre quality assessments emerges from mating genetically superior inbred parents (Hansora et al., 2015). In hybrid breeding, genetic markers must be utilized to select parents with optimal combining ability, yield, and performance in hybrid combinations (Shahzad et al., 2019; Munir et al., 2022). China and India have utilized artificial pollination and emasculation to produce hybrid cotton seeds regularly. Artificial pollination and emasculation are insufficient to maintain the integrity of hybrid seeds, not withstanding the higher cost of seed production. The cytoplasmic male sterility (CMS) system is the most efficient means of developing hybrid cotton seeds (Mohan et al., 2016). In light of the significance of hybrid cotton, numerous scientists have advocated for the commercialization of hybrids. Elite hybrids were developed, which cut seed production costs, increased yield and quality, enhanced disease resistance, and prompted greater use of hybrid cotton (Gao et al., 2016). In Pakistan, hybrid cotton agriculture is indispensable. Phenotypically and genetically pure cotton seeds lessen the challenges created by seed impurity. Hybrid cotton provides superior fibre quality and stress tolerance, can be grown in a broader temperature range and produces a greater yield. Additional advantages of hybrid seed production include uniform maturity and higher profitability. Pakistan has developed only three hybrid cotton cultivars to date, but poor seed care standards and high seed production costs impede the creation of new hybrid cotton cultivars. Additionally, the paucity of commercially available hybrid cotton seed is a considerable obstacle. Notably, developing hybrid breeding procedures based on CMS can facilitate and reduce the cost of hybrid seed production. Utilizing elite hybrids commercially is another option for advancing hybrid cotton agriculture. Cotton ratooning can reduce the cost of producing F1 seeds, utilize heterosis, and maintain male-sterile lines for an extended duration (Zhu et al., 2019).

Progress of mechanization

Effective agricultural mechanization is determined by the move from hand tools to implements drawn by animals to mechanical power technologies, affecting mechanization capacity and farm operating time requirements (Chaudhry et al., 2022). Pakistan produces tractors, front-end loaders, wheat and maize threshers, potato diggers, and various machinery. It is common practice to refurbish obsolete foreign rice milling and ginning equipment. A wide variety of agricultural machinery and equipment are produced locally. Moreover, their output has increased dramatically in recent years (Khalid et al., 2021).

Additionally, a portion of them is exported. However, following trends is difficult in cotton. Modern countries enhanced their cotton production by shifting manual and mechanical harvesting. But unfortunately, in Pakistan, all cotton-grown producers prefer manual harvesting, which increases the cost of production and yield losses (Mudasir et al., 2021).

Conclusion and future prospects

The use of modern genome editing tools, especially CRISPR/Cas, can provide a beneficial alternative platform in addition to conventional breeding techniques for a better understanding of the genetics behind particular phenotypes. It would be better to create biotic and abiotic-resistant cotton cultivars in Pakistan. Also, there is a dire need to utilize mechanical harvesting in Pakistan.

Conflict of interest

The authors declared absence of conflict of interest.

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