J. Appl. Biosci., 50(1): 24-29, January-June, 2024

ISSN (Print) 0975-685X
ISSN (Online) 0975-864X

IMPROVEMENT OF COTTON VARITIES USING BIOTECNOLOGIGAL TOOLS: A REVIEW

ALKA MISRA, P.K. SINGH and S.N. PANDEY*
Department of Botany, University of Lucknow, Lucknow 226007

ABSTRACT

Cotton is an important cash crop, contributes significantly to the agricultural economy, provides income to the farmers and creates numerous jobs in the textile and clothing industries. Cotton cultivation has many advantages, but it also has drawbacks, such as high-water use, pesticide use, and other environmental concerns. The goal is to reduce these problems and make cotton production more eco-friendly using sustainable farming techniques and crop technologies. To meet the ever-growing demands of the expanding population, crop development tactics have now all become reliant on biotechnological advancements. During last three decades, biotechnology has provided a huge range of opportunities, especially in the form of Molecular indicators that can help in identifying transgenic plants which can withstand biotic and abiotic challenges in the more expedient selection of parents and offspring in traditional breeding schemes intended to crop enhancement. This review aimed to acquaint with some fundamental elements, as well as the state and future of cotton biotech research.

KEY WORDS: Cotton, Biotechnology, Molecular indicators, Transgenic plants

INTRODUCTION

Cotton is one of the most significant cash crops in the world's economy and has been farmed for a very long period (Lloyd May, 2002). It is regarded as the foundation of the textile industry and the most commercially significant fibre crop (Gulati *et al.,*1929; Tausif *et al.,* 2018). Cotton production and marketing faces several challenges, including competition from synthetic fibre, yield fluctuations from year to year, and increased fibre quality standards brought about by technical advancements in the textile sector (Hayat *et al.,* 2020). Global cotton crop productivity is greatly reduced due to weeds, diseases, pests, and several other environmental factors. Cotton cultivars have been successfully produced to incorporate a number of beneficial agronomic traits, including early maturity, improved fibre quality, heat tolerance, etc., by utilising standard hybridization and mutation breeding (Bolek *et al.,* 2016). A few crop security strategies can assist in reducing notable crop losses brought on by biotic factors. Recent years have seen groundbreaking achievement made possible by adoption of modern biotechnology techniques (Wilkins *et al.,* 2000; Katageri *et al.,* 2021; Khan *et al.,* 2022).

Cotton plant belongs to the genus, *Gossypium*, family Malvaceae which produces the single most important textile fiber, accounting for ~35% of the world's total annual fiber demands (Fryxell, 1992). Cotton plant is also used as a model system to study plant polyploidization, cell elongation, and cell wall biogenesis (Yang *et al.,* 2020). The *Gossypium* genus comprised 45 diploid species ($2n = 2x = 26$) and seven tetraploid species ($2n = 4x = 52$) with extraordinary morphological variations, including different plant architectures ranging from wild perennial small trees and shrubs to cultivated herbaceous annuals, with variable leaf shapes and different fiber characteristics.

Among the several domesticated taxa of *Gossypium* in the Malvaceae family that are grown extensively, and four species (*Gossypium hirsutum*, *Gossypium barbadense*, *G. herbaceum*, and *Gossypium arboretum*) are cultivated for fiber production. Over 90% of cotton produced in the world comes from Upland cotton (*Gossypium hirsutum*) (Wang *et al.,* 2019). The genetic improvement of cotton plant has been ongoing for centuries, but recent advances in genetic engineering and genomics have made this process faster and more efficient (Fernandez-Cornejo *et al.,* 2002). Due to the development

---

*Corresponding author email: snpandey@gmail.com

of strong transformation and regeneration methods (Flachs, 2017), cotton has been the crop most frequently modified by genetic engineering tools (Chakravarthy *et al.,* 2014; Tarazi *et al.,* 2019). It also contains the most recent information on the genetic improvement of cotton through biotechnological interventions for the improvement of cotton fibre and the control of biotic (disease resistance, etc.) and abiotic (drought, climate resilience, etc.) stresses (Kamburova *et al.,* 2022) and the contribution of epigenetics in increasing cotton fibre productivity and quality has also been addressed (Kohel *et al.,* 2001).

Biotechnological tools have been increasingly employed to enhance the improvement of cotton varieties, aiming to achieve traits such as increased yield, resistance to pests and diseases, improved fiber quality, and tolerance to environmental stress. Some key biotechnological tools and techniques utilized in the improvement of cotton varieties include:

Genetic Engineering (Genetic Modification):

Genetic engineering has provided mankind with unprecedented power to manipulate and develop novel crops towards a safe and sustainable agriculture in the 21st century (Gilbert, 2013; Arora *et al.,* 2017). Technologies and chemical interventions that have proven harmful to human health and environment need to be replaced with safer alternatives to manage insect pests in agricultural ecosystems (Ahmad *et al.,* 2017). Many insecticidal proteins (Debbie *et al.,* 1996) and molecules are available in nature which are effective against agriculturally important pests but are innocuous to mammals, beneficial insects, and other organisms. Insecticidal proteins present in *Bacillus thuringiensis* (Bt), which have shown efficacy as spray formulations in agriculture over the past five decades, have been expressed in many crop species with desirable outcome. Bt technology is reported to be effective against chewing larvae of orders lepidoptera, coleoptera, and diptera but not for sap-sucking pests of order Hemiptera (Palma *et al.,* 2014; Paul & Das, 2021). Next generation transgenics have also been developed by stacking multiple insecticidal genes. Coexpression of two cry genes (Cry1Ac and Cry2Ab) into the crop imparted defense against a wider range of pests and was commercialized in 1999 with a big success (Sivasupramaniam *et al*., 2014). It was highly toxic to *H. armigera* and two species of armyworms *S. frugiperda* and *S. exigua* compared to cotton expressing Cry1Ac (Stewart *et al*., 2001). These insecticidal proteins are highly specific to their target pests and are proven to be biodegradable and safe for mammals and other non-target organisms (Federici, 2003; Oliveira *et al*., 2007). Large scale cultivation of Bt-crops raises concerns about the possible development of resistance in insects. Many strategies have been formulated to prevent/delay the development of resistance.

RNA Interference (RNAi):

RNAi approaches for pest control that do not include transgenic application include soil treatment, foliar spraying, immersing leaf tissues in dsRNA solution, and stem injections (Cagliari *et al*., 2019, Dalakouras *et al*., 2020). The RNAi approach effectively mutes the genes in a short period without causing heritable alterations to the genome and have a higher public acceptability. Spraying of dsRNAs to regulate pest populations is a safe and eco-friendly approach, and dsRNA has short residue period, therefore, it has huge potential for adoption by plant growers (Cagliari *et al*., 2019). RNAi for the control of *B. tabaci* through oral delivery of dsRNA/siRNA was demonstrated (Upadhyay *et al*., 2011) and its potential was further validated in transgenic tobacco as proof of concept for field applications (Thakur *et al.,* 2014, Grover *et al*., 2019).

Marker-Assisted Breeding (MAB):

Cotton genetic resources contain diverse economically important traits that can be used widely in breeding approaches to create of high-yielding elite cultivars with superior fiber quality and adapted to biotic and abiotic stresses. Molecular markers gave a great opportunity to improve the efficiency and precision of crop improvement programs via marker-assisted selection (Collard & Mackill, 2008). The use of DNA markers in plant breeding is called marker-assisted selection (MAS) and it is a component of the molecular breeding approach (Collard & Mackill, 2008). MAS technology allows conducting the selection at any stage of plant growth and development. In short, the development of the MAS technology aimed at the selection of crops led to high achievements in genomics, which became a vital part of agricultural science.

Marker-assisted breeding involves the use of DNA markers associated with desirable traits to accelerate the traditional breeding process (Fakhriddin *et al.,* 2020). This allows breeders to select plants with specific traits more efficiently, such as disease resistance or improved fiber quality.

Genomic Selection:

Whole Genome Sequencing: Advances in genomics enable the sequencing of the entire cotton genome, allowing breeders to identify specific genes associated with desirable traits (Grover *et al.,* 2004). Genomic selection involves predicting the performance of a plant based on its genomic profile, accelerating the breeding process (Char *et al.,* 2017).

Gene Editing:

The past few years have seen, rise in the accessibility and significance of genome editing tools for agricultural production (Gao *et al.,* 2017). Zinc finger nucleases (ZFNs), transcription activator-like effector nucleases (TALENs), and clustered regularly interspaced short palindrome repeats (CRISPR)/CRISPR-associated (Cas) systems are the three main tools for targeted mutagenesis (Gilbert *et al.,* 2014). These tools can all be combined to create extremely specific double-strand breaks in chromosomal DNA (Konermann *et al.,* 2015). Localised mutations and deliberate sequence replacements result from the processing of these breaks by homologous recombination (HR) and nonhomologous end joining (NHEJ) repair mechanisms. The CRISPR/Cas system is high-efficient in producing targeted mutagenesis and is simpler to utilise than the ZFN and TALEN systems (Gao *et al.,* 2017; Wang *et al*., 2019).

Crispr-Cas9 Technology:

A more focused, effective, and rapid GE technique CRISPR/Cas9 (Khatodia *et al.,* 2016) has been successfully used to modify the genomes of many different creatures, including humans. The technique is continuously being improved for its use in both prokaryotes and eukaryotes. Advancements in this methodology have enabled the achievement of high-throughput screening for genomic gene identification (Tsai *et al.,* 2016). The cotton species *G. hirsutum* is the most broadly cultivated, but it is susceptible to various biotic stress which seriously limit fiber yield and quality (Briddon *et al.,* 2000). Genome editing has transformed the agricultural landscape with many success stories of engineering biotic stress tolerance in crop plants (Grohmann *et al.,* 2019). The tremendous potential of genome editing to improve crop plants has been demonstrated using model systems for various traits such as biotic and abiotic stress tolerance, nutritional enhancement, and yield improvement (Kim *et al.,* 2014). In prokaryotes, CRISPR/Cas9 was originally discovered as a natural defence mechanism against viral attacks (Bhaya *et al.,* 2014). CRISPR/Cas has been proved effective for the targeting and redesigning of crop genomes (Doudna *et al*., 2014), especially crop like cotton which are difficult to manipulate with conventional genetic engineering (Xu *et al.,* 2016). Cas9 nuclease has been characterized with two catalytic domains (HNH and RuvC) for creating double-strand breaks (DSBs) in the targeted genomic site. The specificity of CRISPR/Cas9 system to create DSBs is driven by two RNA molecules; trans-activating crRNA (tracrRNA) and CRISPR RNA (crRNA) and a protospacer adjacent motif (PAM) necessary for recognition of target site in the genome (Ma *et al.,* 2015). Although, the CRISPR/Cas9 system has been the most extensively used genome editing system by the scientific community, in recent years, several new CRISPR/Cas variants such as CRISPR/Cas12, CRISPR/CasX, CRISPR/Cas13, CRISPR/Cas3, and CRISPR/Cas14 have been discovered with different PAM requirements, smaller Cas proteins, and improved cleavage efficiency. CRISPR/Cas9, CRISPR/Cas12, and CRISPR/Cas13 have been successfully used for genetic improvement of plants of desired traits (Ma *et al.,* 2015; Ji *et al.,* 2015).

Omics Technologies:

Proteomics, Metabolomics, and Transcriptomics: These technologies enable a comprehensive understanding of the molecular processes within cotton plants. By studying the proteins, metabolites, and gene expression patterns, researchers can identify key pathways and target for improvement. Next-generation sequencing (NGS) has significantly increased sequencing efficiency and reduced cost due to the quick development of sequencing technology. This has led to the generation and distribution of enormous volumes of genomic, transcriptomic, and epigenetic data pertaining to cotton species. The study of population genetic diversity, cotton genomic structure and evolution, and the extensive mining of the genome for exceptional genes pertaining to significant traits are all made possible by these massive data sets. The CottonGen (Yu *et al.,* 2014) provides comprehensive information for cotton genomes, genetic markers, breeding cultivar phenotypes, etc., but its searching and visualization interface needs to be improved; the ccNet (You *et al.,* 2017) focuses mainly on co-expression networks of tetraploid *G. hirsutum* and diploid *G. arboretum*; the CottonFGD (Zhu *et al.,* 2017) is a cotton functional genome database that integrates cotton genomes, transcriptome data and a variety of online tools, but it lacks information for genetic resources; the MaGenDB (Wang *et al.,* 2019) is a comprehensive database for 13 Malvaceae species including cotton, so it is convenient to perform genetic comparative analyses among Malvaceae species; however, its functional analyses on cotton are not complete. Established for cotton research, COTTONOMICS is a dependable platform that combines genetic information, multi-omics data, and integrated genomic resources (Dai *et al.,* 2022).

Bioinformatics:

Bioinformatics plays a crucial role in analysing large-scale genomic and omics data. It helps in the identification of potential genes, the comprehension of gene function, and the forecasting of the consequences of genetic alterations. The sequential integration of individual omics data and its comprehension of the interactions between different cellular molecule types and their roles to enhance resilience to biotic and abiotic stresses and raise lint yield and quality are made possible by bioinformatics. Moreover, multi omics-integrated informatics lend a helping hand in assessing the information flow from one level of omics to another and consequently help in interrelating genotype to phenotype (Aslam, 2022).

Synthetic Biology: Pathway Engineering:

Synthetic biology approaches involve the design and construction of new biological pathways. This can be applied to engineer cotton plants for improved traits, such as enhanced fiber production or resistance to specific stresses.

The combination of these biotechnological tools provides a powerful toolbox for cotton breeders to develop improved varieties that meet the demands of sustainable agriculture, ensuring better yields, reduced environmental impact, and increased resilience to changing climatic conditions (Wen *et al.,* 2023). Additionally, regulatory frameworks and public acceptance are crucial considerations in the deployment of biotechnological advancements in agriculture (Singh, 2021).

CONCLUSION

Despite cotton's susceptibility to variety of illnesses and pests, cotton production relies on a broad range of biotechnological approaches to reduce losses. These biotechnological innovations reduce production costs and provide market and global manufacturing with environmental friendly control systems (Verma *et al.,* 2023). Ag biotech cotton is being used in production areas of the main cotton-producing countries and is gaining trust on a worldwide scale (Geoffery *et al.,* 2014). Continuous development in genome editing and sequencing technologies for cotton, along with the improvement of transgenic technology and marker-assisted selection, will surely lead to the introduction of new stress-tolerant and stress-resistant cotton germplasms in the upcoming years. By utilising these novel resistant germplasms along with enhanced bioagents, phytopathogen sanitation techniques can be completely transformed, leading to a decrease in losses and an improvement in environmental conditions (Herman *et al.,* 2019).

REFERENCES

Ahmad, A., Zia-Ur-Rehman, M., Hameed, U., Qayyum Rao, A., Ahad, A., Yasmeen, A., Akram, F., Bajwa, K.S., Scheffler, J. & Nasir, I.A. (2017). Engineered Disease Resistance in Cotton Using RNA-Interference to Knock down *Cotton leaf curl Kokhran virus*-Burewala and Cotton leaf curl Multan betasatellite Expression. *Viruses*, 9: 257.

Arora, R., Kataria, S.K. & Singh, P. (2017). Breeding for Insect Resistance in Cotton: Advances and Future Perspectives. *Breeding Insect Resistant Crops for Sustainable Agriculture*, ISBN: 978-981-10-6055-7.

Aslam, S., Mehmood, M.A., Rahman, M.U., Noor, F. & Ahmad, N. (2022). Bioinformatics-assisted multiomics approaches to improve the agronomic traits in cotton. *Bioinfor. Agricul.,* 233-251.

Bhaya, D., Davison, M. & Barrangou, R. (2011). *CRISPR-Cas* systems in bacteria and archaea: Versatile small RNAs for adaptive defence and regulation. *Annu. Rev. Genet.,* 45: 273-297.

Bolek, Y., Hayat, K., Bardak, A. & Azhar, M.T. (2016). Molecular Breeding of Cotton [Internet]. *Cotton Research. InTech.*

Briddon, R.W. & Markham, P. (2000). Cotton leaf curl virus disease. *Virus Res.* 71: 151-159.

Cagliari, D., Dias, N.P., Galdeano, D.M., Dos Santos, E.Á, Smagghe, G. & Zotti, M.J. (2019). Management of pest insects and plant diseases by non-transformative RNAi. *Front Plant Sci.,* 10: 1319.

Chakravarthy, V.S.K., Reddy, T.P. Reddy, V.D. & Rao, K.V. (2014). Current status of genetic engineering in cotton (*Gossypium hirsutum* L): An assessment *Critical Reviews in Biotechnol.,* 34(2): 144-160.

Char, S.N., Neelakandan, A.K., Nahampun, H., Frame, B., Main, M., Spalding, M.H., Becraft, P.W., Meyers, B.C., Walbot, V. & Wang, K. (2017). An *Agrobacterium*-delivered CRISPR/Cas9 system for high-frequency targeted mutagenesis in maize. *Plant Biotechnol. J.*, 15: 257-268.

Collard, B.C. & Mackill, D.J. (2008). Marker-assisted selection: an approach for precision plant breeding in the twenty-first century. *Philosophical transactions of the Royal Society of London. Series B, Biological Sciences*, 363(1491): 557-572. https://doi.org/10.1098/rstb.2007.2170.

Constable, G., Llewellyn, D., Walford, S.A., & Clement, J.D. (2015). Cotton Breeding for Fiber Quality Improvement. In: Cruz, V.M.V., Dierig, D.A. (eds*) Industrial Crops. Handbook of Plant Breeding*, (9). Springer,

Dai, F., Chen, J., Zhang, Z., Liu, F., Li, J., Zhao, T., Hu, Y., Zhang, T., & Fang, L. (2022). COTTONOMICS: A comprehensive cotton multi-omics database. *Database: The J. Biolog. Datab. Cur*.

Dalakouras, A., Wassenegger, M., Dadami, E., Ganopoulos, I., Pappas, M. & Papadopoulou, K.K. (2020). GMO-free RNAi: Exogenous application of RNA molecules in plants. *Plant Physiol.,* 182: 38-50.

Debbie, L.N., Kathryn, H.K., Robert, E.B., Randy Deaton, W., William, R.S., Toni, A., Mary, Taylor, L., Christine, C. Ebert, Glennon, J. Rogan, Stephen R. Padgette & Roy L. Fuchs (1996). Glyphosate-Tolerant Cotton:? Genetic Characterization and Protein Expression. *J. Agricul. Food Chem.*, 44(7): 1960-1966.

Doudna, J.A. & Charpentier, E. (2014). The new frontier of genome engineering with *CRISPR-Cas9. Science,* 346: 1077-1087.

Fakhriddin, K. (2020). Application of marker-assisted breeding technology in cotton (*Gossypium spp*).

Federici, B.A. (2003). Effects of Bt on non-target organisms. *J. New Seeds*, 5(1): 11-30.

Fernandez-Cornejo, J. & McBride, W.D. (2002). Adoption of Bioengineered Crops. *Agricultural Economic Report No.* (AER-810): 67.

Flachs, A. (2017) Transgenic cotton: High hopes and farming reality. *Nat. Plants,* 3: 16212.

Fryxell, P.A., (1992). A revised taxonomic interpretation of Gossypium L (Malvaceae). *Rheedea*, 2: 108-116.

Gao, W., Long, L., Tian, X., Xu, F., Liu, J. & Singh, P.K. (2017). Genome editing in cotton with the CRISPR/Cas9 system. *Front. Plant Sci.*, 8: 1-12.

Geoffrey, B. Steven Sexton, S. & Zilberman, D. (2014). "Agricultural Biotechnology: The Promise and Prospects of Genetically Modified Crops." *J. Econ. Perspec.*, 28(1): 99-120.

Gilbert, N. (2013). A Hard Look at GM Crops. *Nat.,* 497: 24-26.

Gilbert, L.A., Horlbeck, M.A., Adamson, B., Villalta, J.E., Chen, Y., Whitehead, E.H., Guimaraes, C., Panning, B., Ploegh, H.L. & Bassik, M.C. (2014). Genome-scale *CRISPR*-mediated control of gene repression and activation. *Cell,* 159: 647-661.

Grohmann, L.J., Keilwagen, N., Duensing, E., Dagand, F., Hartung, R., Wilhelm, J.B. & Sprink, T. (2019). Detection and Identification of Genome Editing in Plants: Challenges and Opportunities. *Front. Plant Sci.,* 10: 77.

Grover, C.E., Kim, H., Wing, R.A., Paterson, A.H., & Wendel, J.F. (2004). Incongruent patterns of local and global genome size evolution in cotton. *Gen. Res.,* 14(8): 1474-1482.

Grover, S., Jindal, V., Banta, G., Taning, C.N.T., Smagghe, G., & Christiaens, O. (2019). Potential of RNA interference in the study and management of the whitefly, *Bemisia tabaci*. *Arch. Insect Biochem. Physiol.*, 100(2): e21522.

Gulati, A.N., & Turner, A.J. (1929). 1—A note on the early history of cotton. *J. Textile Insti. Transac.*, 20(1): T1-T9.

Hayat, K., Bardak, A. & Parlak, D. (2020). Biotechnology for Cotton Improvement. *Cotton Production and Uses,* ISBN: 978-981-15-1471-5.

Herman, R.A., Fedorova, M. & Storer, N.P. (2019). Will Following the Regulatory Script for GMOs Promote Public Acceptance of Gene-Edited Crops? *Trends in Biotechnol.,* 37: 1272-1273.

Ji, X., Zhang, H., Zhang, Y., Wang. Y. & Gao, C. (2015). Establishing a CRISPR–Cas-like immune system conferring DNA virus resistance in plants. *Nat. Plants,* 1: 1-4.

Kamburova, V., Salakhutdinov, I., & Y. Abdurakhmonov, I. (2022). Cotton Breeding in the View of Abiotic and Biotic Stresses: *Challenges and Perspectives*. Intech Open.

Katageri, S., Anjan Gowda, I.S., Biradar, B.N, & Patil, S.R. (2021). Prospects for Molecular Breeding in Cotton, *Gossypium spp. IntechOpen. doi*: 10.5772/intechopen.94613

Khan, Z., Ali, Z., & Khan, A.A. (Eds.). (2022). Cotton Breeding and Biotechnology: *Challenges and Opportunities* (1st ed.). CRC Press.

Khatodia, S., Bhatotia, K., Passricha, N., Khurana, S. & Tuteja, N. (2016). The *CRISPR/Cas* genome-editing tool: Application in improvement of crops. *Front. Plant Sci., 7*: 506.

Kim, H. & Kim, J.S. (2014) A guide to genome engineering with programmable nucleases. *Nat. Rev. Genet.,* 15: 321-334.

Kohel, R.J., Yu, J. & Park, Y.H. (2001). Molecular mapping and characterization of traits controlling fiber quality in cotton. *Euphytica,* 121: 163-172.

Konermann, S., Brigham, M.D., Trevino, A.E., Joung, J., Abudayyeh, O.O., Barcena, C., Hsu, P.D., Habib, N., Gootenberg, J.S. & Nishimasu, H. (2015). Genome-scale transcriptional activation by an engineered *CRISPR-Cas9* complex. *Nat.,* 517: 583-588.

Lloyd May, O. (2002). Quality Improvement of Upland Cotton (*Gossypium hirsutum* L.), *J. Crop Produc.*, 5(1-2): 371-394.

Ma, X., Zhang, Q., Zhu, Q., Liu, W., Chen, Y., Qiu, R., Wang, B., Yang, Z., Li, H. & Lin, Y. (2015). A robust *CRISPR/Cas9* system for convenient, high-efficiency multiplex genome editing in monocot and dicot plants. *Mol. Plant,* 8: 1274-1284.

Oliveira, A.R., Castro, T.R., Capalbo, D.M., & Delalibera, I. (2007). Toxicological evaluation of genetically modified cotton (Bollgard®) and Dipel® WP on the nontarget soil mite Scheloribates praeincisus (Acari: Oribatida). *Experimen. App. Acarol.*, 41(3): 191-201.

Palma, L., Muñoz, D., Berry, C., Murillo, J., & Caballero, P. (2014). *Bacillus thuringiensis* toxins: an overview of their biocidal activity. *Toxins,* 6(12): 3296-3325.

Paul, S., & Das, S. (2021). Natural insecticidal proteins, the promising bio-control compounds for future crop protection. *The Nucleus*, 64(1): 7-20.

Singh, P. (2021). Genetically Modified Crops in India: Politics, Policies, and Political Economy. In Policy Issues in Genetically Modified Crops (pp. 75-96). Academic Press.

Sivasupramaniam, S., Moar, W.J., Ruschke, L.G., Osborn, J.A., Jiang, C., Sebaugh, J.L., & Greenplate, J.T. (2014). Toxicity and characterization of cotton expressing *Bacillus thuringiensis* Cry1Ac and Cry2Ab2 proteins for control of lepidopteran pests. *J. Econ. Entomol.*, 101(2): 546-554.

Sohrab, S.S. (2019). Development of Virus Resistance Transgenic Cotton Using Cotton Leaf Curl Virus Antisense ßC1 Gene. *Methods Mol. Biol*., 1902: 293-305.

Stewart, S.D., Adamczyk, J.J., Knighten, K.S., & Davis, F.M. (2001). Impact of Bt cottons expressing one or two insecticidal proteins of *Bacillus thuringiensis* Berliner on growth and survival of noctuid (Lepidoptera) larvae. *J. Econ. Entomol.*, 94(3): 752-760.

Tarazi, R. Leonardo, Santos Jimenez, J. & Maite, F.S. Vasli (2019). Biotechnological solutions for major cotton (*Gossypium hirsutum*) pathogens and pests. *Biotechnol. Res. Innov.,* (3): Supplement 1, 19-26.

Tausif, M., Jabbar, A., Salman, M., Abdul Basit, N., Ahmad, F. & Cassidy, T. (2018). Cotton in the new millennium: advances, economics, perceptions, and problems. *Textile Progress,* 50(1): 1-66.

Thakur, N., Upadhyay, S.K., Verma, P.C., Chandrashekar, K., Tuli, R., & Singh, P.K. (2014). Enhanced whitefly resistance in transgenic tobacco plants expressing double stranded RNA of v-ATPase A gene. *PloS one*, 9(3): e87235.

Tsai, S.Q. & Joung, J.K. (2016). Defining and improving the genome-wide specificities of *CRISPR–Cas9* nucleases. *Nat. Rev. Genet.,* 17: 300-312.

Upadhyay, S.K., Chandrashekar, K., Thakur, N., Verma, P.C., Borgio, J.F., Singh, P.K., & Tuli, R. (2011). RNA interference for the control of whiteflies *(Bemisia tabaci*) by oral route. *J. Biosci.*, 36(1): 153-161.

Verma, K., Sharma, P., Tripathi, K., Yadav, R. & Singh, S.P. (2023). Recent Advances in Genetic Improvement of Cotton. In: Tiwari, S., Koul, B. (eds) Genetic Engineering of Crop Plants for Food and Health Security. Springer, Singapore.

Wang, D., Fan, W. & Guo, X. (2019). MaGenDB: a functional genomics hub for Malvaceae plants. *Nucleic Acids Res.*, 48.

Wang, M., Tu, L., Yuan, D., Zhu, D., Shen, C. & Li, J. (2019). Reference genome sequences of two cultivated allotetraploid cottons, *Gossypium hirsutum* and *Gossypium barbadense*. *Nat. Gen.*, 51(2): 224-229.

Wen, X., Chen, Z., Yang, Z., Wang, M., Jin, S., Wang, G., Zhang, L., Wang, L., Li, J., Saeed, S., He, S., Wang, Z., Wang, K., Kong, Z., Li, F., Zhang, X., Chen, X. & Zhu, Y. (2023). A comprehensive overview of cotton genomics, biotechnology, and molecular biological studies. *Sci China Life Sci.,* 10: 2214-2256.

Wilkins, T.H., Rajasekaran, K. & Anderson, D. M. (2000). Cotton Biotechnology, *Critical Rev. Plant Sci.*, 19(6): 511-550.

Xu, L., Park, K.H., Zhao, L., Xu, J., El Refaey, M., Gao, Y., Zhu, H., Ma, J. & Han, R. (2016). CRISPR-mediated genome editing restores dystrophin expression and function in mdx mice. *Mol. Ther.,* 24: 564-569.

Yang, Z., Qanmber, G., Wang, Z., Yang, Z. & Li, F. (2020). *Gossypium* Genomics: Trends, Scope, and Utilization for Cotton Improvement. *Trends Plant Sci*., 5: 488-500.

You, Q., Xu, W. & Zhang, K. (2017). ccNET: database of co-expression networks with functional modules for diploid and polyploidy. *Gossypium*. *Nucleic Acids Res.*, 45.

Yu, J., Jung, S. & Cheng, C.H. (2014). CottonGen: a genomics, genetics, and breeding database for cotton research. *Nucleic Acids Res.*, 42.

Zhang, B.-H., Liu, F., Yao, C.-B., & Wang, K.-B. (2000). Recent progress in cotton biotechnology and genetic engineering in China. *Curr. Sci.*, 79(1): 37-44.

Zhang, J., & Manikanda Boopathi, N. (2022). Disease Resistance in Cotton. In: Kole, C. (eds) Genomic Designing for Biotic Stress Resistant Technical Crops. Springer, Cham.

Zhu, T., Liang, C., & Meng, Z. (2017). CottonFGD: an integrated functional genomics database for cotton. *BMC Plant Biol.*, 17: 101-109.doi: 10.1186/s12870-017-1039-x.

Yang, Z., Qanmber, G., Wang, Z., Yang, Z. & Li, F. (2020). *Gossypium* genomics: trends, scope, and utilization for cotton improvement. *Trends Plant Sci*., 25: 488-500.

Tarazi, R., Jimenez, J. L. S. & Vaslin, M.F.S. (2019). Biotechnological solutions for major cotton (Gossypium hirsutum) pathogens and pests, *Biotechnol. Res. Innov.,* 3(1): 19-26, ISSN 2452-0721.