International Journal of Environmental & Agriculture Research (IJOEAR)
ISSN: [2454-1850]
[Vol-12, Issue-3, March- 2026]
Website: www.ijoear.com
Journal DOI: 10.25125/agriculture-journal

Diversity across Ploidy Levels in Mulberry (*Morus* spp.): A Review of Genetic Resources and Their Utilization

Y Surjalata Devi[1*]; Anowar Hossain[2]

[*1]Central Muga Eri & Training institute, Lahdoigarh-785700, Assam.
[2]Department of Genetics and Plant Breeding, IRDM Faculty Centre, Ramakrishna Mission Vivekananda Educational and Research Institute, Narendrapur, Kolkata-700103, West Bengal
*Corresponding Author

Received:- 13 March 2026/ Revised:- 22 March 2026/ Accepted:- 25 March 2026/ Published: 31-03-2026
Copyright @ 2026 International Journal of Environmental and Agriculture Research
This is an Open-Access article distributed under the terms of the Creative Commons Attribution Non-Commercial License (https://creativecommons.org/licenses/by-nc/4.0) which permits unrestricted Non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

Abstract— *Mulberry (Morus spp.) is an economically important perennial crop that serves as the primary food source for the domesticated silkworm (Bombyx mori) and also has potential for fruit production and the utilization of bioactive compounds. This genus exhibits considerable diversity in species characteristics, geographical distribution, chromosome number, and ploidy levels, providing valuable genetic resources for crop improvement. This review surveys mulberry species diversity, chromosome number and genome size variation, and the utilization of genetic resources in the development of improved cultivars. It further summarizes varieties developed through selection, hybridization, mutation breeding, and the use of polyploid germplasm, with emphasis on leaf productivity, environmental adaptation, and suitability for different silkworm-rearing requirements. In addition, reported genes associated with responses to drought, salinity, cold, heat, and powdery mildew are discussed in relation to their potential applications in stress-tolerance improvement. Despite this diversity, mulberry breeding faces challenges associated with variable ploidy levels, high heterozygosity, and long breeding cycles. Integrating conventional breeding with genomics, tissue culture, and emerging genome-editing technologies may help overcome these constraints and facilitate the development of productive, stress-tolerant, and multipurpose cultivars. Overall, this review highlights the importance of conserving and effectively utilizing mulberry genetic resources to support sustainable sericulture and broader agricultural and industrial applications.*

Keywords— Morus, genetic diversity, ploidy, mulberry, stress tolerance, sericulture.

I. INTRODUCTION

Mulberry (*Morus* spp.) is an ancient, perennial, deciduous plant belonging to the family Moraceae. The genus is widely distributed across Asia and other regions, with considerable diversity among its wild and cultivated forms. East Asia and the Himalayan region are important areas of mulberry diversity. Several species, including *Morus indica, M. alba* (white mulberry), *M. serrata* (Himalayan mulberry), and *M. laevigata*, occur in different geographical regions of India [17], [24]. Mulberry is cultivated primarily for its leaves, which provide the principal food source for the domesticated silkworm (*Bombyx mori*). During its larval development, the silkworm feeds on mulberry leaves and subsequently spins a cocoon from which raw silk is extracted. Silk production and quality are influenced by leaf quality and the silkworm strain used, including multivoltine, bivoltine, and their hybrids [8], [9]. Beyond sericulture, mulberry fruits are valued for their nutritional and phytochemical constituents, including anthocyanins, antioxidants, fatty acids, and vitamins [11]. Mulberry leaves are also used in health

beverages and animal feed because they contain bioactive compounds such as flavonoids, phenolic compounds, and coumarins, which have been investigated for potential health benefits [6], [22].

The genus *Morus* exhibits considerable variation in leaf morphology, growth characteristics, reproductive biology, fruit traits, and environmental adaptability [30]. This diversity provides valuable opportunities to identify desirable traits and broaden the genetic base of cultivated mulberry. However, the breeding potential of individual species depends on their agronomic characteristics, environmental adaptation, and reproductive compatibility with existing breeding materials. Systematic characterization and evaluation of mulberry genetic resources are therefore essential for identifying suitable material for specific improvement objectives.

Advances in molecular biology and genomics have created further opportunities for mulberry improvement. Research has identified genes associated with responses to abiotic stresses, including drought, salinity, cold, and heat, as well as biotic stresses such as powdery mildew. Understanding the functions of these genes may facilitate the identification and validation of genetic targets for developing stress-tolerant cultivars [19]. Integrating this knowledge with conventional breeding and emerging biotechnological approaches may help address challenges associated with mulberry productivity, environmental adaptation, and disease resistance.

In this context, the present review examines the genetic diversity of *Morus* species, focusing on geographical distribution, chromosome number, ploidy variation, and genome size. It also summarizes improved mulberry varieties and their utilization, discusses reported stress-responsive genes, and considers the major challenges and future opportunities for integrating conventional breeding with modern biotechnological approaches. The overall aim is to highlight how the conservation and effective utilization of mulberry genetic resources can contribute to the development of productive, stress-tolerant, and multipurpose cultivars for sustainable sericulture and broader agricultural and industrial applications.

II. SPECIES DIVERSITY AND PLOIDY VARIATION

2.1 Diversity and Geographical Distribution

Species diversity represents an important genetic resource for the modification of target traits and the conservation of germplasm in the genus *Morus*. A total of 17 species compiled in this review (Table 1) illustrate the geographical distribution and morphological diversity of mulberry across regions of Asia, North America, and Africa. These species exhibit variation in leaf architecture, foliar characteristics, and reproductive traits [30]. For descriptive purposes, mulberry germplasm can be broadly discussed in terms of cultivated taxa and wild or less-utilized relatives, although the distinction is not always clear-cut. Cultivated taxa, including *Morus alba*, *M. indica*, *M. multicaulis*, *M. atropurpurea*, *M. mizuho*, and *M. nigra*, have been maintained and selected for traits relevant to leaf production, fruit quality, or other uses. In contrast, species such as *M. rubra*, *M. laevigata*, *M. serrata*, *M. microphylla*, and *M. celtidifolia* may provide additional genetic diversity associated with adaptation to different ecological conditions [25], [31].

The sericultural value of mulberry germplasm is influenced by leaf morphology, moisture content, nutritional composition, and digestibility. Leaf quality, including moisture and crude protein content, can affect silkworm growth and cocoon production. Therefore, these characteristics are important considerations in mulberry selection and improvement [14]. In South Asia, *M. indica*-associated germplasm has contributed to sericulture, while *M. multicaulis* is cultivated in parts of East Asia for its leaf-production potential. The nutritional quality of mulberry leaves is also important during the later instars of silkworm development, when larval growth and cocoon formation are strongly influenced by food quality [15].

Leaf surface characteristics and nutritional composition may limit the suitability of some mulberry accessions for silkworm rearing. For example, differences in leaf thickness, surface texture, and fibre content may influence feeding preference and digestibility. However, the suitability of individual species, including *M. nigra*, *M. serrata*, *M. rubra*, *M. microphylla*, and *M. celtidifolia*, should be evaluated using direct feeding and nutritional studies rather than inferred solely from leaf morphology

[10], [18], [23]. Despite differences in their current utilization, wild and underutilized mulberry germplasm may provide valuable variation for broadening the genetic base of cultivated varieties. Their potential use in breeding requires systematic evaluation of target traits, reproductive compatibility, interspecific hybridization success, and field performance.

2.2 Chromosome Number and Ploidy Variation

Chromosome-number variation and differences in ploidy provide important information for understanding chromosome evolution and evaluating genetic resources for mulberry improvement. As summarized in Table 1, *Morus* exhibits considerable cytogenetic diversity, ranging from diploid to highly polyploid forms. This variation provides opportunities for investigating genome evolution and exploring the potential of polyploid germplasm in breeding. The basic chromosome number commonly reported for many *Morus* species is x = 14, with diploid forms having 2n = 2x = 28. Higher-ploidy forms include tetraploids (2n = 4x = 56) and hexaploids (2n = 6x = 84), although chromosome number and ploidy should be verified for the particular species or accession under investigation [25]. The genus also includes *Morus notabilis*, which has been reported with 2n = 14. Comparative chromosome-level genomic analyses have associated this reduced chromosome number with descending dysploidy, a process involving changes in chromosome number during evolution [27].

At the other extreme, *Morus nigra* has been reported with 2n = 22x = 308, representing the highest chromosome number documented in the genus in the cited comparative study [26], [29]. These contrasting chromosome configurations highlight the cytogenetic diversity of mulberry germplasm. However, chromosome number alone does not establish the breeding value of a species; its potential must also be assessed through genetic characterization, reproductive compatibility, and agronomic evaluation.

2.3 Genome Size and Its Relevance to Genetic Resources

Genome size, expressed as nuclear DNA content, provides complementary information for characterizing *Morus* germplasm. Flow cytometry is widely used to estimate nuclear DNA content, and the Mulberry Genome Size, Chromosome Number, and Ploidy Database (MGCPdb) provides data on these characteristics across mulberry germplasm [25]. In that study, genome-size estimates for 323 accessions ranged from approximately 0.36 to 3.08 Gb, while chromosome counts in representative materials covered a range from 14 to 308. The authors reported a strong positive relationship between genome size and chromosome number (R^2 = 0.9853) in their analyzed dataset. This relationship supports the use of genome-size information alongside cytogenetic data for germplasm characterization, although it should not be assumed to apply identically to every species or accession. However, this should not be interpreted as a direct measure of agronomic superiority. A larger genome does not necessarily indicate higher leaf yield, better nutritional quality, or greater stress tolerance. Similarly, differences in chromosome number do not necessarily correspond to proportional differences in total DNA content, because chromosome rearrangements and changes in genome organization can occur during evolution. The reported chromosome-number reduction in *M. notabilis* illustrates the importance of considering chromosome evolution alongside genome-size estimates [20], [27], [28].

2.4 Agronomic Characteristics and Potential Utilization

The morphological and physiological characteristics summarized in Table 1 provide a preliminary basis for evaluating *Morus* germplasm for different agronomic purposes. Traits such as leaf orientation, margin, venation, and trichome density can assist in the initial characterization and selection of accessions. These characteristics may help identify germplasm for leaf production, fruit utilization, and other potential applications [30]. However, morphological descriptions alone are insufficient to establish the breeding value of a species or accession. Effective utilization requires evaluation of trait heritability, stability across generations, adaptability to different environments, and reproductive compatibility with potential breeding parents. In particular, interspecific crosses involving materials with different ploidy levels may encounter reproductive barriers, although the extent of these barriers depends on the parental materials and cross combination. Therefore, the information summarized in Table 1 should be considered a starting point for further evaluation rather than a definitive ranking of genetic resources.

Integrating morphological characterization with cytogenetic information, genome-size estimates, and agronomic evaluation can improve the identification and utilization of valuable *Morus* germplasm. Such an approach can support germplasm conservation, parental selection, and the development of improved mulberry cultivars [31].

TABLE 1
LIST OF DIFFERENT *MORUS* SPECIES WITH DESCRIPTIVE DETAILS

SN	Species	Vernacular name	Origin	Ploidy	Genome Size	Special Use
1	*Morus notabilis*	Sichuan mulberry	China	2n = 14	~342 Mb	Genomic model
2	*Morus alba*	White mulberry	Central & Eastern China	2n = 2x = 28	360–440 Mb	High leaf biomass & silkworm rearing
3	*Morus indica*	Indian mulberry	Himalayan & Indo-China region	2n = 2x = 28	336–360 Mb	High leaf biomass & silkworm rearing
4	*Morus multicaulis*	Lu mulberry	China	2n = 2x = 28	343–380 Mb	High leaf biomass & silkworm rearing
5	*Morus atropurpurea*	Guangdong mulberry	Southern China	2n = 2x = 28	315–360 Mb	Fruit production
6	*Morus mizuho*	Japanese mulberry	Japan & East Asia	2n = 2x = 28	333–370 Mb	High leaf biomass & silkworm rearing
7	*Morus rubra*	Red mulberry	North America	2n = 2x = 28	350–380 Mb	Fruit production & wine making
8	*Morus australis*	Chinese mulberry	East & Southeast Asia	2n = 2x = 28	~354 Mb	Multi-purpose
9	*Morus acidosa*	Korean mulberry	East & South Asia	2n = 2x = 28	~355 Mb	Multi-purpose
10	*Morus mesozygia*	African mulberry	Africa	2n = 2x = 28	330–350 Mb	Quality timber & construction purpose
11	*Morus laevigata*	Wild mulberry	Indian, Himalayan and North-eastern regions	2n = 4x = 56	710–830 Mb	Quality timber & construction purpose
12	*Morus boninensis*	Bonin mulberry	Ogasawara Islands	2n = 4x = 56	~700–750 Mb	Endangered island species
13	*Morus cathayana*	Chinese mulberry	Central & Southern China	2n = 4x = 56	~710–800 Mb	Pharmaceutical
14	*Morus serrata*	Himalayan mulberry	North-western Himalayan region	2n = 6x = 84	940–1100 Mb	Cold and drought tolerance
15	*Morus microphylla*	Texas mulberry	Northern Mexico and South-Western United States	2n = 6x = 84	950–1050 Mb	Drought & heat tolerance
16	*Morus celtidifolia*	Mexican mulberry	Mexico	2n = 6x = 84	950–1000 Mb	Drought & heat tolerance
17	*Morus nigra*	Black mulberry	Western & South-western Iran	2n = 22x = 308	~3080 Mb	Fruit production

III. DEVELOPMENT AND UTILIZATION OF IMPROVED MULBERRY VARIETIES

In India, improved mulberry varieties have been developed through selection, hybridization, mutation breeding, and the utilization of polyploid materials. Many cultivated varieties are associated with *Morus indica*, *M. alba*, *M. multicaulis*, or their hybrids. As summarized in Table 2, these varieties differ in leaf yield, environmental adaptation, disease response, and suitability for specific silkworm-rearing requirements.

Among the varieties developed for different production environments, S-1 is recommended for eastern and northeastern India, while S-1635 is valued for its leaf characteristics and suitability for silkworm rearing. C-2038, derived from the cross C-763 (MI-0124) × CF110, is reported to have broad leaves [4]. C-776, an interspecific hybrid of *M. multicaulis* × *M. indica*, is reported to be suitable for coastal saline conditions, whereas Tr-10, a triploid derivative, is adapted to hill conditions in eastern India [3]. Other varieties have been developed or recommended for specific production requirements. Kanva-2 is reported to show resistance to leaf spot, S-36 is suitable for young-age silkworm rearing and cultivation in red lateritic soils, and Sahana is suited to partially shaded conditions beneath coconut plantations. G-4 is recommended for late-age silkworm rearing, while S-13 is reported to show resistance to leaf rust and powdery mildew [5], [7].

These varieties illustrate how mulberry genetic resources have been utilized to address diverse production requirements. Their characteristics emphasize the importance of selecting cultivars according to local environmental conditions, disease pressure, leaf productivity, and the nutritional requirements of silkworms at different developmental stages. The continued evaluation of existing varieties and underutilized germplasm may help identify additional resources for improving mulberry productivity and resilience.

TABLE 2
LIST OF IMPROVED VARIETIES WITH PRODUCTIVITY AND SELECTION

SN	Variety	Leaf Yield (t/ha/year)	Developed Institute	Pedigree
1	S-1	28–29 at irrigated & 16–18 at rainfed	CSRTI, Berhampore	Introduced from Mandalay, Myanmar
2	S-1635	40–45 at irrigated; 12–17 at rainfed	CSRTI, Berhampore	Triploid selection from CSRS-1
3	C-2038	50–55 at irrigated; 17–21 at rainfed	CSRTI, Berhampore	Developed from a C-763 (MI-0124) × CF110 (a Chinese accession)
4	C-776	45–50	CSRTI, Berhampore	Developed as a cross-pollinated hybrid involving *M. multicaulis* and Black Cherry (*M. indica*)
5	Tr-10	11–15	CSRTI, Berhampore	Triploid derivative of Berhampore S-1
6	Kanva-2	30–35 at irrigated; 10–12 at rainfed	CSRTI, Mysuru	Selected from natural variation in the Mysore Local
7	S-36	38–45 at irrigated	CSRTI, Mysuru	Developed through EMS chemical mutagenesis of Berhampore Local
8	Sahana	40–44 at irrigated	CSRTI, Mysuru	Hybrid of Kanva-2 × Kosen
9	G-4	55–65 at irrigated	CSRTI, Mysuru	Developed from a cross-pollinated hybrid population
10	S-13	8–15 at rainfed	CSRTI, Mysuru	Selected from polycross progeny

IV. STRESS-RESPONSIVE GENES AND THEIR FUNCTIONS

Mulberry responds to abiotic and biotic stresses through a range of molecular and physiological mechanisms. As summarized in Table 3, several reported genes are associated with responses to drought, salinity, cold, heat, and powdery mildew, providing potential targets for further functional characterization and breeding.

4.1 Abiotic Stress

Drought stress affects plant water status and can trigger physiological and biochemical changes that influence growth and productivity. Several genes associated with drought responses in mulberry include MaWRKY48, MaP5CS1, MaP5CS2, MaGγ1, and MaGγ2. WRKY transcription factors are involved in the regulation of stress-responsive gene expression, while pyrroline-5-carboxylate synthetase, encoded by P5CS genes, participates in proline biosynthesis. Proline accumulation may contribute to osmotic adjustment and cellular protection under water deficit [12]. The heterotrimeric G-protein gamma subunits MaGγ1 and MaGγ2 have also been shown to participate in drought responses through interactions with components of abscisic acid (ABA) signalling, highlighting the importance of hormone-mediated stress regulation in mulberry [13].

Under salinity stress, MaNHX encodes a sodium-proton exchanger associated with ion homeostasis and cellular pH regulation. Such transporters may contribute to salt-stress responses by regulating intracellular ion balance [2]. For cold stress, MaFAD2 encodes a fatty-acid desaturase associated with fatty-acid composition and cold-related responses in mulberry [32]. Heat-responsive proteins, including HSP21, HSP70T-2, and DnaJ/HSP co-chaperones, are involved in protein folding, stabilization, and cellular protein quality control. These proteins may help maintain cellular functions under heat stress, although the response of individual genes can vary with stress conditions [21].

4.2 Biotic Stress

In relation to powdery mildew, MnMLO2 and MnMLO6A have been identified as candidate susceptibility genes in mulberry [16]. Their characterization may provide a basis for investigating whether targeted modification of these genes could improve disease resistance. Chalcone synthase (CHS), a key enzyme in flavonoid biosynthesis, has also been investigated in mulberry in relation to powdery mildew disease severity. However, it has been shown to be associated with disease resistance [1]. Overall, these genes and pathways provide useful leads for understanding mulberry stress responses. Their application in breeding will depend on the strength of functional evidence, validation across genetic backgrounds, and demonstrated effects on plant performance (Table 3).

TABLE 3
LIST OF STRESS-RESPONSIVE GENES AND THEIR FUNCTIONS

SN	Stress	Gene	Functions
1	Drought	MaWRKY48	Reducing oxidative damage and water loss
2	Drought	MaP5CS1, MaP5CS2	Involved in proline biosynthesis, which can support osmotic adjustment and protect proteins and cell structures during water deficit
3	Drought	MaGγ1, MaGγ2	Heterotrimeric G-protein γ subunits interact with components of ABA signalling pathway
4	Salinity	MaNHX	Na^+/H^+ exchangers help maintain ion balance and cellular pH by exchanging sodium and protons across membranes
5	Cold	MaFAD2	FAD2 encodes a fatty-acid desaturase that influences membrane lipid composition
6	Heat	HSP21, HSP70T-2	Heat-shock proteins act as molecular chaperones and help protect or refold proteins during thermal stress
7	Heat	DnaJ/HSP	Heat-shock proteins and DnaJ co-chaperones help preserve protein stability
8	Powdery mildew	MnMLO2, MnMLO6A	Targeted functional allele mutation of MLO locus provides resistance
9	Powdery mildew	CHS	CHS catalyses the first committed step of flavonoid biosynthesis, which is associated with powdery mildew severity

V. FUTURE PROSPECTS

Mulberry is a multipurpose perennial crop with substantial diversity in its characteristics and potential uses. Cultivars are selected according to regional requirements, including leaf productivity, leaf size, and suitability for young-age (chawki) or late-age silkworm rearing. Mulberry fruits and leaves are also sources of bioactive compounds, including antioxidants and other secondary metabolites, with potential food, nutraceutical, and industrial applications. Future breeding efforts could therefore focus on developing multipurpose cultivars that combine high leaf yield, suitable nutritional quality, stress tolerance, and desirable fruit or phytochemical traits.

Despite this potential, mulberry improvement faces several challenges, including variation in ploidy, high heterozygosity, and long breeding cycles associated with perennial woody growth. These characteristics can complicate hybridization, genetic analysis, and the selection of superior genotypes. Vegetative propagation methods, including cuttings and layering, remain important for cultivar multiplication and plantation establishment. Tissue culture may further support rapid propagation and, where suitable protocols are available, the development and evaluation of improved plant material.

Advances in genomics and biotechnology offer additional opportunities to accelerate mulberry improvement. Genome editing technologies, including CRISPR-Cas9, base editing, and prime editing, could potentially be used to modify genes associated with stress tolerance, productivity, and secondary-metabolite accumulation. Artificial intelligence-assisted guide RNA design

may facilitate the identification of suitable editing targets and improve guide selection. However, the application of these approaches in mulberry requires appropriate transformation and regeneration protocols, reliable functional validation, and assessment of edited plants under relevant growing conditions. Integrating genomic information and biotechnological approaches with conventional breeding and field evaluation could support the development of productive, stress-tolerant, and multipurpose mulberry cultivars (Figure 1).

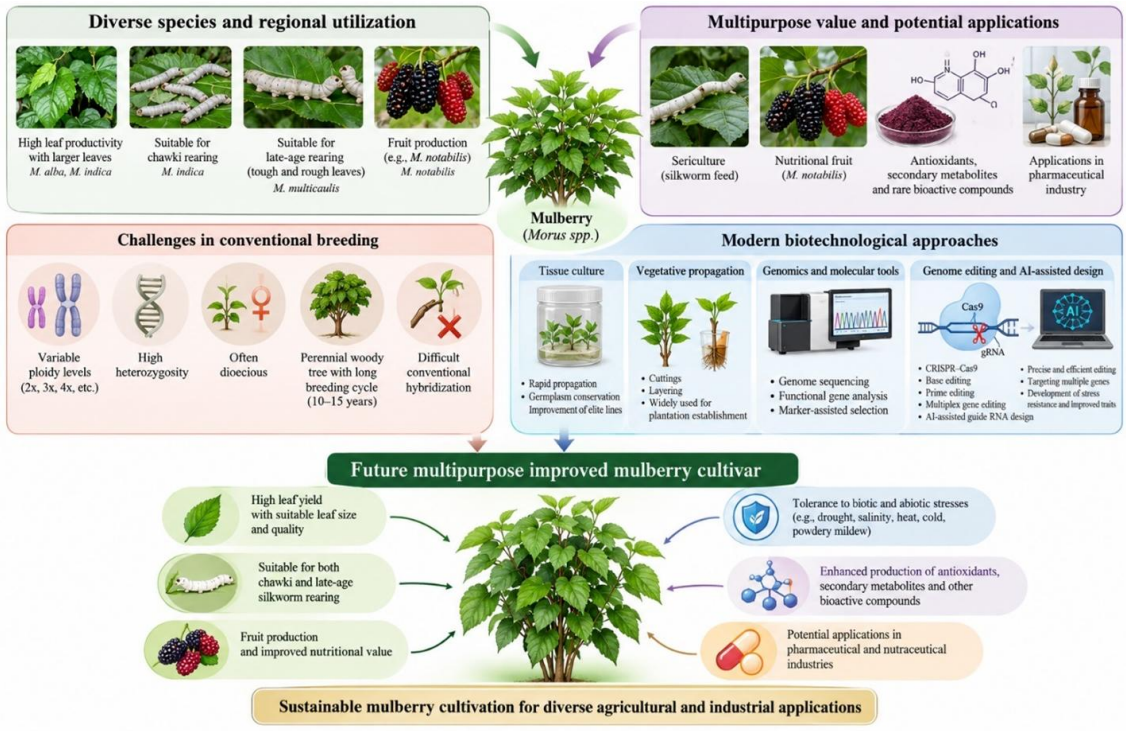


FIGURE 1: Conceptual framework for future research scope for sustainable cultivation.

VI. CONCLUSION

Mulberry (*Morus* spp.) exhibits considerable diversity in chromosome number, ploidy level, genetic characteristics, and potential utilization, providing valuable resources for sericulture, fruit production, and bioactive-compound development. Improved varieties demonstrate how this diversity can be utilized to enhance leaf productivity, meet the feeding requirements of silkworms at different developmental stages, and adapt cultivation to diverse environments. In addition, studies of stress-responsive genes have identified potential molecular targets for improving tolerance to abiotic stresses and diseases. Nevertheless, challenges associated with ploidy variation, high heterozygosity, reproductive biology, and long breeding cycles remain important constraints. Integrating conventional breeding with genomics, tissue culture, and emerging genome-editing technologies may help improve the identification and utilization of valuable genetic resources. Such an integrated approach could contribute to the development of productive, resilient, and multipurpose mulberry cultivars for sustainable sericulture and broader agricultural and industrial applications.

CONFLICT OF INTEREST

The authors declare no conflict of interest.

REFERENCES

[1] Arora, V., Ghosh, M. K., Pal, S., & Gangopadhyay, G. (2017). Allele specific CAPS marker development and characterization of chalcone synthase gene in Indian mulberry (*Morus* spp., family Moraceae). *PLoS One*, *12*(6), e0179189.

[2] Bian, C., Long, D., Liu, X., Wei, C., Gong, J., & Zhao, A. (2015). Cloning and expression to salt stress of Na^+/H^+ antiporter gene (MnNHX1) in mulberry tree. *Scientia Silvae Sinicae*, *51*(8), 16-25.

[3] Central Sericultural Research and Training Institute. (2012). *Mulberry varieties suitable for eastern and north eastern India* [Brochure]. Central Silk Board, Ministry of Textiles, Government of India.
https://www.csrtiber.res.in/Brochure_pamphlets/Mul_ver_E%26NE_India.pdf

[4] Central Sericultural Research and Training Institute. (n.d.). *Improved mulberry varieties*. Central Silk Board, Ministry of Textiles, Government of India. https://www.csrtiber.res.in/Brochure_pamphlets/Brochure.htm

[5] Central Silk Board. (2020). *Note on sericulture: Research and development highlights, 2020–21*. Ministry of Textiles, Government of India. https://www.csb.gov.in/sites/default/files/what_s_new/files/Note-on-Seri-CSB-2020-21.pdf

[6] Chae, J.-Y., Lee, J.-Y., Hoang, I.-S., Wang-Bo, D., Choi, P.-W., Lee, W.-C., Kim, J.-W., Kim, S.-Y., Choi, S.-W., & Rhee, S.-J. (2003). Analysis of functional components of leaves of different mulberry cultivars. *Journal of the Korean Society of Food Science and Nutrition*, *32*(1), 15-21.

[7] Debaraj, Y., Singh, R., & Bajpai, A. K. (2010). Evaluation of some mulberry varieties for yield and quality through bioassay in Manipur, North East India. *Uttar Pradesh Journal of Zoology*, *30*(2), 165-168. https://mbimph.com/index.php/UPJOZ/article/view/276

[8] Devi, Y. S., Hossain, A., Lalremruatpuia, V., & Raviraj, V. S. (2024). Effect of UV radiation on physiological performance of silkworm *Bombyx mori*. *Biological Forum*, *16*(6), 221-229.

[9] Devi, Y. S., Verma, A. K., Nalavadi, C., Hossain, A., & Pramanick, B. (2024). Optimizing preservation duration of mulberry silkworm crossbreed eggs in cold storage. *Biological Forum*, *16*(8), 249-356.

[10] Erarslan, Z. B., Karagöz, S., & Kültür, Ş. (2021). Comparative morphological and anatomical studies on *Morus* species (Moraceae) in Turkey. *Turkish Journal of Pharmaceutical Sciences*, *18*(2), 157.

[11] Kattil, A., Dash, K. K., Shams, R., & Sharma, S. (2024). Nutritional composition, phytochemical extraction, and pharmacological potential of mulberry: A comprehensive review. *Future Foods*, *9*, 100295.

[12] Li, R., Su, X., Zhou, R., Zhang, Y., & Wang, T. (2022). Molecular mechanism of mulberry response to drought stress revealed by complementary transcriptomic and iTRAQ analyses. *BMC Plant Biology*, *22*(1), 36.

[13] Liu, C., Hu, J., Fan, W., Zhu, P., Cao, B., Zheng, S., & Zhao, A. (2021). Heterotrimeric G-protein γ subunits regulate ABA signaling in response to drought through interacting with PP2Cs and SnRK2s in mulberry (*Morus alba* L.). *Plant Physiology and Biochemistry*, *161*, 210-221.

[14] Ma, G., Chai, X., Hou, G., Zhao, F., & Meng, Q. (2022). Phytochemistry, bioactivities and future prospects of mulberry leaves: A review. *Food Chemistry*, *372*, 131335.

[15] Rajan, M. V., Dandin, S. B., Magadum, S. B., & Datta, R. K. (2000). *Nutritional evaluation of mulberry (Morus spp.) genotypes through silkworm growth studies*.

[16] Ramesha, A., Dubey, H., Vijayan, K., Ponnuvel, K. M., Mishra, R. K., & Suresh, K. (2020). Genome wide characterization revealed MnMLO2 and MnMLO6A as candidate genes involved in powdery mildew susceptibility in mulberry. *Molecular Biology Reports*, *47*(4), 2889-2900.

[17] Rao, A. A., Thangavelu, K., & Sharma, K. R. (2005). Distribution and variation of mulberry genetic resources (*Morus* spp.) in the high altitude and cold deserts of Ladakh Himalayan region. *Indian Journal of Plant Genetic Resources*, *18*(2), 255-259.

[18] Sarkar, K. (2020). Studies on the effect of different types of feeding on the commercial characters of mulberry silkworm (*Bombyx mori* L.) in West Bengal: A review. *International Journal of Agriculture, Environment and Biotechnology*, *13*(3), 305-321.

[19] Sarkar, T., Mogili, T., & Sivaprasad, V. (2017). Improvement of abiotic stress adaptive traits in mulberry (*Morus* spp.): An update on biotechnological interventions. *3 Biotech*, *7*(3), 214.

[20] Sliwinska, E., Loureiro, J., Leitch, I. J., Šmarda, P., Bainard, J., Bureš, P., & Galbraith, D. W. (2022). Application-based guidelines for best practices in plant flow cytometry. *Cytometry Part A*, *101*(9), 749-781.

[21] Song, F., Li, Y., Huang, J., Lu, W., Guo, Z., & Deng, W. (2024). Integrated transcriptomic and proteomic analyses reveal the impact of drought and heat stress combination on *Morus alba*. *Environmental and Experimental Botany*, *228*, 105988.

[22] Song, W., Wang, H. J., Bucheli, P., Zhang, P. F., Wei, D. Z., & Lu, Y. H. (2009). Phytochemical profiles of different mulberry (*Morus* sp.) species from China. *Journal of Agricultural and Food Chemistry*, *57*(19), 9133-9140.

[23] Tikader, A., & Dandin, S. B. (2008). *Foliar morphology and venation pattern in different mulberry (Morus spp.)*.

[24] Tikader, A., & Roy, B. N. (2002). Genetic divergence in mulberry (*Morus* spp.). *The Indian Journal of Genetics and Plant Breeding*, *62*(1), 52-54.

[25] Wang, H., Liu, J., Xu, X., Li, Y., Yuan, J., Zeng, Y., & Ma, B. (2024). MGCPdb, a collective resource for mulberry genome size, chromosome number, and ploidy. *Forestry Research*, *4*, e027.

[26] Wang, M., Zhu, M., Qian, J., Yang, Z., Shang, F., Egan, A. N., & Liu, L. (2024). Phylogenomics of mulberries (*Morus*, Moraceae) inferred from plastomes and single copy nuclear genes. *Molecular Phylogenetics and Evolution*, *197*, 108093.

[27] Xia, Z., Dai, X., Fan, W., Liu, C., Zhang, M., Bian, P., & Zhao, A. (2022). Chromosome-level genomes reveal the genetic basis of descending dysploidy and sex determination in *Morus* plants. *Genomics, Proteomics & Bioinformatics*, *20*(6), 1119-1137.

[28] Xuan, Y., Ma, B., Li, D., Tian, Y., Zeng, Q., & He, N. (2022). Chromosome restructuring and number change during the evolution of *Morus notabilis* and *Morus alba*. *Horticulture Research*, *9*, uhab030.

[29] Xuan, Y., Wang, S., Li, S., Yuan, J., Zhou, Q., & He, N. (2023). Chromosome constitution and genetic relationships of *Morus* spp. revealed by genomic in situ hybridization. *BMC Plant Biology*, *23*(1), 428.

[30] Yang, C. X., Liu, S. Y., Zerega, N. J., Stull, G. W., Gardner, E. M., Tian, Q., & Yi, T. S. (2023). Phylogeny and biogeography of *Morus* (Moraceae). *Agronomy*, *13*(8), 2021.

[31] Zeng, Q., Chen, M., Wang, S., Xu, X., Li, T., Xiang, Z., & He, N. (2022). Comparative and phylogenetic analyses of the chloroplast genome reveal the taxonomy of the *Morus* genus. *Frontiers in Plant Science*, *13*, 1047592.

[32] Zhao, M., Zhou, G., Liu, P., Wang, Z., Yang, L., Li, T., & Lin, T. (2024). The role of MaFAD2 gene in bud dormancy and cold resistance in mulberry trees (*Morus alba* L.). *International Journal of Molecular Sciences*, *25*(24), 13341.