

SABRAO Journal of Breeding and Genetics
 58 (4) 1589-1597, 2026
<http://doi.org/10.54910/sabrao2026.58.4.11>
<http://sabraojournal.org/>
 pISSN 1029-7073; eISSN 2224-8978



FLAX (*LINUM USITATISSIMUM* L.) FIBER TRAIT IMPROVEMENT: GERMPLASM RESOURCES, MOLECULAR BREEDING, AND FUTURE PROSPECTS

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SUMMARY

Flax (*Linum usitatissimum* L.) is a strategic fiber crop with increasing importance for sustainable agriculture and textile industries. With crop diversification and development of domestic fiber resources, the renewed interest has emerged in fiber flax cultivation in Uzbekistan. However, the genetic improvement of fiber-related traits—such as fiber yield, length, strength, and fineness—remains challenging because of their quantitative inheritance and robust environmental sensitivity. The present review summarized recent research advancements in flax fiber, particularly focusing on germplasm diversity, conventional and molecular breeding strategies, and the application of DNA marker technology. The local landraces, advanced lines, and introduced accessions have expanded the genetic base for fiber improvement. Modern approaches, including quantitative trait loci (QTL) mapping, genome-wide association studies (GWAS), and marker-assisted selection (MAS), have also enabled the identification of genomic regions and candidate genes involved in the development of fiber quality. This review also discussed future perspectives for flax breeding under Uzbekistan's agro-climatic conditions, emphasizing integrated phenotypic, molecular, and genomic approaches to develop high-yielding, better-quality, and stress-resilient fiber flax cultivars. The results provide a scientific framework to accelerate breeding efficiency and support the sustainable expansion of flax production in Central Asia.

Keywords: Flax (*Linum usitatissimum* L.), fiber traits, breeding, germplasm resources, fiber quality, DNA markers, QTL mapping, marker-assisted selection

Communicating Editor: Dr. Tonette P. Laude

Manuscript received: February 03, 2026; Accepted: November 14, 2025.

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Citation: Bakhadirov USH, Khalmirzaev DK, Andronik EL (2026). Flax (*Linum usitatissimum* L.) fiber trait improvement: Germplasm resources, molecular breeding, and future prospects. *SABRAO J. Breed. Genet.* 58 (4) 1589-1597. <http://doi.org/10.54910/sabrao2026.58.4.11>.

Key findings: This review provides a comprehensive overview of the current status and future prospects of flax (*Linum usitatissimum* L.) fiber traits improvement research in Uzbekistan. The findings highlighted the importance of combining traditional breeding with molecular and genomic approaches to improve fiber yield and quality.

INTRODUCTION

In Uzbekistan, fiber flax (*Linum usitatissimum* L.) germplasm holds a valuable genetic resource for breeding and scope for further improvement of fiber-related traits. Traditionally, flax has succeeded in its cultivation under diverse agro-climatic conditions, which contributed to the formation of locally adapted genotypes with stable fiber yield and better quality. With traditional cultivation and farmer-based selection, flax population gradually adapted to local environments, developing tolerance to drought, temperature fluctuations, and soil salinity, which are the primary characteristics of many regions in Uzbekistan. The local and introduced flax genotypes constitute an important reservoir of genetic diversity for improvement in fiber traits (Ahmed *et al.*, 2019).

Flax fiber-related traits, including fiber yield, length, strength, fineness, and uniformity, underwent quantitative inheritance and considerable influences from genetic and environmental factors. Past studies demonstrated that traditional flax germplasm showed a wide phenotypic variation for fiber traits, proving to be a promising source of donor material in breeding programs (Amangaliev *et al.*, 2023). In particular, the landraces and old cultivars often possess superior fiber quality traits, although with lower productivity than modern cultivars. Therefore, evaluation and conservation of ancient and local flax germplasm remain crucial for sustainable improvement in flax fiber traits (Bakry *et al.*, 2024).

Fiber flax's primary cultivation is in irrigated and partially rainfed areas, where field practices significantly affect fiber development in Uzbekistan. Traditional agronomic practices include autumn and early spring sowing, deep plowing, and moderate nitrogen and phosphorus fertilization that

further enhance the stem elongation and fiber formation. Excessive nitrogen application enhanced the vegetative growth but may negatively alter fiber quality, especially by reducing fiber strength and increasing coarseness (Dawood *et al.*, 2019; Bakry *et al.*, 2024). Therefore, balanced fertilization strategies were notably crucial for maintaining optimal fiber traits under existing environmental conditions.

Several expeditions and collections conducted in different regions of Uzbekistan have accumulated the diverse flax accessions, including local varieties, advanced lines, and introduced material from neighboring countries and international gene banks. These accessions with morphological evaluation revealed substantial variations in stem height, technical stem length, stem diameter, and fiber content, which could serve as key determinants of the fiber yield. Tall flax genotypes with longer technical stems generally exhibited higher fiber yield, whereas shorter genotypes often showed improved adaptability and lodging resistance.

Fiber quality assessment of collected flax accessions disclosed considerable diversity in fiber length and tensile strength. Some local accessions showed relatively fine and stronger fibers suitable for high-quality textile production, while other genotypes were apparently more suitable for industrial and composite applications. Such variability revealing distinct genetic mechanisms controlling fiber development highlighted the importance of integrated evaluation comprising phenotypic screening and molecular analysis (Shuvar *et al.*, 2021). In several studies, fiber content ranged from 18% to 30%, depending on genotypes and environmental conditions, confirming the robust genotype-by-environment interaction effects for fiber-related traits.

Advanced research increasingly emphasized the use of molecular tools to characterize flax germplasm and identify the

genetic loci associated with fiber-related traits. Quantitative trait loci (QTL) mapping and genome-wide association studies (GWAS) have revealed multiple loci linked to fiber yield, stem length, and fiber quality parameters (Turaev *et al.*, 2023). The integration of molecular information with phenotypic data allows breeders to precisely select the parental lines and accelerate the development of superior fiber flax cultivars.

In flax breeding, the application of DNA marker technologies is still at an early stage; however, it showed considerable potential in Uzbekistan. Marker-assisted selection (MAS) can further facilitate the identification of genotypes carrying favorable genes for fiber traits, thereby reducing breeding cycles and time and enhancing selection efficiency (Bakhadirov *et al.*, 2024). Flax germplasm with continued evaluation under diverse environmental conditions, integrated with molecular characterization, will considerably contribute to the development of stable, high-yielding, and high-quality fiber flax cultivars adapted to local agroecological zones (Ahmed *et al.*, 2019).

Overall, ancient and local flax germplasm represents a strategic resource for fiber traits improvement in Uzbekistan. Therefore, comprehensive characterization of these genetic resources, including morphological, agronomic, fiber quality, and molecular analyses, is crucial for exploring their full breeding potential. The knowledge gained from the past and ongoing studies provides a sound base for future breeding programs and supports the sustainable development of the fiber flax sector in Uzbekistan.

Genetic evaluation of the fiber-related traits

Recent advances in genetic mapping technologies have considerably accelerated the identification of DNA markers associated with economically important traits in crop plants, including fiber-related traits in flax (*Linum usitatissimum* L.). Efficient mapping strategies' development has enabled researchers to dissect the complex genetic architecture

underlying fiber yield and quality parameters, such as fiber content, fiber length, tensile strength, and fineness (Sa *et al.*, 2021). These genetic approaches appeared to be particularly vital for flax improvement, where fiber traits entailed quantitative inheritance and considerable influences from environmental conditions.

Classical linkage mapping, linkage disequilibrium (LD)-based association mapping (AM), and GWAS have gained wide usage in the identification of QTLs controlling fiber-related traits in flax (Pali and Mehta, 2016). Traditional biparental QTL mapping studies have successfully identified the genomic regions associated with stem height, technical stem length, and fiber content; however, their resolution was often low due to less allelic diversity and restricted recombination events within mapping populations (Kanapin *et al.*, 2022). Moreover, QTL identified in specific biparental populations may reveal the limited transferability across diverse genetic backgrounds and environments.

LD-based association mapping and GWAS approaches overcome some of these limitations by utilizing natural genetic variation found in diverse germplasm. The first successful GWAS studies evaluated the global germplasm resources and identified the multiple SNP (single nucleotide polymorphism) markers significantly associated with fiber yield and quality traits in flax (Guan-Yu *et al.*, 2016). These studies explored that flax fiber traits sustain the management of multiple loci distributed across the genome, emphasizing the need for high-resolution mapping approaches. Nevertheless, association mapping approaches also obtained alterations from population structure, allele frequency, and historical recombinations that may further lead to false-positive associations if not properly controlled (Manian *et al.*, 2021).

Nested association mapping (NAM) achieved confirmation as a powerful strategy to combine the advantages of linkage mapping and association mapping while minimizing their respective limitations. Kanapin *et al.* (2022) introduced NAM, which was first implemented in flax by Galinousky *et al.* (2020). NAM used a common reference parent crossed with

multiple diverse donor lines to generate a set of recombinant inbred line (RIL) populations. This approach enhanced the allelic diversity and recombination events, thereby improving mapping resolution and statistical power. Although NAM populations have undergone extensive development and application in major crops, such as maize and wheat (Galinousky *et al.*, 2020), NAM application in flax research is still scarce but highly promising.

In flax, the development of NAM populations targeting fiber-related traits could provide valuable insights into the genetic mechanisms managing fiber development and its quality traits. Using a better-characterized fiber flax cultivar as a common parent, crossed with diverse donor genotypes revealing variations in fiber content and quality, would enable the identification of stable QTL and candidate genes across multiple genetic backgrounds. Such an approach would further facilitate the detection of favorable genes associated with fiber traits and enhance their utilization in breeding programs (Galinousky *et al.*, 2020).

The integration of NAM populations with high-throughput genotyping platforms, including SNP arrays and genotyping-by-sequencing (GBS), further strengthens the NAM potential in flax. Combined with precise phenotyping across multiple environments, NAM-based studies can support the development of reliable DNA markers for marker-assisted selection (MAS). Consequently, application of advanced mapping strategies, including NAM and GWAS, represents a crucial step toward accelerating improvement in flax fiber traits and developing high-performing cultivars adapted to diverse

agroecological conditions, including Uzbekistan (Karpov *et al.*, 2021).

QTL mapping, GWAS, and NAM are widely used genetic approaches that differ in population structure and mapping resolution. QTL mapping relies on biparental populations and provides high detection power but low resolution. GWAS uses natural populations and offers higher resolution, although population structure could affect. NAM combines the advantages of both methods, improving resolution and power but requires more complex experimental design. A brief comparison of these approaches is available in Table 1.

Flax cultivar identification using DNA markers

Phenotypic evaluation of flax (*Linum usitatissimum* L.) germplasm relies on morphological traits, such as stem height, technical stem length, stem diameter, flowering time, fiber content, and fiber fineness. Although, these parameters provide valuable information for selection, with considerable influences from environmental conditions, resulting in phenotypic plasticity that is not always stably inherited across the generations (Amangaliev *et al.*, 2023). Therefore, sole reliance on phenotypic traits for cultivar identification can be unreliable, particularly when distinguishing closely related genotypes and breeding lines.

The domestication and long-term selection of flax for fiber quality and agronomic performance resulted in a relatively narrow genetic base in cultivated cultivars compared with wild relatives. These limitations reduced the observable genetic diversity and

Table 1. Comparison of QTL mapping, GWAS, and NAM approaches.

Methods	Population type	Resolution	Advantages	Limitations
QTL mapping	Biparental population	Low-medium	High detection power, simple design	Low resolution, limited genetic diversity
GWAS	Natural population	High	High resolution, captures multiple alleles	Sensitive to population structure, false positives
NAM	Multi-parent population	High	Combines advantages of QTL and GWAS	Complex design, time- and resource-consuming

complicated the accurate identification of new cultivars using morphological descriptors (Pali and Mehta, 2016). Therefore, the application of molecular marker technologies, such as simple sequence repeats (SSRs) and single nucleotide polymorphisms (SNPs), seemed promising approaches for rapid, precise, and environmentally stable characterization of flax genotypes at the DNA level.

DNA barcoding increases its recognition as a reliable tool for cultivar identification, protection of breeders' intellectual property rights, and standardization of germplasm resources. Past studies enunciated that SSR markers associated with fiber quality and stress tolerance traits can be effectively applicable to develop DNA fingerprints for elite flax genotypes (Mokshina *et al.*, 2020). The highly polymorphic SSR and SNP markers use sought to enable the differentiation of closely related genotypes, verification of breeding line authenticity, and accelerating the selection of superior genotypes with desirable fiber traits.

DNA barcoding employment in local elite flax genotypes is possibly a highly viable direction in breeding programs and germplasm conservation. Molecular characterization could complement phenotypic evaluation by providing a robust and reproducible method for assessing genetic diversity, monitoring breeding progress, and preventing misidentification of newly developed genotypes. The integration of DNA barcoding with high-throughput genotyping platform and phenotypic assessment seemed to improve the efficiency of selecting genotypes with high fiber yield, superior fiber quality, and adaptability to local agro-climatic conditions (Wu *et al.*, 2019).

Overall, the DNA barcoding should be beneficial as an essential component of modern flax breeding strategies in Uzbekistan. Therefore, its implementation could facilitate accurate identification, conservation, and effective utilization of elite flax germplasm, thereby supporting the development of high-yielding cultivars with improved fiber traits under diverse environmental conditions (Xie *et al.*, 2018).

DNA marker-based evaluation for fiber traits

In flax (*Linum usitatissimum* L.), the fiber quality and yield are the complex traits controlled by multiple genetic loci and considerably influenced by existing environmental conditions. Phenotypic selection for fiber traits, such as fiber content, technical stem length, fiber fineness, and tensile strength, is time-consuming and has a higher tendency to environmental variations (Drej and Noaman, 2021). Molecular marker-based screening provides a reliable, rapid, and environment-independent method to identify superior genotypes for fiber improvement in breeding programs.

Recent studies have applied DNA markers, including SSRs and SNPs, to screen the flax germplasm for fiber-related traits. For instance, Sa *et al.* (2018) evaluated 120 flax accessions for fiber yield, fiber length, and stem characteristics, using a panel of 40 SSR markers linked to fiber yield and quality. The study exhibited a significant relationship between the specific markers and desirable fiber quality traits, accelerating the identification of flax elite genotypes for further breeding. Similarly, Cloutier *et al.* (2011) used the genome-wide SNP markers to identify QTLs controlling fiber length, fiber fineness, and tensile strength in flax. As a result, identifying several QTLs was consistent across multiple environments, revealing their stability and potential usefulness in MAS.

The flax local germplasm, including landraces and advanced lines, exhibited wide variation in fiber yield and quality traits in Uzbekistan. Marker-assisted genotyping enables breeders to select accessions carrying favorable alleles for high fiber content, longer fibers, and robust tensile strength. For example, markers associated with fiber content (SSR Lu123 and Lu256) and fiber strength (SNP-based loci on chromosomes 1 and 3) have proven to be effective in distinguishing superior lines from diverse flax collections. The integration of molecular screening with conventional phenotyping accelerates the

breeding cycle, reduces field trial requirements, and enhances the efficiency of developing high-performing flax cultivars adapted to local agro-climatic conditions (El-Bassiouny *et al.*, 2024).

Overall, the DNA marker-based screening of flax germplasm represents a powerful tool for improving fiber quality traits. By enabling precise selection of elite genotypes, molecular markers support the sustainable development of flax breeding programs in Uzbekistan and contribute to producing cultivars with high fiber yield and quality suitable for textile and industrial applications (El-Gedwy *et al.*, 2020).

Future perspectives of flax fiber breeding in Uzbekistan

In Uzbekistan, flax (*Linum usitatissimum* L.) cultivation acquires increasing effects from environmental stress factors, including drought, high temperature, and soil salinity, particularly in arid and semi-arid regions. These abiotic stresses reduced the fiber yield and quality, proving it critical to understand the molecular mechanism underlying stress tolerance in flax. Studying genes and QTLs associated with fiber traits and stress resilience will facilitate the development of abiotic stress-tolerant and high-quality flax cultivars using molecular breeding approaches (Cloutier *et al.*, 2011).

Fiber quality genes and marker-assisted selection

Flax (*Linum usitatissimum* L.) fiber quality and yield are crucial for industrial applications and ecological requirements. Key fiber traits include fiber length, thickness, flexibility, and chemical composition, including cellulose, lignin, and pectin content. The flax fiber quantitative traits involved polygenic inheritance, incurring high impacts from environmental conditions. Therefore, identifying genes controlling fiber traits at the molecular level and performing MAS is a key approach for improving fiber quality traits and their stability (Turaev *et al.*, 2023).

Past studies revealed that genes involved in flax fiber quality traits include the *LuCesA* (cellulose synthase) gene family, *LuLAC* (laccase), and *LuPAL* (phenylalanine ammonia-lyase) genes. These genes regulate the fiber composition and structure, ensuring stable fiber yield under various stress conditions (Soto-Cerda *et al.*, 2018).

The application of MAS approaches have been successful using SSR and SNP markers associated with these genes. For instance:

- a. The markers Xlnu-15 and Xlnu-24 SSR appeared to link with cellulose content and fiber yield, used to select high-quality fiber genotypes (Cloutier *et al.*, 2011).
- b. *LuCesA2*-SNP marker use helped identify long and robust fibers (Yurkevich *et al.*, 2017).
- c. The marker *LuPAL1*-SSR, as applied, sought to optimize the lignin and pectin content in fiber (Cloutier *et al.*, 2011).

In selection using markers, it considerably accelerates the breeding process, allows precise differentiation among different genotypes, and facilitates the development of stable and high-quality fiber flax cultivars. Molecularly targeted selection ensures that newly developed cultivars are not only superior in fiber quality but also tolerant to abiotic stress factors such as drought, heat, and salinity (Galinousky *et al.*, 2020).

Future studies should focus on examining the expression of *LuCesA* and *LuLAC* genes across the different genotypes, as well as identifying QTLs associated with specific SSR and SNP markers. Such a type of approach will enable more effective identification of fiber quality genes and their incorporation into marker-assisted breeding programs, ultimately supporting the development of high-quality and stress-resilient flax cultivars in Uzbekistan (Yurkevich *et al.*, 2017).

Fiber flax disease management

Fiber flax (*Linum usitatissimum* L.) productivity and quality attain negative effects from various fungal diseases, including pasmo disease (*Melampsora lini*) and powdery mildew (*Oidium*

lini). These pathogens reduce the fiber yield, degrade fiber quality, and affect the cellulose content, ultimately limiting industrial applications (Karpov *et al.*, 2021).

Future strategies for improving disease resistance in flax and ensuring high fiber quality include:

- a. Availability of suitable germplasm: Screening local and exotic flax accessions for resistance to fiber-degrading pathogens while maintaining high cellulose and long fiber traits.
- b. Strengthening screening and testing facilities: Enhancing field evaluation plots, greenhouse experiments, and molecular analyses to evaluate disease resistance accurately.
- c. Capacity building: Training of young researchers in flax pathology, molecular marker analysis, and fiber quality assessment.
- d. Germplasm exchange and international collaboration: Collaborating with the International Center for Agricultural Research in the Dry Areas, or ICARDA, the Food and Agriculture Organization (FAO), and regional breeding centers to introduce disease-resistant flax genotypes and exchange molecular marker information.
- e. Marker-assisted selection and molecular breeding: Using molecular markers linked to fiber quality genes (*LuCesA*, *LuLAC*, and *LuPAL*), as well as resistance loci to accelerate the development of disease-resistant and high-fiber genotypes (Povkhova *et al.*, 2021).
- f. Advanced breeding technologies: Implementing double haploid techniques and genomic selection to reduce breeding cycles and rapidly release superior cultivars in disease-prone areas (Al-Rawi and Noman, 2020).

With the integration of disease resistance screening, molecular markers for fiber quality, and modern breeding tools, breeders can develop flax cultivars with high-quality fiber and stable disease resistance, ensuring sustainable production for textile and industrial applications in Uzbekistan. Continuous field and molecular research approaches will be crucial for understanding pathogen diversity, fiber degradation mechanisms, and improving selection efficiency (Amangaliev *et al.*, 2023). The information

presented will serve as a valuable scientific basis for future flax breeding programs and support the development of competitive fiber flax cultivars suited to Uzbekistan's agroecological conditions.

CONCLUSIONS

The review summarized the current status of flax (*L. usitatissimum* L.) fiber traits' improvement research in Uzbekistan. Both local and introduced flax germplasm resources have played a remarkable role in improving fiber-related traits. Molecular studies focusing on genes involved in cellulose biosynthesis and fiber quality have provided valuable insights into the genetic basis of fiber improvement. The application of DNA marker-based screening and marker-assisted selection (MAS) has considerably enhanced the accuracy and efficiency of identifying superior genotypes. Accumulated genetic resources and experimental findings offer a robust platform for future breeding efforts. Advanced molecular approaches, such as genome-wide association studies (GWAS), genomic selection, and CRISPR (clustered regularly interspaced short palindromic repeats)/Cas-based technologies, will surely support the development of high-quality and stress-resilient flax cultivars in Uzbekistan.

ACKNOWLEDGMENTS

The authors express their sincere gratitude to all researchers and institutions who contributed to this review article by providing scientific guidance, experimental results, and genetic materials. Their valuable support and collaboration are greatly appreciated.

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