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GENETIC AND AGRONOMIC CHARACTERISTICS OF SUNFLOWER (*HELIANTHUS ANNUUS* L.) AND ITS RESISTANCE TO PESTS AND DISEASES

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SUMMARY

Sunflower (*Helianthus annuus* L.) is an important oilseed crop, valued for its high-quality edible oil and protein-rich byproducts. Its economic and agricultural significance continues to grow due to increasing demand for vegetable oil and renewable resources worldwide. The following research provides a comprehensive analysis of sunflower biology, agronomy, and genetics, emphasizing traits crucial for its sustainable crop production. The description of sunflower taxonomy, classification, and morpho-biological features succeeded in highlighting its structural diversity and adaptability to diverse agroecological zones. Physiological and agronomic traits, such as growth dynamics, yield potential, and oil composition, attained examination in interaction with environmental factors and cultivation practices. Special attention focused on the sunflower's resistance to major pests and diseases influencing global production. Furthermore, the study reviewed the genetic resources and molecular seed production tools, including marker-assisted selection and genomic mapping, which accelerate the development of improved cultivars with higher yield, better oil quality, and enhanced stress tolerance. The summary of data from national and international genetic collections resulted in tabular form. The findings underline the importance of integrating classical selection with molecular approaches to meet the challenges based on climate change and sustainable agricultural development.

Keywords: Sunflower (*H. annuus* L.), genetics, morphology, physiology, resistance, stress, seed production, molecular markers

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Key findings: The study confirmed the substantial genetic and morphological diversity in the regional and global sunflower (*H. annuus* L.) collections, providing valuable resources for seed production. The integration of molecular markers and genomic technologies has considerably accelerated the identification of desirable traits, enabling the development of improved sunflower cultivars with enhanced yield, oil quality, and resistance to biotic and abiotic stresses.

INTRODUCTION

Agriculture, being a key sector, plays an important role in strengthening food security, economic growth, and social stability worldwide. As of 2024, the global population has surpassed eight billion, intensifying the demand for sustainable food and feed production worldwide (FAO, 2024). According to the Food and Agriculture Organization, the agriculture sector contributes over 10% to global GDP and employs around 27% of the world’s workforce. In agriculture, the oilseed crops have acquired a pivotal role, providing high-energy food, essential fatty acids, protein-rich animal feed, and raw material for various industries, including biofuel, cosmetics, and pharmaceuticals (García-Vila *et al.,* 2012; Guo *et al.,* 2017).

Sunflower (*Helianthus annuus* L.) is one of the most essential oilseed crops globally for its economic and nutritional values (Pandey, 2018; El-Hamidi and Zaher, 2018). Sunflower oil is distinct with the highest content of linoleic and oleic acids, low saturated fats, and an abundance of vitamins E and A, which makes it a recognized, highly desirable vegetable oil for human consumption and industrial use. In 2023, the global sunflower seed production reached approximately 56.5 million metric tons cultivated on more than 27.3 million hectares (USDA, 2024). The leading sunflower producers were Ukraine, Russia, the European Union, Argentina, and the USA, collectively accounting for over 80% of the global production (Grieve *et al.,* 2019).

The leading and strategic importance of sunflower extends to developing and transition economies. In Uzbekistan, sunflower attains high regard as a priority crop for national food security and import substitution. The national agricultural statistics indicated that sunflower acreage has grown by 15% over the last five years, with production rising from 182,000 tons in 2019 to over 220,000 tons in 2023 (Ministry of Agriculture of Uzbekistan, 2024). Therefore, the policy initiatives aimed at diversifying cropping patterns, increasing oilseed self-sufficiency (Muminov *et al.,* 2025), and supporting farmer cooperatives have considerably contributed to this sustainable development (Kodirova *et al.,* 2024; Khodjayeva *et al.,* 2025).

However, despite these advances, constraints to sunflower production are due to several biotic and abiotic stress factors. The critical diseases, such as downy mildew (*Plasmopara halstedii*), Sclerotinia stem rot (*Sclerotinia sclerotiorum*), and sunflower rust (*Puccinia helianthi*), are the most destructive, causing significant yield losses, ranging from 15% to 40% in epidemic years. Insect pests, most notably the sunflower moth (*Homoeosoma electellum*) and aphids (*Aphis gossypii*), are also responsible for further reductions in seed yield and oil quality. Abiotic stresses, i.e., drought, soil salinity, and extreme temperatures, are also increasingly prevalent under climate change scenarios, posing new challenges for crop resilience and productivity. According to the Intergovernmental Panel on Climate Change (IPCC, 2023), Central Asia, including Uzbekistan, is particularly vulnerable to shifts in precipitation patterns and rising temperatures, which may also threaten the stability of the existing and traditional cropping systems (Pachauri and Meyer, 2014; Hladni and Jocić, 2021).

Addressing all these multifaceted challenges requires an integrative approach. Classical seed production based on the phenotypic variation and selection, while effective, is often slow and labor-intensive. Recent advances in molecular genetics, such as marker-assisted selection (MAS), genomic selection, and gene editing, have revolutionized sunflower improvement, enabling the rapid identification and incorporation of genes conferring disease resistance, abiotic stress tolerance, and improved oil quality (Hladni *et al.,* 2021). Genetic resource banks and international collaboration play a vital role in exploring and utilizing the extensive genetic diversity of sunflowers, which is critical for developing resilient cultivars. For instance, recent past studies have demonstrated the utility of wild *Helianthus* species as donors of novel resistance genes and the application of high-throughput genotyping for mapping quantitative trait loci (QTL) related to higher seed yield and oil content (Seiler and Brothers, 2017).

In this context, the presented research aimed to provide a comprehensive and up-to-date review of the sunflower's taxonomic classification, morpho-biological and physiological traits, genetic resources, and resistance to various diseases and pests. The said review synthesizes the regional and global data, revealing findings from national and international genetic collections and discussing the prospects for integrating molecular and conventional seed production approaches. By offering a critical analysis of current trends and research gaps, this study contributes to the scientific base necessary for developing sustainable and resilient sunflower production systems, both in Uzbekistan and worldwide (Seiler and Gulya, 2016; Hladni *et al.,* 2021).

Taxonomic classification of sunflower

Helianthus annuus L. is a member of the order Asterales and the largest and most evolutionarily successful angiosperm family, Asteraceae, characterized by composite inflorescences (capitula), specialized secondary metabolites (sesquiterpene lactones), and a unique pappus structure. Within Asteraceae, sunflower falls under the subfamily Asteroideae and tribe *Heliantheae*, which integrate the genera exhibiting helicoid and trichome-covered stems and involucral bracts arranged in two distinct series (Elemike *et al.,* 2019). The genus *Helianthus* comprises approximately 70 species, divided into two main sections, viz., the perennial section (*H. maximiliani* and *H. tuberosus*), and the annual section *Agrestis*, to which *H. annuus* also belongs (Andrew *et al.,* 2013).

The modern phylogenetic analyses based on chloroplast DNA sequences confirm the monophyly of *Helianthus* and place the *H. annuus* in a clade with its closest wild relatives, such as *H. petiolaris* and *H. argophyllus*. This indicated a recent divergence during the late Pleistocene. Linnaeus's original description in Species *Plantarum* (Linnaeus, 1753) established *H. annuus* based on key diagnostic features, i.e., large, solitary capitula with yellow ray florets, a glabrous receptacle, and ovate-cordate leaves with serrate margins. Domestication of *H. annuus* likely occurred in eastern North America over 4000 years ago, where Indigenous peoples selected for increased achene size and oil yield. The said endemic process generated distinct landraces that form the primary gene pool for current improvement in the sunflower (Blackman *et al.,* 2011).

The cultivated sunflower classification has four major cultivar groups based on seed use and morphological traits, as follows:

- Oilseed group—characterized by small achenes, thin hulls (<20% of seed weight), and high oil content (≥45%);
- Confectionery group—exhibits large kernels, thick hulls (>30%), and protein-rich meal (≥25%);
- Intermediate group—combines the moderate oil and seed size traits for dual-purpose; and
- Ornamental group—selected for diverse head diameter (8–30 cm), ray floret color polymorphism, and branch architecture.

Wild sunflower subspecies (*H. annuus* subsp. *texanus*) remain indispensable reservoirs of genes for biotic (disease resistance) and abiotic (drought and salinity) stress tolerance. In gene banks, the ex-situ collections, such as the U.S. Department of Agriculture–Agricultural Research Service (USDA–ARS) National Sunflower Repository and the Vavilov Institute, currently maintain over 9000 accessions, preserving the genetic breadth essential for pre-seed production and advanced molecular selection strategies. However, significant advancements have resulted in previous years in improving sunflower oilseed quality. Selection efforts have focused primarily on modifying fatty acid profiles to considerably enhance the proportion of health-beneficial fatty acids. Additionally, the bioactive compounds, such as tocopherols and phytosterols, have also gained enhancements, contributing to improved oil stability and nutritional values (Fernández-Martínez *et al.,* 2015).

Morpho-biological characteristics of sunflower

Sunflower demonstrates a coherent suite of morpho-biological traits that underlie its agronomic success and ecological plasticity. Vegetatively, the sunflower plants develop a single and erect stem, ranging from 1.5 to 2.5 m in height; specialized seed production has produced dwarf hybrids (0.8–1.2 m) for mechanical harvesting, and the mammoth types exceed 3.5 m for maximal biomass (Škorić *et al.,* 2016). The stem has a dense covering of unicellular, multicellular, and glandular trichomes, which enhance the structural rigidity, reduce transpiration, and deter herbivory. The internodes vary between 15 and 30 cm, modulated by photoperiod and temperature during early development. The root system comprises a dominant taproot that penetrates 2–3 m into the soil profile, supported by a fibrous network of lateral roots concentrated in the top 30 cm. This type of root architecture confers superior access to deep soil moisture, contributing to drought resilience, even under water-limited conditions (Seiler and Marek, 2011). Under well-watered regimes, lateral root proliferation correlates with enhanced nutrient uptake, particularly of phosphorus and micronutrients, supporting its vigorous vegetative growth.

In sunflowers, the optimum leaf morphology for highest photosynthetic efficiency has leaves that are alternate, simple, and ovate-cordate (15–30 cm long), bearing serrate margins. At the anthesis stage, the canopy achieves a leaf area index (LAI) of 4–5, maximizing light interception. Stomatal density (120–180 mm^{-2}) and aperture control allow a net CO_2 assimilation rate of 18–22 $\mu mol\ m^{-2}s^{-1}$ under non-limiting conditions while maintaining water use efficiency of approximately 2.5 mmol CO_2 mol^{-1} H_2O. Reproductively, the composite capitulum (8–30 cm diameter) comprises 800–2000 florets arranged on a convex receptacle. Sterile ray florets (20–30 per head) form an attractant perimeter, whereas fertile disc florets open centripetally over 5–7 days, ensuring sequential pollination. Photoperiod sensitivity is minimal between 12 and 16 h of day length, facilitating cultivation across the latitudes. Collectively, these integrated morpho-biological features—stem architecture, root depth, leaf physiology, inflorescence dynamics, and seed biochemistry—provide a holistic framework for targeted seed production aimed at yield optimization, oil quality enhancement, and resilience to biotic and abiotic stress conditions (Jan and Seiler, 2022).

Physiological and agronomic traits of sunflower

Physiological traits

Growth and development stages

In the sunflower vegetation period, the plants undergo several developmental phases: seed germination, seedling emergence, flowering, and seed formation. Depending on the variety and agro-climatic conditions, the vegetation period lasts 80–130 days (Seiler and Marek, 2011).

Photosynthetic activity

During photosynthesis, plants produce and accumulate organic matter. The total amount of this organic matter depends on the intensity of photosynthesis and respiration, that is, the ratio of organic matter produced during photosynthesis to organic matter consumed for respiration. Given its large leaf area and high chlorophyll content, the sunflower demonstrates a high intensity of photosynthesis, which enhances the plant’s ability to accumulate considerable biomass.

Water and moisture requirements

Sunflower is considerably a moderately moisture-loving crop. Its moisture demand significantly increases during the flowering and seed formation stages. However, certain sunflower hybrids exhibited relative drought tolerance (Liviero *et al.,* 2021).

Response to light and temperature

Sunflower, being a light- and heat-loving plant, grows optimally at 20 °C–25 °C. Lower temperature slows down its growth, while excessively high temperatures may negatively affect its pollination process (Qi *et al.,* 2016).

Agronomic traits

Productivity

Depending on the cultivar and hybrid, the crop yield ranges between 2,000 and 5,000 kg ha^{-1}. However, the use of intensive cultivation technologies allows for stable and higher yields.

Seed oil content

Sunflower seeds contain an average of 40%–55% oil. The oil is of high quality, rich in useful unsaturated fatty acids, such as linoleic acid. During the cropping season of 2021, the exotic sunflower genotypes 9853 and 9848 (from Russia) showed the highest oil content (54.4%±0.87% and 53.99%±0.14%, respectively) (Omonov *et al.,* 2023).

Disease and pest resistance of sunflower

In fungal and oomycete pathogens, the resistance to downy mildew (*Plasmopara halstedii*) has the control of major R-genes (Pl1–Pl17), effectively inhibiting both seedling and systemic infection (Seiler and Jan, 2006). However, efforts to map resistance QTL against maize mosaic virus are ongoing, with initial screens identifying the low-level partial resistance in the Central Plains germplasm.

In insect pests, the sunflower moth (*Homoeosoma electellum*) and cutworms (*Agrotis ipsilon*) resistance incur mediation from antixenosis and antibiosis mechanisms associated with glandular trichomes and sesquiterpene lactone production (Smith *et al.,* 2010). Partial resistance to sunflower head weevil (*Smicronyx fulvus*) and sunflower beetle (*Zygogramma exclamationis*) correlates with capitulum toughness and phenolic glucoside content; a major resistance QTL on chromosome 6 is currently under marker-assisted selection.

In seed production and integrated management, combining monogenic resistance (Pl-genes for downy mildew) with quantitative resistance loci for Sclerotinia and Alternaria via marker-assisted backcrossing accelerates the cultivars' development (Seiler and Jan, 2006). Integrated pest management practices, including crop rotation, biological control agents (*Trichoderma* spp. and *Bacillus thuringiensis*), and judicious insecticide application, can enhance the durability of resistance. Emerging genomic selection platforms enable simultaneous selection for multiple resistance loci and key agronomic traits, promising the rapid deployment of resilient hybrid cultivars (Seiler and Gulya, 2016).

Under drought stress conditions, the integrated transcriptome and metabolome analyses of sunflower revealed that drought tolerance receives mediation from coordinated regulation of genes involved in photosynthesis, osmolyte biosynthesis, and antioxidant defense. In this context, several transcription factors showed increased expression under drought conditions, suggesting their pivotal role in the transcriptional regulatory network governing stress response (Liviero *et al.,* 2021). The upregulation of genes involved in osmotic adjustment, reactive oxygen species scavenging, and hormonal signaling pathways highlighted their crucial roles in drought tolerance. Functional validation confirmed these genes enhanced the sunflower's ability to withstand water-deficit conditions by modulating cellular homeostasis and stress signaling (Lee *et al.,* 2022).

Sunflower genetic resources and collections

The preserved genetic diversity within national and global sunflower (*H. annuus* L.) collections constitute a cornerstone for sustainable seed production, further genetic improvement, and long-term food security. The continuous domestication, intensive hybridization, and directional selection during the 20th and 21st centuries have narrowed the genetic base of elite cultivars, rendering the conservation and systematic study of the primary, secondary, and tertiary gene pools as an urgent scientific priority (Seiler and Gulya, 2016; Hladni *et al.,* 2021).

Scope and structure of sunflower collections

International gene banks, such as the USDA-ARS National Plant Germplasm System (NPGS, USA), the Vavilov All-Russian

Table 1. Sunflower genetic resources - major global collection (Seiler and Brothers*,* 2017)**.**

Collection/repository	Country	Number of accessions	Types of accessions	Notable features
USDA-ARS NPGS	USA	3700+	Cultivated, wild, landraces	Largest wild species diversity
VIR (Vavilov Institute)	Russia	2000+	Landraces, wild, historic	Historic landraces, wild *Helianthus* spp.
INRAE	France	1000+	Seed production lines, hybrids	High-oil, broomrape-resistant lines
EMBRAPA	Brazil	800+	Local and adapted lines	Abiotic stress tolerance collection
National Genebank of China	China	900+	Land races, wild, seed production lines	Regional adaptation, disease resistance
INTA	Argentina	600+	Hybrids, wild, seed production lines	South American wild relatives
Others (India, Turkey)	Various	2000+ (total)	National accessions, wild spp.	Local adaptation, unique genotypes

Table 2. Structure and utilization of sunflower gene pools in modern seed production (Seiler and Gulya, 2016).

Gene pool	Representative species / taxa	Crossability with cultivated sunflower	Key traits introduced to cultivated sunflower	Practical seed production applications
Primary	*H. annuus* (cultivated and wild), *H. petiolaris*	Direct, high compatibility	Yield, oil content, plant architecture, phenology, and basic disease resistance	Hybrid and open-pollinated variety development and direct-trait selection
Secondary	*H. tuberosus*, *H. maximiliani*, *H. nuttallii*, *H. grosseserratus*, other perennial *Helianthus* spp.	Partial; requires bridging crosses or embryo rescue	Durable disease resistance (downy mildew, rust, broomrape), abiotic stress tolerance (drought, salinity, and cold), cytoplasmic diversity	Pre-seed production, introgression of stress, and disease resistance
Tertiary	Distant wild *Helianthus* spp. (*H. deserticola*, *H. arizonensis*, *H. debilis*), interspecific hybrids	Difficult; needs advanced biotechnological approaches (somatic hybridization and molecular markers)	Cytoplasmic male sterility (CMS), novel resistances (*Sclerotinia* and insects), unique, adaptive, and metabolic traits	CMS system development, creation of unique cytoplasms, and advanced gene discovery

Institute of Plant Genetic Resources (VIR, Russia), and the INRAE (National Research Institute for Agriculture, Food, and the Environment—France), maintained over 10,000 sunflower accessions representing cultivated, wild, landrace, and related *Helianthus* species (Seiler and Brothers, 2017). The USDA sunflower collection alone comprises more than 3700 accessions, including wild taxa, primitive landraces, obsolete cultivars, and advanced seed production lines. The national repositories in Argentina, China, India, Turkey, and other countries collectively add several thousand unique accessions, further broadening the global gene pool of sunflower (Tables 1 and 2).

Utilization and characterization

Ex-situ collections comprising relative characteristics include morphological descriptors (plant height, flowering time, and capitulum diameter), phenological plasticity, oil and protein content, and resistance to major pathogens (downy mildew, rust, broomrape, and Sclerotinia). Over the past decade, molecular marker systems (SSR, SNP, AFLP, and GBS) have become standard for assessing genetic structure, diversity indices, and core collection assembly (Qi *et al.,* 2015; Kaya *et al.,* 2020).

The current studies employing high-density genotyping arrays and next-generation sequencing have uncovered novel quantitative trait loci (QTL) for drought tolerance, fatty acid biosynthesis, and resistance to broomrape (*Orobanche cumana*) and Sclerotinia stem rot, facilitating marker-assisted selection (MAS) and genomic selection pipelines (Badouin *et al.,* 2017; Hübner *et al.,* 2019).

Global importance for seed production

The genetic resources of sunflower are indispensable for seed production programs aimed at increasing yield potential, oil quality, climate resilience, and resistance to emerging biotic threats. Introgression from wild species has resulted in the release of selectively bred hybrids with enhanced drought and salt tolerance (Jan and Seiler, 2022), as well as improved resistance to diseases and parasitic weeds. International pre-seed production consortia and collaborative projects, such as the Sunflower Association Genetics Network (SAGNET) and the International Sunflower Genomics Initiative, accelerate the germplasm evaluation and data exchange, promoting global research synergies.

Challenges and prospects

Despite advances in gene bank management and high-throughput genotyping, several challenges persist, i.e., underrepresentation of wild and primitive landraces, limited passport and phenotypic data for the accessions, and the gaps in collection of endemic *Helianthus* taxa. Conservation strategies increasingly prioritize in situ protection, digital gene banking (genome sequencing), and coordinated core collection development to maximize genetic utility and minimize redundancy. In conclusion, the efficient conservation, characterization, and utilization of sunflower genetic collection explored the scientific progress of crop improvement and resilience and sustainability of future agricultural systems in the face of climate and market volatility (Miller and Seiler, 2017).

Molecular genetics of sunflower

The molecular genetics application has fundamentally transformed sunflower (*H. annuus* L.) seed production and research, enabling the dissection of complex traits and accelerating the development of superior cultivars. Advances in DNA marker technologies, genome sequencing, transcriptomics, and functional genomics have also provided unprecedented insights into the structure, diversity, and regulatory mechanisms underlying key agronomic traits, such as oil composition, disease resistance, abiotic stress tolerance, and flowering time (Badouin *et al.,* 2017; Hübner *et al.,* 2019).

Genome Sequencing and Structure: The sequencing of sunflower reference genome 3.6 Gb revealed a large, highly repetitive genome with extensive segmental duplication (Badouin and Gouzy*,* 2017). The genome encodes approximately 52,000 predicted genes, including gene families associated with lipid metabolism, disease resistance (NBS-LRR), photoperiod sensitivity, and environmental adaptation. Pan-genome analyses have demonstrated that hybridization, introgression from wild relatives, and ongoing selection have resulted in substantial structural and copy-number variation, particularly at loci controlling disease resistance and oil biosynthesis (Hübner *et al.,* 2019).

Molecular Marker Systems and Diversity Analysis: Molecular marker platforms, such as simple sequence repeats (SSR), single nucleotide polymorphisms (SNP), amplified fragment length polymorphisms (AFLP), and genotyping-by-sequencing (GBS), have revolutionized the assessment of genetic diversity, population structure, and phylogenetic relationship within and among *Helianthus* species (Kaya *et al.,* 2020). High-density SNP arrays now enable genome-wide association studies (GWAS), quantitative trait loci (QTL) mapping, and genomic selection for complex traits and also dramatically increase the efficiency and precision of seed production systems (Qi *et al.,* 2015).

Marker-Assisted and Genomic Selection: Marker-assisted selection (MAS) has become a standard approach for introgressing resistance genes from wild relatives (Pl6 for downy mildew and Or5 for broomrape) into elite germplasm (Jan and Seiler, 2022). Genomic selection models, incorporating thousands of SNP markers, now allow for the prediction of seed production values for polygenic traits, leading to more rapid and cost-effective cultivar development compared with conventional methods. Recent GWAS have identified the QTLs for drought tolerance, resistance to key pathogens, seed yield, and oil content and composition (Qi *et al.,* 2015; Hladni *et al.,* 2021).

Functional genomics and gene editing: Functional genomics approaches, such as RNA-Seq, proteomics, and metabolomics, have elucidated the transcriptional networks and metabolic pathways governing flowering, oil biosynthesis, and stress responses. These studies provided candidate genes and molecular targets for genome editing. With the advent of CRISPR/Cas9 and related technologies, targeted mutagenesis of genes associated with fatty acid desaturation, plant height, and resistance mechanisms has numerous reports (Qi *et al.,* 2016; Jin *et al.,* 2023).

Integration of phenotypic selection and seed production

The combined strategy of molecular tools and high-throughput phenotyping with traditional seed production will enhance the resolution, speed, and reliability of cultivar development. International collaborative initiatives, such as the International Sunflower Genomics Consortium and national genomics programs in the USA, France, and China, continue to expand the functional annotation of the sunflower genome. Furthermore, such initiatives helped identify allelic variants relevant to productivity, oil quality, disease resistance, and climate adaptation (Hübner *et al.,* 2019). In summary, molecular genetics has become indispensable for modern sunflower seed production, enabling the identification, mapping, and manipulation of genetic factors controlling agronomic traits (Miller and Seiler, 2017).

The integration of genomic resources, marker technologies, and functional gene analysis is accelerating the delivery of resilient, high-yielding, and quality-improved sunflower cultivars for global agriculture. In total, the *H. annuus* EST collection (93,428 sequences) contained just over half of the genes in our search (82 of 155 total). Expanding the search to the EST collection of related sunflower species (189,585 additional sequences) led to the identification of homologs of 31 additional genes (Blackman *et al.,* 2011). Plant height at flowering, flowering date, and percent humidity of seed at harvest are characters regularly measured in sunflower breeding programs. This is mostly to avoid very tall and very late-maturing breeding materials and to have a complete knowledge of inbred lines and hybrids (Vear, 2016).

Sunflower oilseed quality is a key trait for both edible oil production and industrial applications. Recent advances in genomics, breeding technologies, and biotechnological tools have sufficiently enhanced our understanding of the genetic basis underlying important quality traits, such as oil content, fatty acid composition, and resistance to environmental stress conditions (Velasco and Fernández-Martínez, 2019). Genetic improvement of the sunflower for resistance to *Sclerotinia sclerotiorum* has made significant progress in past years. Identification of resistant sources and the application of molecular markers have considerably accelerated the breeding programs. However, the resistance is quantitatively inherited, with influences from environmental factors, which further complicates the selection (Hladni *et al.,* 2018; Wu *et al.,* 2021).

MADS-box* genes play a crucial role in plant growth and development, particularly in plant growth and development, flowering, and seed formation. In sunflower, the MADS-box gene family underwent identification and systematic analysis at the whole-genome level. The identified 89 MADS-box genes received type I and type II group classifications (Wang *et al.,* 2019). (*Acronym origin of MADS: Derived from the first four identified members:

MCM1 [yeast], AGAMOUS [Arabidopsis], DEFICIENS [Antirrhinum], and SRF [human]).

CONCLUSIONS

The genetic, morphological, and molecular diversity of sunflower (*H. annuus* L.) forms the scientific basis for sustainable sunflower seed production. The integration of molecular and traditional seed production methods enabled the development of high-yielding, oil-rich, and stress-resistant cultivars that address the challenges of climate change and evolving pathogens. Comprehensive conservation and systematic utilization of global genetic resources are essential for ensuring future food and oil security. In molecular genetics and genomics, the continued investment will further accelerate the development of resilient and market-oriented sunflower genotypes for global agriculture.

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