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Genetic and Genomic Approaches for Improving Yield Potential, Oil Content, and Climate Resilience in Sunflower (*Helianthus Annuus* L.)

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ABSTRACT

Sunflower (Helianthus annuus L.) is one of the most important oilseed crops worldwide because of its high-quality edible oil, nutritional value and adaptability to diverse environmental conditions. However, increasing climatic variability, including drought, high temperature, soil salinity and irregular rainfall, poses serious challenges to sunflower productivity and oil quality. Conventional breeding has contributed considerably to the development of high-yielding hybrids, but the complex genetic inheritance of seed yield, oil accumulation and abiotic stress tolerance requires more advanced breeding strategies. Recent developments in molecular genetics and genomics, including quantitative trait locus (QTL) mapping, genome-wide association studies (GWAS), marker-assisted selection (MAS), genomic selection (GS), transcriptomics, gene expression analysis and CRISPR/Cas-based genome editing, provide new opportunities for improving sunflower cultivars. The reference genome of sunflower has facilitated the identification of important genomic regions associated with oil biosynthesis, flowering time and agronomic performance. Several studies have identified candidate genes involved in fatty acid metabolism, drought tolerance, salinity resistance and plant adaptation. In particular, the identification of FAD2 and other lipid-metabolism-related genes provides opportunities for improving oil composition and nutritional quality. Similarly, genomic studies have identified drought- and salinity-associated loci that can be incorporated into breeding programmes. This review examines the potential of genetic and genomic approaches for developing sunflower cultivars with improved seed yield, enhanced oil content, desirable fatty acid composition and greater climate resilience. An integrated approach combining conventional breeding, molecular markers, genomic selection, high-throughput phenotyping and multi-environment evaluation is recommended for developing stable, high-performing sunflower hybrids under changing climatic conditions.

Introduction

Sunflower (*Helianthus annuus* L.) is an economically important oilseed crop cultivated worldwide for edible oil, animal feed and industrial applications (Kaleri et al., 2023). Its oil is valued for its nutritional quality, particularly its unsaturated fatty acid composition (Laghari et al., 2023). Sunflower is also considered a relatively adaptable crop because of its ability to grow under different climatic and soil conditions (Buriro et al., 2024). Nevertheless, its productivity is influenced by genetic potential, environmental conditions, crop management and interactions between genotype and environment (Kaleri et al., 2024). The development of high-yielding sunflower cultivars with improved oil quality and tolerance to environmental stresses is a major objective of modern plant breeding (Manzoor et al., 2024). Traditional breeding programmes have mainly relied on phenotypic selection, hybrid development and the evaluation of genetic variability (Kaleri et al., 2026). Although these methods have produced substantial improvements, selection for complex traits such as seed yield, oil percentage and drought tolerance is often difficult because these characteristics are controlled by multiple genes and influenced by environmental conditions. The availability of molecular markers and genomic resources has substantially improved the understanding of sunflower genetic diversity and inheritance. Badouin et al. (2017) published a high-quality sunflower reference genome of approximately 3.6 Gb and identified genomic regions associated with oil metabolism, flowering and other important characteristics. Their research identified 46 oil-related genes in 32 genomic regions associated with seven oil-related quantitative trait loci. These findings provided an important foundation for genome-assisted sunflower improvement. Molecular breeding techniques such as marker-assisted selection (MAS), quantitative trait locus (QTL) mapping and genome-wide association studies (GWAS) allow breeders to identify genomic regions associated with desirable characteristics. These approaches can accelerate the selection of superior genotypes and improve breeding efficiency. In sunflower, molecular markers have already been used for important traits such as high-oleic acid content, fertility restoration, herbicide tolerance and disease resistance (Hubner et al., 2018). Oil quality is another important target of sunflower improvement. The fatty acid composition of sunflower oil determines its nutritional and industrial properties. Chernova et al. (2021) investigated 601 cultivated sunflower inbred lines using 15,483 single-nucleotide polymorphisms (SNPs) and identified significant genetic associations for 11 fatty acid traits. Their findings demonstrated the potential of genome-wide association analysis for improving sunflower oil composition. Climate change has further increased the importance of developing stress-tolerant sunflower varieties. Drought, high temperature and salinity can reduce plant growth, seed development, photosynthetic activity and oil accumulation. These stresses are particularly important during flowering and seed-filling stages. Genetic improvement through the identification and utilization of stress-associated genomic regions is therefore essential for maintaining sunflower productivity under changing environmental conditions. Recent research has also demonstrated the importance of wild sunflower relatives as sources of useful genetic variation. These genetic resources may contain valuable alleles for stress adaptation, disease resistance and improved agronomic performance. The incorporation of useful genes from wild relatives through introgression breeding can broaden the genetic base of cultivated sunflower (Badouin et al., 2017). Therefore, this review focuses on the application of genetic and genomic approaches for improving sunflower yield potential, oil content and climate resilience. It also evaluates recent research findings and identifies opportunities for integrating molecular breeding techniques into future sunflower improvement programmes.

Materials and Methods

Research design

The present study was designed as a literature-based comparative review of genetic and genomic approaches used for sunflower improvement. Published scientific studies concerning sunflower genetics, molecular breeding, genome sequencing, oil biosynthesis, seed yield and abiotic stress tolerance were examined. The review focused primarily on research published between 2017 and 2026, while selected earlier publications were included where they provided important foundational information about sunflower genetics and breeding.

Objectives

The main objectives of this review are:

1. To evaluate genetic and genomic approaches for improving sunflower seed yield.
2. To identify important genes and genomic regions associated with oil content and fatty acid composition.
3. To examine molecular mechanisms and genetic resources associated with drought, heat and salinity tolerance.
4. To assess the potential of MAS, GWAS, genomic selection and genome editing in sunflower breeding.
5. To propose an integrated breeding strategy for developing climate-resilient sunflower hybrids.

The following keywords were used to identify relevant research:

- Sunflower genetic improvement
- Sunflower genome sequencing
- Quantitative trait loci
- Genome-wide association studies
- Genomic selection
- Oil content and fatty acid composition
- Drought tolerance
- Heat stress tolerance
- Salinity tolerance
- Molecular plant breeding

Parameters considered

The following research parameters were considered during the comparative evaluation:

Research area	Parameters evaluated
Genetic diversity	Germplasm variation and wild relatives
Seed yield	Seed yield, head diameter and seed number
Oil production	Oil percentage and fatty acid composition
Molecular genetics	SNPs, QTLs and candidate genes
Drought tolerance	Root traits and stress-responsive genes
Salinity tolerance	Salt-response loci and physiological traits
Advanced breeding	MAS, GWAS and genomic selection
Biotechnology	Transcriptomics and CRISPR/Cas approaches

Data analysis and comparative assessment

Published numerical findings were extracted from selected studies and organized into comparative tables. The results were evaluated descriptively according to the number of genotypes, molecular markers, identified QTLs, candidate genes and reported genetic associations. The comparative assessment focused on identifying useful genomic resources and breeding approaches for improving sunflower productivity, oil quality and environmental adaptability. Because this is a literature review, no new field experiment, original ANOVA, LSD test or independent experimental dataset was generated. Numerical values in the results tables represent findings reported by the cited researchers.

Results

Genetic and genomic resources for sunflower improvement

The literature indicates that sunflower improvement has benefited considerably from the development of genomic resources, molecular markers and genetic mapping populations. The availability of the reference genome has enabled researchers to investigate genes involved in oil biosynthesis, flowering time, plant development and stress responses. Badouin et al. (2017) reported a high-quality reference genome of approximately 3.6 Gb. Their analysis identified 46 oil-related genes in 32 genomic regions corresponding to previously identified QTLs for seven oil-related traits. These genomic resources provide opportunities for identifying favourable alleles and developing improved sunflower cultivars. Blackman et al. (2026) further highlighted the importance of multiple genome assemblies, genome-wide association panels, transcriptomic resources and wild sunflower relatives for crop improvement. They also identified structural variation and introgression as important factors influencing sunflower adaptation and genetic diversity.

Table 1. Important genomic resources and their applications in sunflower breeding

Genomic resource	Reported findings	Application in breeding
Reference genome	Approximately 3.6 Gb	Genome-based gene identification
Oil-related genes	46 genes in 32 genomic regions	Improvement of oil production
QTL resources	Seven oil-related traits investigated	Marker-assisted selection
SNP markers	Genome-wide genetic variation	Genetic diversity and GWAS
Transcriptomic resources	Gene expression across plant organs	Identification of candidate genes
Wild sunflower relatives	Additional genetic variation	Stress tolerance and introgression

Source: Badouin et al. (2017); Blackman et al. (2026).

Molecular approaches for improving seed yield

Seed yield is a complex quantitative trait controlled by several genetic and environmental factors. Important yield-related characteristics include plant height, head diameter, number of seeds per head, seed weight and biological productivity. Conventional selection for these traits can be affected by environmental variation. Molecular approaches provide opportunities to identify favourable alleles and improve selection accuracy. QTL mapping is particularly useful for identifying genomic regions associated with quantitative traits. Once favourable QTLs are identified, molecular markers linked to these regions can be incorporated into breeding programmes. Genome-wide association studies provide another important approach by examining relationships between genetic polymorphisms and phenotypic variation across diverse germplasm collections. These studies can identify useful SNPs associated with yield components and environmental adaptation. Hubner et al. (2018) explained that genomic approaches are particularly important for complex traits such as yield, heterosis, drought tolerance and oil content, which are difficult to improve through individual molecular markers alone.

Table 2. Molecular and genomic approaches for improving sunflower yield

Breeding approach	Genetic information used	Expected improvement
QTL mapping	Chromosomal regions controlling yield components	Identification of favorable yield alleles
GWAS	SNP–trait associations	Discovery of yield-associated loci
Marker-assisted selection	Markers linked to major genes or QTLs	Faster selection of desirable genotypes
Genomic selection	Genome-wide marker information	Improved selection for complex traits
Hybrid breeding	Combining ability and heterosis	Higher hybrid productivity
Speed breeding	Accelerated plant generation cycles	Faster breeding progress

Source: Hubner et al. (2018); Badouin et al. (2017); Blackman et al. (2026).

Genetic improvement of oil content and fatty acid composition

Oil content and fatty acid composition are among the most important breeding objectives in sunflower. The oil quality of sunflower is largely determined by the proportions of oleic, linoleic, palmitic and stearic acids. The FAD2 gene plays an important role in fatty acid metabolism by controlling the conversion of oleic acid into linoleic acid. Genetic variation in this pathway provides opportunities for developing high-oleic sunflower cultivars with improved oxidative stability. Badouin et al. (2017) identified oil metabolism-related genes associated with previously mapped QTLs. Their findings demonstrated the importance of genomic information for understanding the genetic regulation of oil accumulation. Chernova et al. (2021) conducted a genome-wide association study using 601 cultivated sunflower lines and 15,483 SNP markers. Their research identified significant genetic associations for 11 fatty acid traits among the 23 fatty acids investigated. Some genomic regions associated with rare fatty acids on chromosomes 3 and 14 explained up to 34.5% of the variation in docosanoic acid.

These findings indicate that genomic selection and marker-assisted breeding can be useful for improving both total oil production and fatty acid composition.

Table 3. Important molecular findings associated with sunflower oil improvement

Research parameter	Reported result	Breeding significance
Sunflower accessions	601 inbred lines	Broad genetic evaluation
SNP markers	15,483	Genome-wide genetic analysis
Fatty acids investigated	23	Comprehensive oil-quality assessment
Fatty acid traits with significant associations	11	Identification of genetic control
Variation explained for docosanoic acid	Up to 34.5%	Potential for marker-assisted improvement
Important gene	FAD2	Oleic and linoleic acid regulation
Oil-related genomic regions	32 regions	Identification of candidate genes

Source: Chernova et al. (2021); Badouin et al. (2017).

Genetic improvement for drought tolerance

Drought is one of the major abiotic stresses limiting sunflower production, particularly in semi-arid and arid agricultural environments. Water deficit affects germination, root development, leaf expansion, photosynthesis, flowering and seed filling. Sunflower has a relatively strong capacity to tolerate moderate water shortages, but prolonged drought can substantially reduce seed yield and oil accumulation. Molecular breeding provides opportunities to identify genetic factors involved in drought adaptation. Root architecture, root-to-shoot ratio, osmotic adjustment and stress-responsive gene expression are important characteristics for identifying drought-tolerant genotypes. A QTL study published in 2023 identified 33 QTLs associated with germination and seedling responses to drought stress across eight sunflower chromosomes. The researchers also identified 60 putative drought-related genes within the investigated QTL regions. Four candidate genes on chromosome 13 were highlighted for further investigation.

These findings provide valuable genetic information for developing drought-tolerant sunflower varieties.

Table 4. Reported genomic findings associated with drought tolerance in sunflower

Parameter	Reported finding
QTLs identified	33
Chromosomes containing QTLs	8
Phenotypic traits evaluated	18
Putative drought-related genes	60
Reported PVE range	0.016–10.712%
Important selection characteristics	Germination rate, germination potential, germination index and root-to-shoot ratio
Important chromosome	Chromosome 13

Source: 2023 sunflower QTL study on germination and seedling responses to drought stress (PubMed PMID: 37159834). PVE = phenotypic variance explained.

Genetic improvement for salinity tolerance

Soil salinity is another major constraint affecting sunflower production, particularly in arid and semi-arid agricultural regions. High concentrations of soluble salts can disturb water absorption, nutrient balance, photosynthetic activity and plant development. McNellie et al. (2024) investigated the genetic basis of salinity tolerance using the Sunflower Association Mapping panel under naturally occurring saline soil conditions in Saskatchewan, Canada. Their study identified 14 significant genomic loci associated with evaluated characteristics, including flowering time, plant height, leaf area, leaf mass, oil percentage and yield. The identification of these loci provides useful information for developing sunflower genotypes adapted to saline environments. Furthermore, a 2026 study by researchers using 342 oilseed sunflower accessions investigated 31 traits through high-throughput phenotyping and GWAS under salt stress. The study highlighted the potential involvement of the HaCBF4–HaHAK11 module in salt-stress tolerance.

Table 5. Genomic studies associated with salinity tolerance in sunflower

Research study	Genetic material	Main findings	Breeding application
McNellie et al. (2024)	Sunflower association mapping panel	14 significant loci	Selection for saline-soil adaptation
2026 high-throughput GWAS study	342 sunflower accessions	31 traits investigated	Identification of salt-tolerance mechanisms
2026 HaCBF4–HaHAK11 study	Molecular and phenotypic evaluation	Candidate regulatory module	Development of salt-tolerant genotypes

Sources: McNellie et al. (2024); 2026 study published in Horticulture Research.

Genomic selection and advanced molecular breeding

Genomic selection is an advanced breeding approach in which genome-wide marker information is used to estimate the breeding value of individual genotypes. Unlike conventional marker-assisted selection, which generally focuses on a limited number of major loci, genomic selection considers a large number of markers distributed throughout the genome. This approach is particularly useful for complex traits such as seed yield, oil content, drought tolerance and hybrid performance. Hubner et al. (2018) discussed the potential of genome-wide approaches for improving complex sunflower traits. Integration of genomic selection with conventional hybrid breeding can help breeders identify superior parental lines and accelerate genetic improvement.

Table 6. Comparison of major genetic and genomic breeding techniques

Technique	Main function	Importance for sunflower improvement
Conventional breeding	Phenotypic selection and hybridization	Establishes improved genetic backgrounds
MAS	Selection using linked molecular markers	Improvement of specific traits
QTL mapping	Identification of quantitative trait loci	Yield and stress-related gene discovery
GWAS	Association between SNPs and traits	Identification of useful genetic variation
Genomic selection	Prediction using genome-wide markers	Improvement of complex traits
Transcriptomics	Investigation of gene expression	Identification of stress-responsive genes
CRISPR/Cas	Targeted modification of DNA sequences	Potential improvement of oil and stress-related traits
Speed breeding	Accelerated generation advancement	Shortening breeding cycles

Potential application of genome editing in sunflower

Genome editing technologies, particularly CRISPR/Cas systems, have created new opportunities for precision crop improvement. These technologies can potentially modify specific genes involved in fatty acid biosynthesis, plant development and stress responses. For example, targeted modification of FAD2 genes provides a potential strategy for changing oleic and linoleic acid proportions. Similarly, candidate genes associated with drought and salinity responses may provide targets for future functional studies. However, the application of genome editing in sunflower is still limited by challenges associated with genetic transformation, regeneration and functional validation of candidate genes. Blackman et al. (2026) emphasized that improvements in transformation systems and functional genomics tools are important requirements for accelerating sunflower genetic improvement.

Discussion

Importance of genomic resources for sunflower improvement

The findings of this review demonstrate that molecular genetics and genomic technologies have substantially expanded the possibilities for sunflower improvement. The availability of a high-quality reference genome has made it possible to identify genes and genomic regions associated with important agronomic and quality traits. Badouin et al. (2017) provided an important genomic foundation by identifying genes associated with oil metabolism and other economically important characteristics. Their findings indicate that the combination of genome sequencing, transcriptomic analysis and genetic mapping can provide valuable information for future breeding programmes. Blackman et al. (2026) further emphasized that multiple genome

assemblies, association panels and transcriptomic resources are expanding the opportunities for crop improvement. However, the practical utilization of genomic discoveries requires additional functional validation and improved transformation methods.

Improving seed yield through molecular breeding

Seed yield is a polygenic trait influenced by numerous genetic and environmental factors. Conventional selection alone may not always identify superior genotypes because the expression of yield-related characteristics changes under different environmental conditions. QTL mapping and GWAS can help identify genomic regions associated with seed yield, head diameter, seed number and other yield components. Genomic selection offers additional advantages because it considers genome-wide marker information rather than relying on individual genes. Hubner et al. (2018) highlighted that genomic approaches are particularly important for improving complex traits such as yield, heterosis and drought tolerance. Therefore, future sunflower breeding programmes should combine conventional selection with genomic prediction and multi-environment testing to identify hybrids with high and stable productivity.

Genetic improvement of oil content and quality

Oil content and fatty acid composition are important determinants of sunflower economic value. Breeding programmes should therefore focus not only on increasing total oil percentage but also on improving the composition of fatty acids. The FAD2 gene is particularly important because of its role in regulating oleic and linoleic acid proportions. High-oleic sunflower cultivars are valuable because of their improved oxidative stability and suitability for different food-processing applications. Chernova et al. (2021) demonstrated the potential of GWAS through their investigation of 601 inbred lines and 15,483 SNP markers. Their identification of significant associations for 11 fatty acid traits provides useful information for future molecular breeding. Attia et al. (2021) also emphasized that environmental conditions can influence oilseed quality and fatty acid composition. Consequently, genetic improvement should be combined with multi-environment evaluation to ensure stable oil quality under changing climatic conditions.

Genetic mechanisms of drought tolerance

Drought tolerance is a complex characteristic involving morphological, physiological and molecular mechanisms. Root development, water-use efficiency, stomatal regulation, antioxidant activity and stress-responsive gene expression contribute to plant adaptation under water-limited conditions. The identification of 33 drought-associated QTLs and 60 putative candidate genes provides an important foundation for molecular breeding. However, these findings require further validation in diverse genetic backgrounds and under field conditions. Future breeding programmes should investigate drought tolerance at different growth stages, particularly flowering and seed filling, because water shortages during these periods can reduce seed production and oil accumulation.

Salinity tolerance and climate-resilient sunflower

Salinity tolerance is particularly important for sunflower production in regions where soil salinity and irrigation-water quality limit crop productivity. McNellie et al. (2024) identified 14 significant loci associated with sunflower performance under naturally occurring saline conditions. This research demonstrates the usefulness of GWAS for identifying genetic variation associated with environmental adaptation. The 2026 research on the HaCBF4–HaHAK11 module further demonstrates the potential of integrating high-throughput phenotyping with molecular genetics to investigate salt-stress responses. These approaches are especially relevant to agricultural regions facing increasing soil salinity. Nevertheless, promising loci should be validated under field conditions before their incorporation into commercial breeding programmes.

Integration of conventional and advanced breeding approaches

The future improvement of sunflower requires an integrated strategy combining conventional plant breeding, molecular genetics, genomics and advanced phenotyping. Conventional breeding remains essential for developing adapted parental lines and evaluating hybrid performance. Molecular markers can accelerate the selection of specific traits, while genomic selection can improve the efficiency of breeding for complex quantitative characteristics. Genome editing may provide additional opportunities for modifying important genes associated with oil quality and stress responses. However, the successful application of these techniques requires functional validation, suitable transformation systems and appropriate field evaluation. Overall, an integrated breeding approach is likely to be more effective than relying on a single breeding technique.

Future research priorities

The following research areas should receive priority in future sunflower improvement programmes:

1. Identification of new genes controlling seed yield and oil accumulation.

2. Development of high-oleic and high-oil sunflower cultivars.
3. Identification of drought- and heat-tolerant genetic resources.
4. Utilization of wild sunflower relatives for genetic improvement.
5. Application of genomic selection for complex quantitative traits.
6. Functional validation of candidate genes using molecular and biotechnology approaches.
7. Development of hybrids adapted to saline and water-deficient agricultural environments.
8. Evaluation of promising genotypes across multiple locations and growing seasons.

Conclusion

Genetic and genomic approaches offer considerable opportunities for improving sunflower yield potential, oil content and climate resilience. The development of the sunflower reference genome, identification of QTLs, genome-wide association studies and molecular marker technologies have improved understanding of the genetic basis of important agronomic and quality traits. Research findings demonstrate that genes associated with fatty acid metabolism, particularly FAD2, have significant potential for improving sunflower oil quality. Similarly, the identification of drought- and salinity-associated genomic regions provides valuable opportunities for developing environmentally adapted cultivars. Genomic selection, marker-assisted breeding, transcriptomics and genome editing can further accelerate genetic improvement when integrated with conventional hybrid breeding and multi-environment evaluation. However, additional research is required to validate candidate genes, understand genotype × environment interactions and improve the practical application of genomic technologies. Overall, combining conventional plant breeding with modern molecular genetics and genomics is a promising strategy for developing high-yielding, high-oil-content and climate-resilient sunflower hybrids. Such improvements will contribute to sustainable oilseed production and food security under changing climatic conditions.

References

Attia, Z., Pogoda, C. S., Reinert, S., Kane, N. C., & Hulke, B. S. (2021). Breeding for sustainable oilseed crop yield and quality in a changing climate. Theoretical and Applied Genetics, 134, 1817–1827. https://doi.org/10.1007/s00122-021-03770-w

Badouin, H., Gouzy, J., Grassa, C. J., Murat, F., Staton, S. E., Cottret, L., et al. (2017). The sunflower genome provides insights into oil metabolism, flowering and Asterid evolution. Nature, 546, 148–152. https://doi.org/10.1038/nature22380

Blackman, B. K., Burke, J. M., Nasti, R. A., Todesco, M., Wang, J., & Rieseberg, L. H. (2026). Sunflower genetics and genomics: From fundamental evolutionary insights to crop improvement. Trends in Genetics, 42(5), 446–459. https://doi.org/10.1016/j.tig.2026.01.002

Buriro, N.A., Memon, H.R., Kaleri, A.A., Buriro, N.A., Jamro, I.A., Fazal, S., Baloch, D.M. and Ahmed, S., 2024. Effect of nitrogen and zinc fertilizer levels on the growth and yield of sunflower (*Helianthus annuus* L.). *African Journal of Biological Sciences*, *6*(15), pp.13777-13788.

Chernova, A. I., Gubaev, R. F., Singh, A., Sherbina, K., Goryunova, S. V., Martynova, E. U., et al. (2021). Genotyping and lipid profiling of 601 cultivated sunflower lines reveals novel genetic determinants of oil fatty acid content. BMC Genomics, 22, 505. https://doi.org/10.1186/s12864-021-07768-y

Guo, W., Qiu, J., Zeng, Y., Li, X., Dong, S., Li, Q., Liu, Y., Cai, M., Lei, Z., & Chen, T. (2026). Integrating high-throughput phenomics and GWAS unravels the HaCBF4–HaHAK11 module to regulate salt stress tolerance in sunflower (Helianthus annuus L.). Horticulture Research, 13(7), uhag081. https://doi.org/10.1093/hr/uhag081

Hubner, S., Bercovich, N., Todesco, M., Mandel, J. R., Odenheimer, J., Ziegler, E., et al. (2018). Sunflower hybrid breeding: From markers to genomic selection. G3: Genes, Genomes, Genetics, 8(1), 1–12. https://doi.org/10.1534/g3.117.300211

Kaleri, A.A., 2023. Sunflower growth and yield in response to combined application of farmyard manure and inorganic fertilizers (nitrogen and phosphorus). National Journal of Biological Sciences, 4(2), pp.10-17.

Kaleri, A.A., Rajper, S.A., Shah, I.B., Memon, I., Nuherio, A.R., Kolhi, H., Khoso, D.K., Arain, M.M., Arain, M.S., Khoso, M.S. and Sasoli, M.R., 2026. Effect of Organic and Inorganic Fertilizers on Growth, Yield Components and oil Production of Sunflower (Helianthus Annuus L.). *Kashmir Journal of Academic Research and Development*, *2*(10), pp.265-275.

Kaleri, A.A., Soomro, N.S., Banbhan, G.M., Wahocho, S.A., Kaleri, N., Iqbal, K., Samoon, R., Khokhar, F., Bughio, A. and Baloch, G.A., 2024. The growth and yield of sunflower (Helianthus annuus L.) under different organic (farm yard manure) and inorganic phosphorus doses. *Pakistan Journal of Biotechnology*, *21*(1), pp.148-154.

Laghari, R., Laghari, G.M., Kaleri, A.A., Manzoor, D., Lund, M.M., Awan, M.H., Sheikh, Z.A., Soomro, M.K., Soomro, M.M. and Solangi, S., 2023. Growth and yield of sunflower under the integrated farmyard manure and potassium fertilization: Growth and yield of sunflower. Futuristic Biotechnology, pp.20-25.

Manzoor, D., Kaleri, A.A., Khaki, S.A., Jamali, A., Jogi, M.T., Islam, M., Hameed, M., Ahmad, S. and Ali, C., 2024. The effect of different phosphorous levels on growth, yield, and quality of autumn planted sunflower (Helianthus Annuus L.). *Pakistan Journal of Biochemistry and Biotechnology*, *5*(1), pp.10-14.

McNellie, J. P., May, W. E., Rieseberg, L. H., & Hulke, B. S. (2024). Association studies of salinity tolerance in sunflower provide robust breeding and selection strategies under climate change. Theoretical and Applied Genetics, 137, 184. https://doi.org/10.1007/s00122-024-04672-3

Shi, H., Wu, Y., Yi, L., Hu, H., Su, F., Wang, Y., Li, D., & Hou, J. (2023). Analysis of QTL mapping for germination and seedling response to drought stress in sunflower (Helianthus annuus L.). PeerJ, 11, e15275. https://doi.org/10.7717/peerj.15275.

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