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Review paper

Molecular marker utilization in oilseed crop breeding: a review

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Abstract: It has been observed that molecular markers are one of the most important tools in the advancement of oilseed crops and in developing varieties capable of withstanding drought, salinity, and high-temperature stresses. The present review focuses on the use of DNA-based molecular markers such as SSRs and SNPs in oilseed crop breeding. These markers, in addition to being able to identify and locate QTLs associated with stress tolerance, by using Marker-Assisted Selection (MAS) will aid in accelerating selection. Although the oilseed crops, including canola, soybean, and sunflower, have achieved certain levels of environmental stress tolerance, their inability to overcome abiotic stresses such as drought, salinity, and temperature extremes further dampens growth and productivity to contribute to the existing yield gap. However, the integration of molecular markers into breeding programs saves not only genetic diversity but also contributes to the quicker release of high-yielding varieties under extreme conditions. This review, therefore, enumerates examples of successful applications and emphasizes the future research needs of using molecular markers in breeding these under-investigated oilseed crops to build more robust world food systems resilient to global warming.

Keywords: Genetic variability, global warming, marker-assisted selection, quantitative trait loci.

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Introduction

With time, molecular markers have developed as one of the important tools for improvement in oilseed crops and can develop tolerant varieties against adverse environmental conditions like drought, salinity, and high temperatures. These markers allow for the identification of specific genetic traits linked to stress tolerance, enabling breeders to select and multiply only those plants which are most capable of surviving harsh climatic conditions.

Genetic mapping and marker-assisted selection (MAS)

Molecular markers are segments of DNA that may be associated with a specific plant trait. Genetic mapping requires them to locate the genes that control desirable traits such as drought tolerance and heat resistance. MAS uses these markers, therefore enabling its use to accelerate breeding processes and hence allowing new varieties of oilseeds to be developed more rapidly than would be possible by the use of traditional methods alone. This approach is crucial for crops like soybean, canola, and sunflower, which, in these years, have increasingly been cultivated at the mercy of climate change and attendant stresses.

Improvement of stress tolerance

Tolerance against abiotic stresses, such as drought or salinity, is one of the keys for preserving crop yields against unpredictable environmental changes (Lesk et al., 2022). Research has shown that molecular markers offer a shortcut to the identification of genes which may be involved in the stress response mechanism such as maintenance of osmotic balance and ion transport in plants (Teixido et al., 2021). Some of these genes are associated with water use efficiency and root depth, both being very important for drought tolerance (Kühn et al., 2022). In addition, identification of the genetic mechanisms underlying salinity resistance allows breeders to generate cultivars that can be cultivated in saline soils, which are increasingly becoming more common due to irrigation practices and climate change (Holsman, 2023).

Challenges and future directions

These advantages of molecular markers in developing resilient oilseed crops are encompassed by a number of challenges. Most of the resilient-related traits, for example, heat tolerance, generally result from a large number of genes interacting together. Such polygenic traits are challenging to identify and manipulate through conventional breeding approaches. Additionally, the complexity involved in isolating, cloning, and transforming quantitative traits, along with the public concerns and strict regulatory hurdles associated with GMOs, make developing crops with tolerance to abiotic stresses especially challenging (Lynas et al., 2022). Overcoming these challenges, research studies have continuously strived to integrate molecular markers into genomic technologies, such as CRISPR and other gene-editing tools (Segelbacher et al., 2022). These developments hold bright prospects for improving precision in breeding programs and for making rapid strides toward the development of oilseed varieties (Sinha et al., 2023). In other words, molecular markers, a revolutionary methodology, are now contributing to changing the face of oilseed crop breeding through the facilitation of developing varieties that are tolerant to drought, salinity, and high temperature (Soltabayeva et al., 2021). As this research goes on, this tool will undoubtedly contribute to developing more robust agricultural systems against a shifting climate (Lawrence et al., 2023). Application of different DNA-based molecular markers in the improvement of oilseed crops has resulted in a sea change in the breeding methodology to produce varieties with enhanced environmental stress tolerance and more suitable agricultural requirements. Among these, SSRs, RAPD, SNPs, and other types of molecular markers carry out genetic diversity enhancement, identification of desirable features within the crop, and speed up the breeding process (Malgaonkar et al., 2020; Adje et al., 2023).

Overview of DNA-based molecular markers

Simple sequence repeats (SSRs)

SSRs or microsatellites are small fragments of DNA that form tandem repeats and are highly polymorphic. Due to their abundance and stability over generations, they find wide applications in genetic mapping and diversity studies (Sunde et al., 2020; Baba Nitsa et al., 2023).

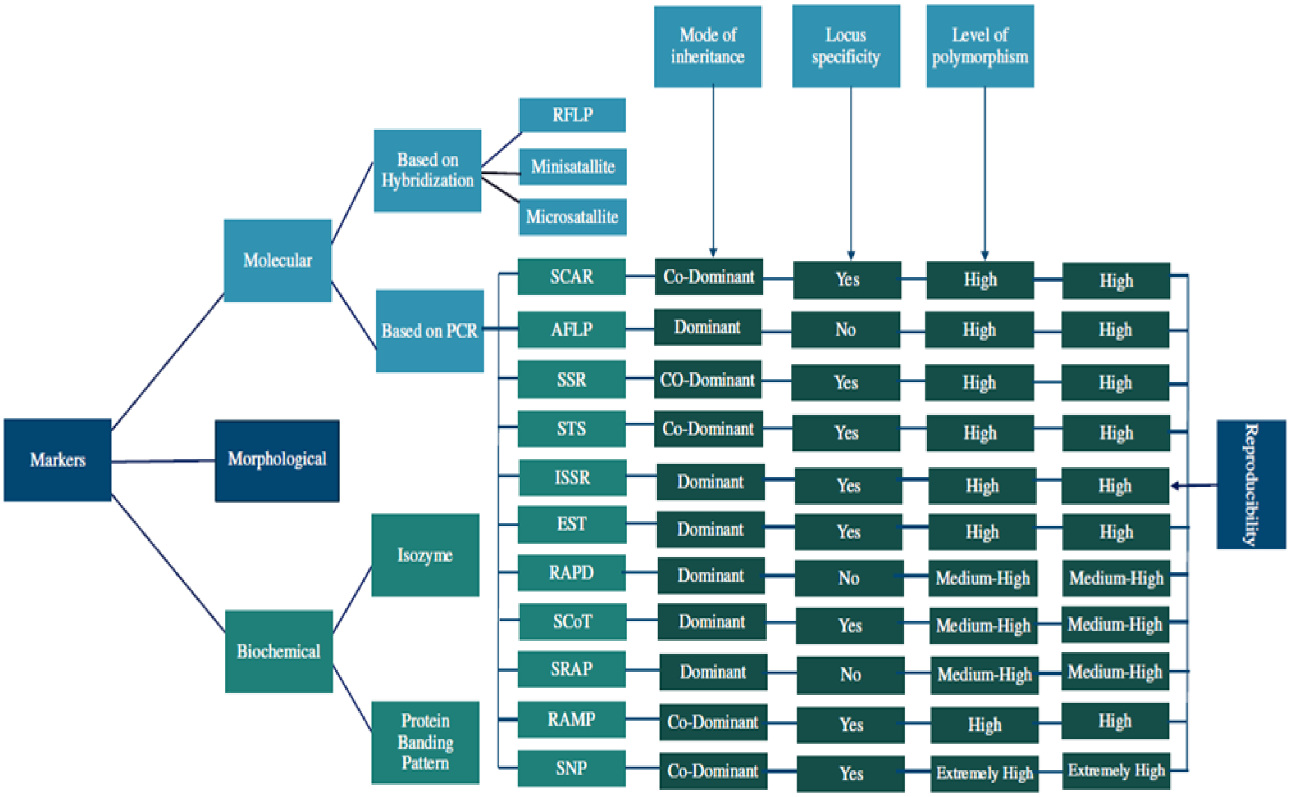

Figure 1. A flowchart that classifies various genetic markers based on their distinct features. Abbreviations represent RFLP: Restriction Fragment Length Polymorphism; SCAR: Sequence Characterized Amplified Region;AFLP: Amplified Fragment Length Polymorphism; SSR: Simple Sequence Repeat; STS: Sequence Tag Site; ISSR: Inter-Simple Sequence Repeat; RAPD: Random Amplified Polymorphic DNA;SCOT: Start Codon Targeted Polymorphism;SRAP: Sequence Related Amplified Polymorphism;RAMP: Random Amplified Microsatellite Polymorphism;SNP: Single Nucleotide Polymorphism.

In oilseed crops, SSRs allow the identification of genetic variation among cultivars, thereby enabling breeders to choose the best parental lines for hybridization (Heidari et al., 2023; Kour et al., 2023). Their codominant inheritance allows detailed insight into the genetic constitution of populations, which is a prerequisite for effective breeding strategies (Martin-Gutierrez et al., 2022).

Random amplified polymorphic DNA

In RAPD markers, random segments of the genomic DNA are amplified using short primers (usually 10 bases). The technique has the advantage of speed and reasonable low cost. As no prior information is required on the genome sequence, genetic diversity of improvement can easily be estimated using this marker. In oilseed crop improvement, RAPD has been utilized for detecting variation within and among cultivars that enable breeders to select the most promising lines in breeding programs (O'Brown et al., 2019; Hosseinpour Azad, 2023).

Single nucleotide polymorphisms

SNPs are the most common form of genetic variation among individuals in a population, where the variation involves a change in only one nucleotide (Walker et al., 2021). Because of their high density across the genome, they have been very important in studies of complex traits. They have widely been used in fine-mapping QTLs related to important agronomic traits such as yield and stress tolerance (Yang et al., 2021). High-throughput SNP genotyping enables the testing of very large populations with high efficiency and contributes to the acceleration of crop improvement (Allen et al., 2017). Figure 1 and Table 1 categorize different types of molecular markers along with their applications and characteristics.

Amplified fragment length polymorphism

Amplified fragment length polymorphism (AFLP) markers have been employed in oilseed research covering analysis of genetic diversity, identification of cultivars and mapping genes linked with tolerance to abiotic stress (Čurn et al., 2002). Oilseed rape has also been assessed for suitability as a subject of fluorescence-based AFLPs as molecular markers (Sobotka et al., 2004). Such technique was also compared with other marker types including, isozyme, RAPD and SSR markers in determining genetic similarity among oilseed lines (Havlíčková et al., 2014).

Random amplified microsatellite polymorphism

Random amplified microsatellite polymorphism (RAMP) markers are often employed in oilseeds research regarding the study of genetic diversity, identification of the traits associated with drought tolerance. For instance, RAMP markers have been successfully applied to studying genetic diversity among oilseed sunflower under conditions of different irrigations (Akbari and Darvishzadeh, 2024). Furthermore, RAMP markers are based on PCR that may detect various types of induced genetic variations and mechanisms similar to SSRs (Hasan et al., 2021).

NGS: a game changer in marker development

Next-Generation Sequencing (NGS) is a swift, economical sequencing method that facilitates the concurrent sequencing of millions of DNA and RNA fragments, transforming genomics through the efficient analysis of intricate genomes (Hashemi-Petroudi et al., 2022; Satam et al., 2023). The history of NGS commenced in the early 2000s with the launch of 454 Life Sciences' GS20 in 2005, succeeded by Illumina's sequencing technology, which gained prominence owing to its precision and scalability (Akacin et al., 2022). Innovative NGS techniques like Ion Torrent and PacBio offer distinct advantages for read length, accuracy, and versatility, with several platforms demonstrating particular attributes (Hu et al., 2021). Various types of NGS platforms are presently accessible, each possessing unique characteristics:

- *Illumina Sequencing:* Illumina sequencing, recognized for its high throughput and precision, is extensively utilized in genomics and transcriptomics. It utilizes a sequencing-by-synthesis technique, wherein fluorescently labeled nucleotides are integrated into elongating DNA strands (Abdi et al., 2024)
- *Ion Torrent Sequencing:* Ion Torrent Sequencing use semiconductor technology to monitor pH variations as nucleotides are incorporated into a developing DNA strand. It provides expedited sequencing at reduced costs, rendering it appropriate for many applications (Kumar et al., 2024).
- *PacBio Sequencing:* PacBio's Single Molecule Real-Time (SMRT) sequencing offers extended read lengths, advantageous for elucidating intricate genomic areas and structural changes (Zhou et al., 2022b).

Genetic Markers: MAS, QTL mapping, and transferability

Marker-assisted selection (MAS)

A biotechnological approach known as Marker-Assisted Selection (MAS) utilizes molecular markers to select for desired traits in breeding programs. The application of molecular markers in MAS has accelerated the breeding process by allowing breeders to select individuals carrying desirable alleles linked to specific QTLs early in the breeding cycle. This method has been particularly beneficial in oilseed crops, where traits such as oil yield and disease resistance can be efficiently selected based on marker data (Teixido et al., 2021). At the outset of the breeding cycle, it is possible to enhance decision-making by pinpointing specific markers linked to desired traits, thereby significantly boosting the efficiency and accuracy of crop development (Mahjoob et al., 2016). With the incorporation of molecular markers into plant breeding program during the late 1980s and early 1990s, the concept of MAS emerged. Methods such as SSR and RFLP enable the mapping of Quantitative Trait Loci associated with important agronomic traits (Wenzl et al., 2006). Progress in genomics and the emergence of NGS in recent years have significantly enhanced the applicability of MAS, facilitating more precise marker identification and selection (Pandey et al., 2016).

Quantitative Trait Loci (QTL)

Quantitative Trait Loci (QTL) are specific regions of the genome that correlate with variation in a quantitative trait (Aguet et al., 2023). The identification and mapping of QTLs are crucial for breeding programs as they provide insight into the genetic basis of traits that can be selected for improvement. The ability to locate these loci on chromosomes using molecular markers enhances the precision of breeding efforts.

Recent studies have focused on developing chromosome-specific markers that allow for precise localization of QTLs on specific chromosomes. For instance, researchers have utilized gene-based markers such as Conserved Ortholog Set (COS) markers to map QTLs related to starch granule content in wheat, demonstrating their effectiveness in facilitating gene introgression from wild relatives into cultivated species. This approach not only aids in identifying QTLs but also enhances our understanding of chromosomal relationships among different species (Lindqvist-Kreuze et al., 2013). The integration of NGS technologies has significantly advanced the ability to identify and characterize molecular markers linked to QTLs. NGS allows for comprehensive genome-wide scans to detect SNPs associated with traits of interest, leading to more accurate QTL mapping (Yang et al., 2010). This technology enables breeders to develop high-density genetic maps that improve the resolution at which QTLs can be identified.

Transferability of markers

The transferability of markers opens up avenues for tapping into genetic diversity present in the related species, particularly for crops with low genetic variation.low genetic variation. With markers from closely related species, breeders can introduce new alleles enhancing traits of interest. Transferable markers can acceleratebreeding programs by enabling the identification of specific trait more quickly. These increases in speed are invaluable for oilseed crops, as global food security challenges demand the development of high-yielding and resilient crop varieties (Huang et al., 2016).

Applications of molecular markers in improvement of oilseed crop

This has been possible with the integration of these molecular markers into breeding strategies, where significant strides have been made in the improvement of oilseed crops (Table 1).

Genetic diversity analysis

Breeders are allowed, through molecular markers, to investigate the genetic diversity present in the oilseed germplasm collections. This becomes very important for choosing appropriate parents to hybridize and also for ensuring a broad genetic base for further breeding programs. For instance, research has shown the use of SSRs together with other markers to effectively characterize the genetic diversity among oilseed cultivars, hence informing breeding decisions.

In MAS, breeders can select plants that have the desired trait at an early growth stage. This advances the pace of breeding and helps in the more rapid development of cultivars with improved tolerance to abiotic stresses such as drought and salinity (Hasan et al., 2021). MAS enables selection with significantly greater precision than before, potentially reducing the time required to develop new varieties by several years compared to traditional methods (Table 1). QTL Mapping: QTL mapping studies allowed the identification of genomic regions responsible for relevant traits such as heat tolerance or disease resistance by molecular markers (Zhou et al., 2022a). Such information is important for targeted breeding focused on improving such traits in oilseed crops. For example, QTLs concerning drought tolerance in soybean were mapped by using SNP markers (Wang et al., 2022). SNP markers enable genomic selection methodologies to project the performance of untested individuals based on their genomic profile. This approach simplifies the selection process, and shortens the length of the breeding cycle since breeders can be extremely informed on which plants to advance.

Addressing abiotic stresses

Abiotic stresses, including drought, salinity, heat, and flooding, have wholly taken their toll on oilseed crops. Molecular marker applications helped in developing stress-resistant varieties. To cite a few examples, studies have demonstrated how SSRs and SNPs have been mapped with QTL associated with drought resistance in major oilseed crops of rapeseed and soybean (Song et al., 2021). Such efforts are being directed toward closing the gap between actual and potential yields by enhancing

Table 1. List of some studies involving molecular markers for Genetic diversity and improvement of oilseeds. Abbreviations are as defined in Figure 1.

Trait	Marker used/ linked to QTL	Crop	Reference
Oil content	SSR	Sesame	(Li et al., 2014)
Cadmium toxicity	SSRs	Soybean	(Jegadeesan et al., 2010)
Cold stress	RFLPs, AFLPs	Mustard and Canola	(Kole et al., 2002))
Cold stress	SSRs	Soybean	(Funatsuki et al., 2005; Ikeda et al., 2009; Zhang HaiYang et al., 2012)
Cold stress	ESTs	Sunflower	(Hewezi et al., 2006; Fernandez et al., 2008)
Cyst Nematodes	AFLP, RFLP	Sunflower, Soybean	(Ali et al., 2017)
Drought stress	AFLPs	Safflower	(Poodineh et al., 2021)
Drought stress	SSR	Soybean	(Chen et al., 2021)
Drought and salt stress	SNPs	Sesame	(Li et al., 2018)
Drought tolerance	SSRs	Groundnut	(Ravi et al., 2011; Gautami et al., 2012)
Drought tolerance	SSRs and ISSRs	Safflower	(Mirzahashemi et al., 2015)
Drought tolerance	SNPs	Sesame	(Dossa et al., 2019)
Drought tolerance	SSR	Soybean	(Specht et al., 2001; Bhatnagar et al., 2005; Monteros, 2006)
Drought tolerance	RFLP	Soybean	(Mian et al., 1998)
Drought stress	RFLP	Soybean	(Mian et al., 1996)
Flooding stress	SSRs	Soybean	(VanToai et al., 2001; Cornelious et al., 2005; Githiri et al., 2006; Dhungana et al., 2021)
Flooding stress	SSRs and SNPs	Soybean	(Nguyen et al., 2012)
Fungal diseases	SSRs, SNPs	Sunflower	(Dimitrijevic and Horn, 2018)
Sclerotinia stem rot	IRAP, REMAP	Canola, Soybean	(Negi et al., 2016)
Genetic diversity	EST-SSRs	Multiple oil crops	(Miladinović et al., 2019)
Genetic diversity	EST-SSRs	Cotton	(Yu et al., 2008)
Genetic diversity	EST-SSR, SCoT	Sesame	(Bhattacharjee et al., 2020)
Heat stress	AFLPs, SCARs	Rapeseed	(Zeng et al., 2014)
Manganese toxicity	SSRs	Soybean	(Kassem et al., 2004)
Oil content	EST	Soybean, Peanut, Sesame, Rapeseed	(Ke et al., 2015)
Root-knot nematodes	SSRs, SNPs	Soybean, canola	(Ragimekula et al., 2013)
Salt stress	SSRs	Soybean	(Lee et al., 2004; Chen et al., 2008; Hamwieh et al., 2011)
Tobacco streak virus	IRAP, REMAP	Canola	(Negi et al., 2016)
Viruses	SNPs, SSRs	Soybean	(Jones et al., 2021)

the capacity of crops to withstand severe abiotic pressures (Figure 2).

Improving oil content

Application of molecular markers to improve oilseed crops' oil content is extremely encouraging. Recent innovations in genomics have enhanced our knowledge of the genes involved in oil production that are targets for genetic alteration, claim Chao et al. (2023). Based on the findings of Savadi et al. (2017), candidates found through studies on such genes offer useful resources for enhancing oil content through the application of transgenic and gene editing technologies. Molecular markers associated with fatty acid components also contribute to the enhancement of overall crop quality. Molecular markers associated with fatty acid components also contribute to the enhancement of overall crop quality. For example, several markers that would enhance the oil content and composition of seeds have been found in *Lepidium campestre* (Lodenius, 2023).

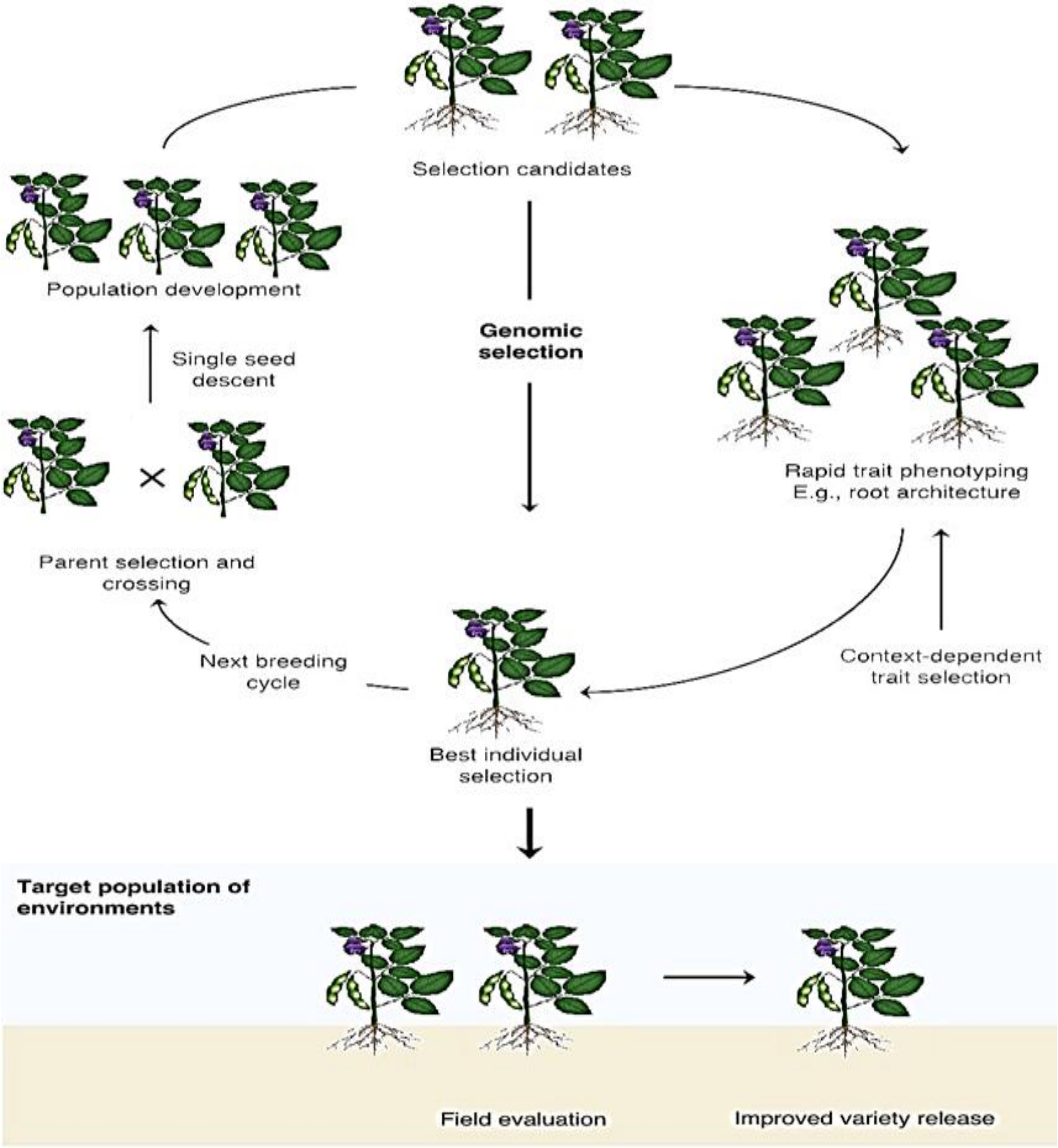

Figure 2. The connection between traditional plant breeding and molecular plant breeding in developing Soybean varieties withstand environmental stresses.

Challenges and future perspectives

In conclusion, the application of molecular markers towards the improvement in oilseed crops is doubtlessly a jump upwards in breeding methodologies. Not only does it advance the selection with increased efficiency concerning tolerance to various abiotic and biotic stresses, but the pace of breeding also accelerates, while new possibilities emerge due to enhanced usage of genetic variability and using methods of modern genetic manipulation. Therefore, such inventions are important in the development of resilient oilseed crops that will be resistant to climate change and continue to ensure food security for future generations. Further research, in fact still ongoing in the fields, promises to expand possibilities for sustainable varieties of oilseeds and contribute immensely to the resilience of global agriculture. Otherwise, apart from that, the potentials of molecular markers, coupled especially with state-of-the-art genome editing techniques such as CRISPR-Cas9, among others, cannot be left aside in ensuring additional dimensions of accuracy in plant improvement. For all these, integrated use of traditional breeding in amalgamation with progressive biotechnology is likely to effect total transformation for developing better improved varieties toward enhancement of nutritional profiles and enhanced quality of oils and a superior level of yields thereof in oilseed crops. Secondly, investments in research and development related to the technology of molecular markers and training of the next generation of plant breeders and geneticists should be done on a continuous basis. The progress needs to reach varieties, regions, economies, and farmers for truly fair agricultural development to take place. After all, the successful use of molecular markers in oilseed crop breeding contributes not only to agricultural sustainability but also plays a very important role in solving such challenges as overpopulation of the globe, changes in eating habits, and the need for more efficient land use. All the present molecular markers, along with related technologies, have considerable promise in attempting to secure the future productivity of the oilseed crops for the aspects of food security and sustainability.

Supplementary Materials

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Author Contributions

These authors contributed equally.

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Conflict of Interest Statement

The authors declare no potential conflict of interest with respect to the research, authorship, and/or publication of this article.

References

Abdi, G., Tarighat, M.A., Jain, M., Tendulkar, R., Tendulkar, M., and Barwant, M. (2024). "Revolutionizing Genomics: Exploring the Potential of Next-Generation Sequencing," in *Advances in Bioinformatics*. Springer), 1-33.

Adje, C., Missihoun, A.A., Sedah, P., Adoukonou Sagbadja, H., Achigan Dako, E., and Agbangla, C. (2023). Genetic diversity and structure of Benin pineapple (*Ananas comosus* (L) Merr.) germplasm collection using Simple Sequence Repeat (SSR) markers. *J Plant Mol Breed.* 11(2): 94-106.

Aguet, F., Alasoo, K., Li, Y.I., Battle, A., Im, H.K., Montgomery, S.B., and Lappalainen, T. (2023). Molecular quantitative trait loci. *Nat. Rev. Methods Primers.* 3(1): 4.

Akacin, I., Ersoy, Ş., Doluca, O., and Güngörmüşler, M. (2022). Comparing the significance of the utilization of next generation and third generation sequencing technologies in microbial metagenomics. *Microbiolog. Res.* 264: 127154.

Akbari, N., and Darvishzadeh, R. (2024). Identification of REAMP markers related to morpho-phisiological and agronomic traits in oilseed sunflower (*Helianthus annuus* L.) under normal and limited irrigation conditions. *Cro Sci Res Arid Reg.* 6(2): 245-260.

Ali, M.A., Azeem, F., Abbas, A., Joyia, F.A., Li, H., and Dababat, A.A. (2017). Transgenic strategies for enhancement of nematode resistance in plants. *Front. Plant Sci.* 8: 750.

Allen, A.M., Winfield, M.O., Burridge, A.J., Downie, R.C., Benbow, H.R., Barker, G.L., Wilkinson, P.A., Coghill, J., Waterfall, C., and Davassi, A. (2017). Characterization of a Wheat Breeders' Array suitable for high‐throughput SNP genotyping of global accessions of hexaploid bread wheat (*Triticum aestivum*). *J. Plant Biotech.* 15(3): 390-401.

Baba Nitsa, M., Odiyi, A.C., Akinyele, B.O., Aiyelari, O.P., and Fayeun, L.S. (2023). Genetic diversity assessment of thirty nine *Coffea canephora* accessions using EST-SSR markers. *J Plant Mol Breed.* 11(1): 17-27.

Bhatnagar, S., King, C.A., Purcell, L., and Ray, J.D. (Year). "Identification and mapping of quantitative trait loci associated with crop responses to water-deficit stress in soybean [*Glycine max* (L.) Merr.]", in: *The ASACSSA-SSSA International annual meeting poster abstract*).

Bhattacharjee, M., Prakash, S., Roy, S., Soumen, S., Begum, T., and Dasgupta, T. (2020). SSR-based DNA fingerprinting of 18 elite Indian varieties of sesame (*Sesamum indicum* L.). *The Nucleus.* 63: 67-73.

Chao, H., Kilaru, A., and Liu, L. (2023). Editorial: Genetics, breeding and engineering to enhance oil quality and yield. *Front. Plant Sci.* 14. doi: 10.3389/fpls.2023.1265897.

Chen, H., Cui, S., Fu, S., Gai, J., and Yu, D. (2008). Identification of quantitative trait loci associated with salt tolerance during seedling growth in soybean (*Glycine max* L.). *Aust. J. Agric. Res.* 59(12): 1086-1091.

Chen, H., Kumawat, G., Yan, Y., Fan, B., and Xu, D. (2021). Mapping and validation of a major QTL for primary root length of soybean seedlings grown in hydroponic conditions. *BMC genom.* 22: 1-9.

Cornelious, B., Chen, P., Chen, Y., De Leon, N., Shannon, J., and Wang, D. (2005). Identification of QTLs underlying water-logging tolerance in soybean. *Mol. Breed.* 16: 103-112.

Čurn, V., Ovesna, J., Sakova, L., and Sobotka, R. (2002). Identification of oilseed rape cultivars using AFLP markers. *J Cent Eur Agric.* 3(4): 285-292.

Dhungana, S.K., Kim, H.-S., Kang, B.-K., Seo, J.-H., Kim, H.-T., Shin, S.-O., Oh, J.-H., and Baek, I.-Y. (2021). Identification of QTL for tolerance to flooding stress at seedling stage of soybean (*Glycine max* L. Merr.). *Agronomy.* 11(5): 908.

Dimitrijevic, A., and Horn, R. (2018). Sunflower hybrid breeding: from markers to genomic selection. *Front. Plant Sci.* 8: 2238.

Dossa, K., Li, D., Zhou, R., Yu, J., Wang, L., Zhang, Y., You, J., Liu, A., Mmadi, M.A., and Fonceka, D. (2019). The genetic basis of drought tolerance in the high oil crop *Sesamum indicum*. *Plant Biotechnol. J.* 17(9): 1788-1803.

Fernandez, P., Di Rienzo, J., Fernandez, L., Hopp, H.E., Paniego, N., and Heinz, R.A. (2008). Transcriptomic identification of candidate genes involved in sunflower responses to chilling and salt stresses based on cDNA microarray analysis. *BMC Plant Biol.* 8: 1-18.

Funatsuki, H., Kawaguchi, K., Matsuba, S., Sato, Y., and Ishimoto, M. (2005). Mapping of QTL associated with chilling tolerance during reproductive growth in soybean. *Theor. Appl. Genet.* 111: 851-861.

Gautami, B., Pandey, M., Vadez, V., Nigam, S., Ratnakumar, P., Krishnamurthy, L., Radhakrishnan, T., Gowda, M., Narasu, M., and Hoisington, D. (2012). Quantitative trait locus analysis and construction of consensus genetic map for drought tolerance traits based on three recombinant inbred line populations in cultivated groundnut (*Arachis hypogaea* L.). *Mol. Breed.* 30: 757-772.

Githiri, S.M., Watanabe, S., Harada, K., and Takahashi, R. (2006). QTL analysis of flooding tolerance in soybean at an early vegetative growth stage. *Plant Breed.* 125(6): 613-618.

Hamwieh, A., Tuyen, D.D., Cong, H., Benitez, E.R., Takahashi, R., and Xu, D. (2011). Identification and validation of a major QTL for salt tolerance in soybean. *Euphytica.* 179: 451-459.

Hasan, N., Choudhary, S., Naaz, N., Sharma, N., and Laskar, R.A. (2021). Recent advancements in molecular marker-assisted selection and applications in plant breeding programmes. *J Gen Eng Biotech.* 19(1): 128.

Hashemi-Petroudi, S.H., Arab, M., Dolatabadi, B., Kuo, Y.-T., Baez, M.A., Himmelbach, A., Nematzadeh, G., Maibody, S.A.M.M., Schmutzer, T., and Mälzer, M. (2022). Initial description of the Genome of *Aeluropus littoralis*, a halophile grass. *Front. Plant Sci.* 13: 906462.

Havlíčková, L., Jozova, E., Rychla, A., Klima, M., Kučera, V., and Čurn, V. (2014). Genetic diversity assessment in winter Oilseed Rape (*Brassica napus* L.) collection using AFLP, ISSR and SSR markers. *Czech J Gene. Plant* 50(3).

Heidari, P., Hasanzadeh, S., Faraji, S., Ercisli, S., and Mora-Poblete, F. (2023). Genome-wide characterization of the sulfate transporter gene family in oilseed crops: *Camelina sativa* and *Brassica napus*. *Plants* 12(3): 628.

Hewezi, T., Léger, M., El Kayal, W., and Gentzbittel, L. (2006). Transcriptional profiling of sunflower plants growing under low temperatures reveals an extensive down-regulation of gene expression associated with chilling sensitivity. *J. Exp. Bot.* 57(12): 3109-3122.

Holsman, K.K. (2023). *Climate Change 2022 :Impacts, Adaptation and Vulnerability.22p.*

Hosseinpour Azad, N. (2023). Genetic diversity of *Satureja bachtiarica* Bunge species collected from north-west Iran. *J Plant Mol Breed.* 11(2): 31-38.

Hu, T., Chitnis, N., Monos, D., and Dinh, A. (2021). Next-generation sequencing technologies: An overview. *Human Immunol.* 82(11): 801-811.

Huang, L., Wu, B., Zhao, J., Li, H., Chen, W., Zheng, Y., Ren, X., Chen, Y., Zhou, X., and Lei, Y. (2016). Characterization and transferable utility of microsatellite markers in the wild and cultivated Arachis species. *PLoS One.* 11(5): e0156633.

Ikeda, T., Ohnishi, S., Senda, M., Miyoshi, T., Ishimoto, M., Kitamura, K., and Funatsuki, H. (2009). A novel major quantitative trait locus controlling seed development at low temperature in soybean (*Glycine max*). *Theor. Appl. Genet.* 118: 1477-1488.

Jegadeesan, S., Yu, K., Poysa, V., Gawalko, E., Morrison, M.J., Shi, C., and Cober, E. (2010). Mapping and validation of simple sequence repeat markers linked to a major gene controlling seed cadmium accumulation in soybean [*Glycine max* (L.) Merr]. *Theor. Appl. Genet.* 121: 283-294.

Jones, R.A., Sharman, M., Trębicki, P., Maina, S., and Congdon, B.S. (2021). Virus diseases of cereal and oilseed crops in Australia: current position and future challenges. *Viruses.* 13(10): 2051.

Kassem, M.A., Meksem, K., Kang, C., Njiti, V., Kilo, V., Wood, A., and Lightfoot, D. (2004). Loci underlying resistance to manganese toxicity mapped in a soybean recombinant inbred line population of 'Essex2019; x 'Forrest'. *Plant Soil.* 260: 197-204.

Ke, T., Yu, J., Dong, C., Mao, H., Hua, W., and Liu, S. (2015). ocsESTdb: a database of oil crop seed EST sequences for comparative analysis and investigation of a global metabolic network and oil accumulation metabolism. *BMC Plant Biol.* 15: 1-11.

Kole, C., Thormann, C., Karlsson, B., Palta, J., Gaffney, P., Yandell, B., and Osborn, T. (2002). Comparative mapping of loci controlling winter survival and related traits in oilseed Brassica rapa and *B. napus*. *Mol. Breed.* 9: 201-210.

Kour, M., Kumari, L., and Sharma, S. (2023). Association of SSR Markers for primary branches in *Brassica Juncea* L. *J Plant Mol Breed.* 11(2): 77-92.

Kühn, N., Spiegel, M.P., Tovar, C., Willis, K.J., and Macias-Fauria, M. (2022). Seeing roots from space: aboveground fingerprints of root depth in vegetation sensitivity to climate in dry biomes. *Environ. Res. Lett.* 17(11): 114062.

Kumar, K.R., Cowley, M.J., and Davis, R.L. (Year). "Next-generation sequencing and emerging technologies", in: *Seminars in thrombosis and hemostasis*: Thieme Medical Publishers).

Lawrence, T.J., Vilbig, J.M., Kangogo, G., Fèvre, E.M., Deem, S.L., Gluecks, I., Sagan, V., and Shacham, E. (2023). Shifting climate zones and expanding tropical and arid climate regions across Kenya (1980–2020). *Reg. Environ. Change.* 23(2): 59.

Lee, G., Boerma, H., Villagarcia, M., Zhou, X., Carter, T., Li, Z., and Gibbs, M. (2004). A major QTL conditioning salt tolerance in S-100 soybean and descendent cultivars. *Theor. Appl. Genet.* 109: 1610-1619.

Lesk, C., Anderson, W., Rigden, A., Coast, O., Jägermeyr, J., McDermid, S., Davis, K.F., and Konar, M. (2022). Compound heat and moisture extreme impacts on global crop yields under climate change. *Nat. Rev. Earth Environ.* 3(12): 872-889.

Li, C., Miao, H., Wei, L., Zhang, T., Han, X., and Zhang, H. (2014). Association mapping of seed oil and protein content in *Sesamum indicum* L. using SSR markers. *PLoS One.* 9(8): e105757.

Li, D., Dossa, K., Zhang, Y., Wei, X., Wang, L., Zhang, Y., Liu, A., Zhou, R., and Zhang, X. (2018). GWAS uncovers differential genetic bases for drought and salt tolerances in sesame at the germination stage. *Genes.* 9(2): 87.

Lindqvist-Kreuze, H., Cho, K., Portal, L., Rodríguez, F., Simon, R., Mueller, L.A., Spooner, D.M., and Bonierbale, M. (2013). Linking the potato genome to the conserved ortholog set (COS) markers. *BMC Genetics* 14: 1-12.

Lodenius, N. (2023). *Identifying molecular markers for breeding a future oil crop, Lepidium campestre.* Master Program, Swedish University of Agricultural Sciences.

Lynas, M., Adams, J., and Conrow, J. (2022). Misinformation in the media: global coverage of GMOs 2019-2021. *GM Crops & Food*: 1-10.

Mahjoob, B., Zarini, H., Hashemi, S., and Shamasbi, F. (2016). Comparison of ISSR, IRAP and REMAP markers for assessing genetic diversity in different species of *Brassica* sp. *Rus J Gen.* 52: 1272-1281.

Malgaonkar, M., Shirolkar, A., Murthy, S.N., Mangal, A.K., and Pawar, S.D. (2020). DNA Based Molecular Markers: A Tool for Differentiation of Ayurvedic Raw Drugs and their Adulterants. *Phcog Rev.* 14(27).

Martin-Gutierrez, M.P., Schiff, E.R., Wright, G., Waseem, N., Mahroo, O.A., Michaelides, M., Moore, A.T., Webster, A.R., Arno, G., and Consortium, G.E.R. (2022). Dominant cone rod dystrophy, previously assigned to a missense variant in RIMS1, is fully explained by co-inheritance of a dominant allele of PROM1. *Invest. Ophthalmol Vis. Sci.* 63(9): 14-14.

Mian, M., Ashley, D., and Boerma, H. (1998). An additional QTL for water use efficiency in soybean. *Crop Sci.* 38(2): 390-393.

Mian, M., Bailey, M., Ashley, D., Wells, R., Carter Jr, T., Parrott, W., and Boerma, H. (1996). Molecular markers associated with water use efficiency and leaf ash in soybean. *Crop Sci.* 36(5): 1252-1257.

Miladinović, D., Vollmann, J., Molinero-Ruiz, L., and Torres, M. (2019). "advances in oil crops research—classical and new approaches to achieve sustainable productivity". Frontiers Media SA).

Mirzahashemi, M., Mohammadi-Nejad, G., and Golkar, P. (2015). A QTL linkage map of safflower for yield under drought stress at reproductive stage. *Iran. J. Genet. Plant Breed.* 4(2): 20-27. (In Persian).

Monteros, M. (Year). "Identification and confirmation of QTL conditioning drought tolerance in Nepalese soybean", in: *The 11th Biennial Conference on the Molecular and Cellular Biology of the Soybean, August 5-8, Lincoln, NE, 2006*).

Negi, P., Rai, A.N., and Suprasanna, P. (2016). Moving through the stressed genome: emerging regulatory roles for transposons in plant stress response. *Front. Plant Sci.* 7: 1448.

Nguyen, V., Vuong, T., VanToai, T., Lee, J., Wu, X., Mian, M.R., Dorrance, A., Shannon, J., and Nguyen, H. (2012). Mapping of quantitative trait loci associated with resistance to Phytophthora sojae and flooding tolerance in soybean. *Crop Sci.* 52(6): 2481-2493.

O'Brown, Z.K., Boulias, K., Wang, J., Wang, S.Y., O'Brown, N.M., Hao, Z., Shibuya, H., Fady, P.-E., Shi, Y., and He, C. (2019). Sources of artifact in measurements of 6mA and 4mC abundance in eukaryotic genomic DNA. *BMC Genom.* 20: 1-15.

Pandey, M.K., Roorkiwal, M., Singh, V.K., Ramalingam, A., Kudapa, H., Thudi, M., Chitikineni, A., Rathore, A., and Varshney, R.K. (2016). Emerging genomic tools for legume breeding: current status and future prospects. *Front. Plant Sci.* 7: 455.

Poodineh, M., Nezhad, N.M., Mohammadi-Nejad, G., Fakheri, B.A., and Ebrahimi, F. (2021). Identification of safflower (*Carthamus tinctorius* L.) QTL under drought stress and normal conditions. *Ind. Crops Prod.* 171: 113889.

Ragimekula, N., Varadarajula, N.N., Mallapuram, S.P., Gangimeni, G., Reddy, R.K., and Kondreddy, H.R. (2013). Marker assisted selection in disease resistance breeding. *J. Plant Breed.* 1(2): 90-109.

Ravi, K., Vadez, V., Isobe, S., Mir, R., Guo, Y., Nigam, S., Gowda, M., Radhakrishnan, T., Bertioli, D., and Knapp, S. (2011). Identification of several small main-effect QTLs and a large number of epistatic QTLs for drought tolerance related traits in groundnut (*Arachis hypogaea* L.). *Theor. Appl. Genet.* 122: 1119-1132.

Satam, H., Joshi, K., Mangrolia, U., Waghoo, S., Zaidi, G., Rawool, S., Thakare, R.P., Banday, S., Mishra, A.K., and Das, G. (2023). Next-generation sequencing technology: current trends and advancements. *Biology.* 12(7): 997.

Savadi, S., Lambani, N., Kashyap, P.L., and Bisht, D.S. (2017). Genetic engineering approaches to enhance oil content in oilseed crops. *J. Plant Growth Regul.* 83: 207-222.

Segelbacher, G., Bosse, M., Burger, P., Galbusera, P., Godoy, J.A., Helsen, P., Hvilsom, C., Iacolina, L., Kahric, A., and Manfrin, C. (2022). New developments in the field of genomic technologies and their relevance to conservation management. *Conserv. Genet.* 23(2): 217-242.

Sinha, D., Maurya, A.K., Abdi, G., Majeed, M., Agarwal, R., Mukherjee, R., Ganguly, S., Aziz, R., Bhatia, M., and Majgaonkar, A. (2023). Integrated genomic selection for accelerating breeding programs of climate-smart cereals. *Genes.* 14(7): 1484.

Sobotka, R., Dolanska, L., Curn, V., and Ovesná, J. (2004). Fluorescence-based AFLPs occur as the most suitable marker system for oilseed rape cultivar identification. *J Appl Genet.* 45(2): 161-174.

Soltabayeva, A., Ongaltay, A., Omondi, J.O., and Srivastava, S. (2021). Morphological, physiological and molecular markers for salt-stressed plants. *Plants.* 10(2): 243.

Song, X., Yang, Q., Bai, Y., Gong, K., Wu, T., Yu, T., Pei, Q., Duan, W., Huang, Z., and Wang, Z. (2021). Comprehensive analysis of SSRs and database construction using all complete gene-coding sequences in major horticultural and representative plants. *Hortic. Res.* 8.

Specht, J., Chase, K., Macrander, M., Graef, G., Chung, J., Markwell, J., Germann, M., Orf, J., and Lark, K. (2001). Soybean response to water: a QTL analysis of drought tolerance. *Crop Sci.* 41(2): 493-509.

Sunde, J., Yıldırım, Y., Tibblin, P., and Forsman, A. (2020). Comparing the performance of microsatellites and RADseq in population genetic studies: Analysis of data for pike (*Esox lucius*) and a synthesis of previous studies. *Front. Genet.* 11: 218.

Teixido, C., Castillo, P., Martinez-Vila, C., Arance, A., and Alos, L. (2021). Molecular markers and targets in melanoma. *Cells.* 10(9): 2320.

VanToai, T.T., St. Martin, S.K., Chase, K., Boru, G., Schnipke, V., Schmitthenner, A.F., and Lark, K.G. (2001). Identification of a QTL associated with tolerance of soybean to soil waterlogging. *Crop Sci.* 41(4): 1247-1252.

Walker, F.C., Hassan, E., Peterson, S.T., Rodgers, R., Schriefer, L.A., Thompson, C.E., Li, Y., Kalugotla, G., Blum-Johnston, C., and Lawrence, D. (2021). Norovirus evolution in immunodeficient mice reveals potentiated pathogenicity via a single nucleotide change in the viral capsid. *PLoS Pathog.* 17(3): e1009402.

Wang, L., Xun, H., Aktar, S., Zhang, R., Wu, L., Ni, D., Wei, K., and Wang, L. (2022). Development of SNP markers for original analysis and germplasm identification in *Camellia sinensis*. *Plants.* 12(1): 162.

Wenzl, P., Li, H., Carling, J., Zhou, M., Raman, H., Paul, E., Hearnden, P., Maier, C., Xia, L., and Caig, V. (2006). A high-density consensus map of barley linking DArT markers to SSR, RFLP and STS loci and agricultural traits. *BMC Gene.* 7: 1-22.

Yang, J., Benyamin, B., McEvoy, B.P., Gordon, S., Henders, A.K., Nyholt, D.R., Madden, P.A., Heath, A.C., Martin, N.G., and Montgomery, G.W. (2010). Common SNPs explain a large proportion of the heritability for human height. *Nat. Genet.* 42(7): 565-569.

Yang, W., Liang, J., Hao, Q., Luan, X., Tan, Q., Lin, S., Zhu, H., Liu, G., Liu, Z., and Bu, S. (2021). Fine mapping of two grain chalkiness QTLs sensitive to high temperature in rice. *Rice.* 14: 1-10.

Yu, Y., Zhi-Wei, W., Chang-Hui, F., Zhang, Y.-X., Zhong-Xu, L., and Zhang, X.-L. (2008). Genetic evaluation of EST-SSRs derived from *Gossypium herbaceum*. *Acta Agron. Sin.* 34(12): 2085-2091.

Zeng, X., Li, W., Wu, Y., Liu, F., Luo, J., Cao, Y., Zhu, L., Li, Y., Li, J., and You, Q. (2014). Fine mapping of a dominant thermo-sensitive genic male sterility gene (*BntsMs*) in rapeseed (*Brassica napus*) with AFLP- and Brassica rapa-derived PCR markers. *Theor. Appl. Genet.* 127: 1733-1740.

Zhang HaiYang, Z.H., Wei LiBin, W.L., Miao HongMei, M.H., Zhang TiDe, Z.T., and Wang CuiYing, W.C. (2012). Development and validation of genic-SSR markers in sesame by RNA-seq. *BMC Genom.* 13.

Zhou, H.J., Li, L., Li, Y., Li, W., and Li, J.J. (2022a). PCA outperforms popular hidden variable inference methods for molecular QTL mapping. *Genome Biol.* 23(1): 210.

Zhou, K., Chen, Z., Du, X., Huang, Y., Qin, J., Wen, L., Pan, X., and Lin, Y. (2022b). SMRT sequencing reveals candidate genes and pathways with medicinal value in Cipangopaludina chinensis. *Front. Gene.* 13: 881952.

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استفاده از نشانگرهای مولکولی در به‌نژادی دانه‌های روغنی: مقاله مروری

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مقاله مروری

چکیده: نشانگرهای مولکولی به عنوان ابزارهای حیاتی برای بهبود محصولات دانه‌های روغنی و ایجاد ارقام با قابلیت تحمل شرایط خشکی، شوری و دماهای بالا مطرح هستند. در این این مقاله مروری بر کاربرد نشانگرهای مولکولی مبتنی بر DNA، مانند ردیف‌های تکراری ساده (SSRs) و پلی‌مورفیسم‌های نوکلئوتید منفرد (SNPs) در اصلاح گیاهان زراعی دانه‌های روغنی متمرکز است. این نشانگرها در شناسایی و مکان‌یابی ژنی کنترل کننده صفات کمی (QTL) که مرتبط با تحمل به استرس هستند، کمک نموده و فرایند انتخاب را از طریق انتخاب مبتنی بر نشانگرها (MAS) تسریع می‌بخشند. اگرچه دانه‌های روغنی مانند کلزا، سویا و آفتابگردان از تحمیل بالاتری نسبت به تنش‌های محیطی برخوردارند، ولی از دلایل اصلی شکاف عملکرد موجود ناتوانی آنها در مدیریت اثرات تنش غیرزیستی مانند خشکسالی، شوری، و دمای شدید بوده، که به طور قابل توجهی بر رشد و بهره وری تاثیر می‌گذارد. گنجاندن نشانگرهای مولکولی در برنامه‌های اصلاحی نه تنها به حفاظت تنوع ژنتیکی کمک می‌کند بلکه به توسعه سریع‌تر ارقام با عملکرد بالا که می‌توانند شرایط سخت را تحمل کنند نیز تاثیرگذار خواهد بود. در این بررسی، مثال‌هایی از کاربردهای موفق این فناوری‌ها ارائه گردیده، ضمن اینکه تحقیقات بیشتر بر روی کاربرد نشانگرهای مولکولی در اصلاح دانه‌های روغنی کمتر مطالعه شده به منظور بهبود امنیت غذایی در برابر تهدیدات گرم شدن کره زمین را ضروری می‌داند.

کلمات کلیدی: تنوع ژنتیکی، گرمایش زمین، انتخاب مبتنی بر نشانگرها، مکان‌یابی ژنی کنترل کننده صفات کمی.

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