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REVIEW ARTICLE

Genetic approaches for trait improvement in sesame: Progress and prospects

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Abstract

Sesame (*Sesamum indicum* L.) is the most ancient oilseed crops cultivated by humans, widely known as the 'queen of oilseeds' due to its high oil content, nutritional richness and health-promoting properties. The global demand for sesame has risen significantly in recent years, largely driven by its excellent oil quality, high protein levels, antioxidant compounds such as sesamin and sesamolin and its remarkable adaptability to a wide range of agro-climatic and soil conditions. Despite being widely grown and self-sustaining in terms of acreage, sesame continues to exhibit low average productivity. This is primarily due to limited genetic improvement, environmental stress susceptibility and poor adaptation to diverse agro-ecological regions. To overcome these challenges, genetic enhancement of sesame is essential. Recent advancements in molecular biology and genomics have opened new avenues for sesame improvement through the use of molecular markers, QTL mapping, mutation breeding and genome-assisted selection. This article aims to explore the genetic approaches currently employed in sesame crop improvement. It highlights the evolutionary history of sesame research, development and utilization of genetic resources, progress in molecular breeding and the challenges faced by breeders. Emphasis is also placed on prospects and the integration of modern biotechnological tools to enhance sesame productivity and resilience.

Keywords: functional genes; molecular markers; QTLs; trait improvement

Introduction

Sesame (*Sesamum indicum* L.), an oilseed crop used in ancient times, belongs to the family Pedaliaceae and is cultivated mainly in tropical regions (1). Having been utilised for nearly 5000 years, sesame was first domesticated in ancient Pakistan and the Indian subcontinent, dating back to the Harappa and Anatolian eras (2). It eventually spread to several nations, including Malaysia and China. Sesamum (2n = 26) belongs to the family Pedaliaceae and the genus *Sesamum* (3). Sesame seeds are widely grown for their oil-bearing nature, toppings and cakes. Sesame is a monoecious, diploid and self-pollinating plant valued for its oil quality. Sesame is referred to as the "queen of oilseeds" due to its high oil content of nearly 63 %, surpassing other oilseed crops such as groundnut (45 % - 56 %), sunflower (45 %) and rapeseed (40 %) (4). Sesame seeds comprise of around 83 % - 90 % of unsaturated fatty acids, like 37 % - 47 % of linoleic acid, (35 % - 43 %) of oleic acid, (9 % - 11 %) of palmitic and (5 % - 10 %) of stearic acid (5).

Sesamin and sesamolin are the two major antioxidants in sesame, while sesamol further stabilises the oil quality (6). India boasts remarkable sesame diversity, consisting of cultivated *S. indicum* along with six other species. Despite having a large area under sesame cultivation, India experiences low productivity due to its shattering plant type. In the last two decades, the popularity of sesame has increased significantly due to its exceptional oil quality. It possesses good protein levels, antioxidant properties and the ability to thrive in diverse agro-ecological conditions (7). Sesame seeds are recognised for their anticancer, anti-ageing, antioxidant, anti-hypersensitive and cholesterol-lowering properties (8). Major factors considered while cultivating sesame include tolerance to phyllody, waterlogging and resistance to root rot, as well as morphological traits like determinate growth, prostrate growth habit, indehiscent capsule, reduction of seed shattering loss and leveraging wild relatives in wide hybridisation to adapt to existing climate change. This can be achieved by genetic improvement at the trait level in the plant breeding of sesame.

Challenges in sesame breeding

The primary factors that affect sesame production and productivity are the absence of high-yielding cultivars. Additionally, locally adapted varieties are having issues with the capsule shattering, seed loss and uneven maturity, driven by additional factors like biotic stress and abiotic stress (4). Significant yield loss is observed due to its indeterminate plant architecture, that are prone to capsule-shattering (9). Globally, 99 % of sesame varieties are vulnerable to capsule shattering, which is a major negative factor (7). The non-availability of molecular data across the sesame cultivated genotypes and wild germplasm is due to a lack of

information about the evolution of sesame. Mechanisation of the sesame harvest is difficult due to its indeterminate habit. Substances that hinder the digestion and absorption of nutrients are antinutrients, which can adversely impact animal health and growth (10). Oxalic acid, phytic acid and small amounts of tannins are the main anti-nutritional factors present in sesame seeds. It is reported that sesame hulls contain 13 % oxalic acid and 1.12 % phytic acid (1).

Pests and diseases in sesame

The main insect pests affecting sesame include the webworm (*Antigastra catalaunalis*), gall midge (*Asphondylia sesame*) and seed bug *(Elasmolomus sordidus*) (11). Mostly sesame varieties are susceptible to diseases caused by bacteria, such as blight (*Xanthomonas campestris* pv. *sesame*), fungi, including charcoal rot (*Macrophomina phaseolina*), stem anthracnose (*Colletotrichum* spp.), mildew (*Erysiphe cichoracearum*), Fusarium wilt (*Fusarium oxysporum* f.sp. sesame) and root rot (*Rhizoctonia solani*), as well as viruses like phyllody (*Orosius albicinctus*) (7).

Waterlogging in sesame

Sesame is sensitive to waterlogging, salinity and low temperatures, so effective water management practices should be carried out to mitigate these negative effects (12). Waterlogging can negatively impact sesame by hindering its growth and development, reducing leaf area index, chlorophyll concentration, dry matter accumulation and the number of capsules, while also increasing seed abortion, ultimately leading to a decline in yield (13). The seedling establishment stage (around 20 days after sowing) is the most sensitive phase for sesame under waterlogged conditions, during which exposure can result in yield reductions of up to 35 % (14).

Resources for crop improvement

Genetic resources

Wild relatives: The Indian subcontinent is known for its rich diversity, inclusive of cultivated *S. indicum,* six more wild species are reported, with seed colour ranging from black to pure white (15). High-throughput genome sequencing technology found that *Utricularia gibba* is taxonomically related to sesame and it diverged from that species 98 million years ago (16). Early *Sesamum* species were classified based on morphological and microscopic observations. The taxon consists of both *S. orientale* var. *malabaricum* and *S. mulayanum*. A morphological, cytogenetic and molecular closeness is observed in the *S. indicum* sub sp. *malabaricum,* a species is being cultivated in India (17-19). *Sesamum* genus comprises of 17 species mostly of African origin recognised by International Plant Genetic Resource Institute (IPGRI) and National Bureau of Plant Genetic Resources (NBPGR) in the year 2004 (IPGRI and NBPGR, 2004). *S. laciniatum* wild was merged with the *S. prostratum* and the species rank is reduced to a subspecies under *S. Indicum* (20). Wild relatives contribute many useful genes which we have lost during the domestication process. The conservation and utilisation of wild relatives is important in breeding programmes. Some wild relatives are found to be an important source of pests and diseases resistance, i.e., resistance to *Cercospora* spot, *Phytopthora* blight, *Alternaria* leaf spot, phyllody, leaf curl virus and tolerance to waterlogging, drought and salinity stress. Association analysis of sesame germplasms found that traits like number of branches, number of capsules and thousand seed weight recorded a positive correlation and direct effect on cultivated and wild species; there is a significant difference between the cultivated and wild species (21). Wild relatives of sesame are mentioned in Fig. 1.

Germplasm conservation: Germplasm conservation serves as the source for valuable genes which have been lost in the domestication process. The repository of these genetic resources will have a huge impact on the cultivated crops (22). Wild relatives and local land races are the sources of genetic variation, which comprises novel genes that are a source of various biotic and abiotic resistance. They can be conserved *in situ* or *ex-situ*. A major source of genetic diversity is an available genetic repository. The selection is effective due to the presence of genetic diversity, which can be used in plant breeding and future genetic improvement programmes. A substantial collection of various sesame genetic resources, including both wild and cultivated species, is maintained at gene banks worldwide (23).

Around 95 % of sesame genetic resources are conserved in Asia and the remaining 5 % in the United States of America. The key sesame gene banks are the NBPGR in India and the National Agro Biodiversity Centre of the Rural Development Administration in South Korea (24). In China, the Oil Crops Research Institute of the Chinese Academy of Agricultural Sciences and the US Department of Agriculture's Agricultural Research Service Plant Genetic Resources Unit (USDA-ARS-PGRA) in the United States serve as major platforms (25). For crop improvement, the important factor taken into consideration is genetic diversity and

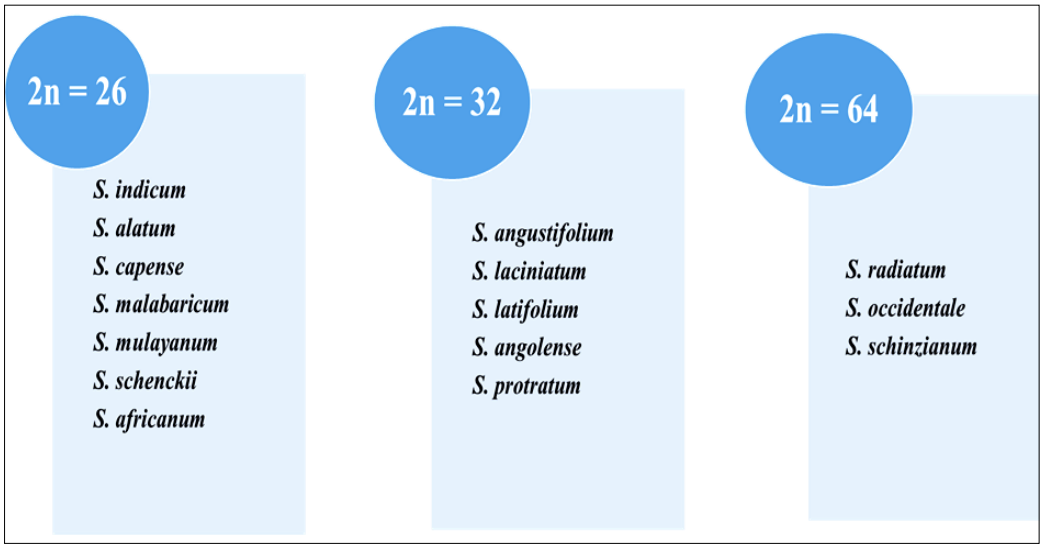

Fig. 1. Wild relatives of sesame.

population structure of the germplasm collection. It forms the foundation for conservation and it ensures robust development in the field of plant breeding (26).

Genomic resources

Functional genes

Advances in molecular biology and genome mapping have enabled the association of specific loci with agronomic traits. Some trait defining genes identified for oil content (*SIN_1010931-LG1* and *SIN_1019167-LG10)* and other functional genes of sesame are mentioned in Fig. 2.

Molecular markers

The cultivated sesame has a chromosome no of 2n = 26, with a relatively similar size for each chromosome (27). Genetic studies using molecular markers can be done for phenotypic selection in the breeding programme (4). Molecular marker studies can assess extremely diverse genotypes and population interactions in breeding operations and pinpoint target genes in various crops. Molecular markers are DNA-specific sequences used to identify the genetic diversity present in that population. Molecular markers are used in breeding programmes for the reduction of the number of cycles in breeding programmes, genetic gain, genetic diversity studies, generation of genetic linkage maps, molecular characterisation, the creation of functional online databases and the detection of genomic regions (QTLs) for various traits (28).

Markers play an important role in understanding the diversity of a crop and the study of important traits present in the wild and cultivated species of sesame. This approach has oriented plant breeding towards genetic gain and the reduction of crop production cycles. To assess the genetic diversity of sesame accessions, amplified fragment length polymorphism (AFLP), random amplified polymorphic DNA (RAPD), inter simple sequence repeat (ISSR), microsatellites or simple sequence repeat (SSR) and single-nucleotide polymorphisms (SNPS) (16).

Sesame germplasms and diversity studies

The molecular markers paved the way for genetic diversity studies in sesame. In crop improvement programme, the idea is to exploit the available genetic diversity, also a key factor in effective breeding programmes and conservation strategies (26). Many studies have been conducted on sesame and found that there is a mismatch in the geographical area and genetic distance (29). Sesame genomic sequences are available globally and markers like SSRs, SNPs and Indels have been developed for the entire genome, eventually, it has been utilised in the breeding programmes (25, 30, 31). Wild sesame species are found to be highly diverse. There is no cross-pollination during the domestication process, as is evident from the clustering pattern of wild and cultivated sesame species. There is a considerable loss in genetic diversity during domestication (32, 33). *S. indicum* and its wild relative *S. malabaricum* have a high rate of marker transferability (30).

Random amplified polymorphic DNA (RAPD) marker

RAPD markers are amplified products of anonymous DNA sequences using single, short and oligonucleotide primers, they do not require prior knowledge of the DNA sequence (4). It is used for assessing genetic diversity. Diversity studies of RAPD markers are given in Table 1.

Amplified fragment length polymorphism (AFLP)

Amplified fragment length polymorphism (AFLP) is a PCR-based marker that undergoes selective amplification of a subset of digested DNA segments to generate and compare unique genomic fingerprints. A study with twenty commercial cultivars in Venezuela with 339 AFLP, divided into four clusters, have 91 % polymorphism and a 0.28 PIC value (42). Another study of genome diversity in India, Sudan, Venezuela and Western Asia, with 10 sesame accessions, shows 95 % polymorphism (43). A study was conducted with 40 accessions of *S. radiatum* from Benin were divided into three clusters and 77 out of 224 were polymorphic (44). Diversity research of 96 accessions from various parts of the globe with AFLP markers, divided into two clusters and shows 35 % polymorphism (45).

Simple sequence repeat (SSR)

SSR genotyping utilises simple sequence repeats (SSRs) as DNA markers. SSRs, known as microsatellites and repetitive sequences

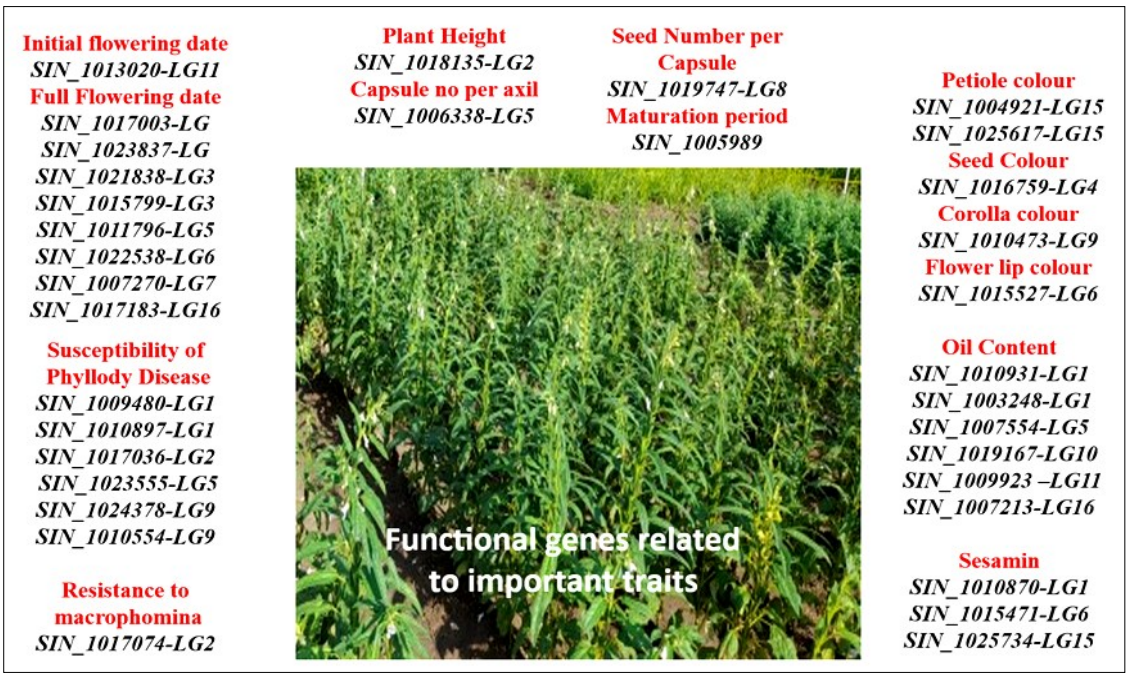

Fig. 2. Functional genes related to important traits in sesame.

Table 1. Diversity studies carried out with RAPD markers.

Materials	No. of markers	No. of genotypes	No. of clusters	Polymorphic % / no. of polymorphic bands	PIC	References
Accessions from 18 different states of India	24 RAPD	48 of total 58 accessions	6 clusters			(34)
Turkey	7 RAPD	35 out of 38 accessions	6 clusters	78 %		(35)
Venezuela	12 RAPD	Two commercials cultivars and seven	2 clusters	All of them are polymorphic	0.37	(36)
Cambodia and Vietnam	10 RAPD	22 sesame accession	4 clusters	83 %		(37)
Pakistan	10 RAPD	20 accessions	2 clusters	75 %		(38)
Iran	15 RAPD	27	5 clusters	111 out of 171 were polymorphic		(39)
India	22 RAPD	47	2 clusters	191 out of 256 is polymorphic	0.186	(40)
India	10 RAPD	9 cultivars	2 clusters	46 out of 102 is polymorphic		(41)

PIC = polymorphic information content.

found in most plant genomes. Diversity studies using SSR markers are mentioned in Table 2.

Inter simple sequence repeat (ISSRs)

A study of 128 genotypes (comprising 119 land races and nine from Ethiopia using 17 ISSR primers were divided into nine clusters, consisting of 92.2 % polymorphic percent and 0.26-0.76 PIC values (29). In the same year, a study conducted in Ethiopia with 120 accessions using six ISSR primers shows 2 main clusters and 3 outliers, showing 75.86 % polymorphic content (54). A study conducted comprising 10 genotypes from various regions of Ethiopia was divided into four clusters and contained 56.25 % polymorphic content (55). A study of 31 genotypes from the Tadla area in Morocco with 24 ISSR primers that have PIC values of 0.002 -0.350 (56).

Single nucleotide polymorphism (SNPs)

A study of 366 germplasm accessions from 18 provinces of China and 11 other countries of the world, using 89924 SNPs, were divided into 3 subgroups (57). Another study using 198 sesame accessions from four different continents, with 5292 high-quality SNPs, was also classified into three subgroups (58).

Functional markers

Functional markers are DNA markers associated with phenotypic traits and offer complete linkage to target loci, making them highly reliable for molecular breeding. Functional markers related to oil and protein content are given in Fig. 3.

Online databases

Genomic tools and techniques are significant for molecular

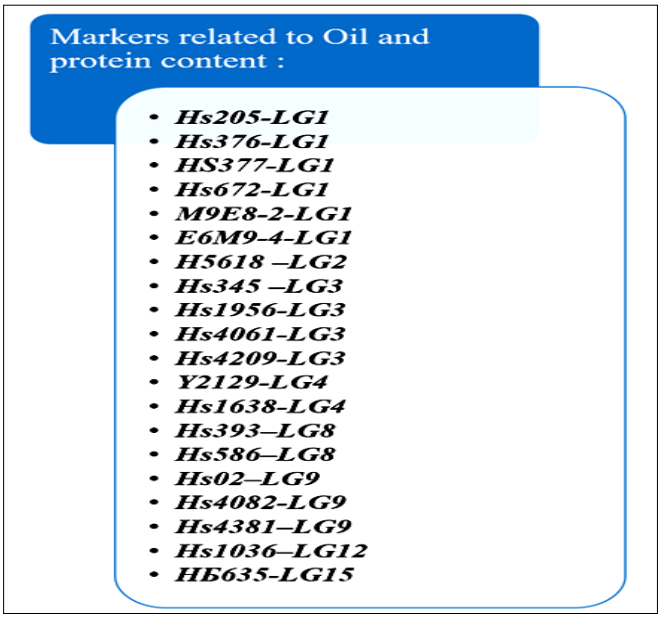

Fig. 3. Functional markers related to oil and protein content.

Table 2. SSR marker studies in diversity analysis.

Materials	Markers	No. of genotypes	No. of clusters	Polymorphic %	PIC	Reference
China	88 polymorphic SSR	Four wild germplasm accessions, 44 landraces and 82 cultivars	2 main and 5 sub-groups		0.365	(46)
12 countries	218 polymorphic SSRs	31 accessions	2 clusters		>0.60	(47)
Korea	23 informative SSR	129 sesame cultivars and landraces	2 major and 6 minors	23 out of 70	0.33-0.86	(48)
Northern Ghana	38 SSR	25 sesame landraces	Two main clusters: cluster A subdivided into four sub-clusters and cluster B sub-divided into three sub-clusters		0.91	(49)
India	10 SSR markers	36 sesame accessions	9 groups		0.27	(50)
India	eight polymorphic EST-SSR	60 globally collected genotypes	Two major groups			(51)
Bulgaria, Greece, Italy and several Asian	seven EST-SSR	35 sesame landraces	3 clusters		0.82	(52)
Nigeria	12 SSR markers	22 sesame germplasm	Three major clusters and one outlier		0.36-0.76	(53)
Accessions collected from Tigray, Afar, Amhara, Gambela and Oromiya	27 SSR markers	100 sesame accessions	4 clusters		0.25	(45)

PIC = polymorphic information content.

breeding and trait discovery (59). Sesame comprises around 554.05 Mbp; the core and dispensable accounts for 258.79 and 295.26 Mbp, respectively (60). The genome of sesame consists of 26472 orthologous gene clusters, in which 15890 genes are variety specific. Genomic resources are important for crop improvement, breeding programmes and genetic analysis (61). The information on the diversity of sesame is limited (42). So, for sesame functional genomics, an integrated database named SesameFG was created to provide sesame genomic data, phenotypic information and acts as a centralised resource for researchers to access (62). Sinbase 2.0 was an interactive and comprehensive multi-omics tool developed for sesame bioinformatics analysis (45). Sesame online databases are given in Fig. 4.

Approaches for trait improvement

Conventional breeding

The source of new genetic variations is conventional breeding. Using this method, the new variety and crop improvement activities are carried out. The presence of genetic variations is important for sesame crop varietal descriptors, morphological evaluation, genetic analysis and improvement in breeding programmes (26). For effective utilisation of germplasms, the knowledge of genetic variability, heritability and correlation among the morpho-agronomic traits is important (4, 63). Phenotypic selection is the basis for conventional breeding; high genetic advance and high heritability are the prerequisites for phenotypic selection (7). Yield shows a positive correlation among most of the important agronomic traits (64). Seed oil and oleic content show a negative correlation among the genotypes (4, 65).

Mutation breeding

Mutation breeding induces genetic variation through spontaneous or artificial mutagens, like physical or chemical agents. This method reduces the reliance of the breeding programme on the wild species and other cultivars for genetic enhancement; they have created drastic contributions to the sesame breeding. The major drawback in this programme is the production of numerous mutants, which results in undesirable effects. To introduce genetic diversity, mutation techniques have been successfully employed in sesame cultivation. A coordinated research project has been initiated by FAO to improve sesame genetically, using physical and chemical mutagens, the development of 142 mutants related to various agronomic traits. This research project also established a holistic approach to mutation breeding in sesame (66). Mutants with important agronomic traits, including enhanced plant structure, higher yield and better quality, improved seed retention, larger seed size and diverse seed colours, were identified in larger numbers in sesame. Sesame's indeterminate growth habit has also been tackled using mutation breeding techniques (67-69). An indehiscent mutant, "id," which is naturally occurring, was identified in Venezuela in the year 1942 (70). The adaptation of the mutant varieties in commercial cultivation is difficult due to undesirable factors and lower yield. Some of the varieties developed through induced mutation in sesame are shown in Table 3.

Quantitative trait locus (QTL) studies

Target quantitative traits from a population for major gene regions can be detected with the help of QTL analysis (72). The QTLs for agronomically important traits are identified for sesame crop improvement; they can be used to increase yield, identify key genes and manipulate genes in correspondence with simple and complex traits in sesame. For sesame plant breeding and genetic

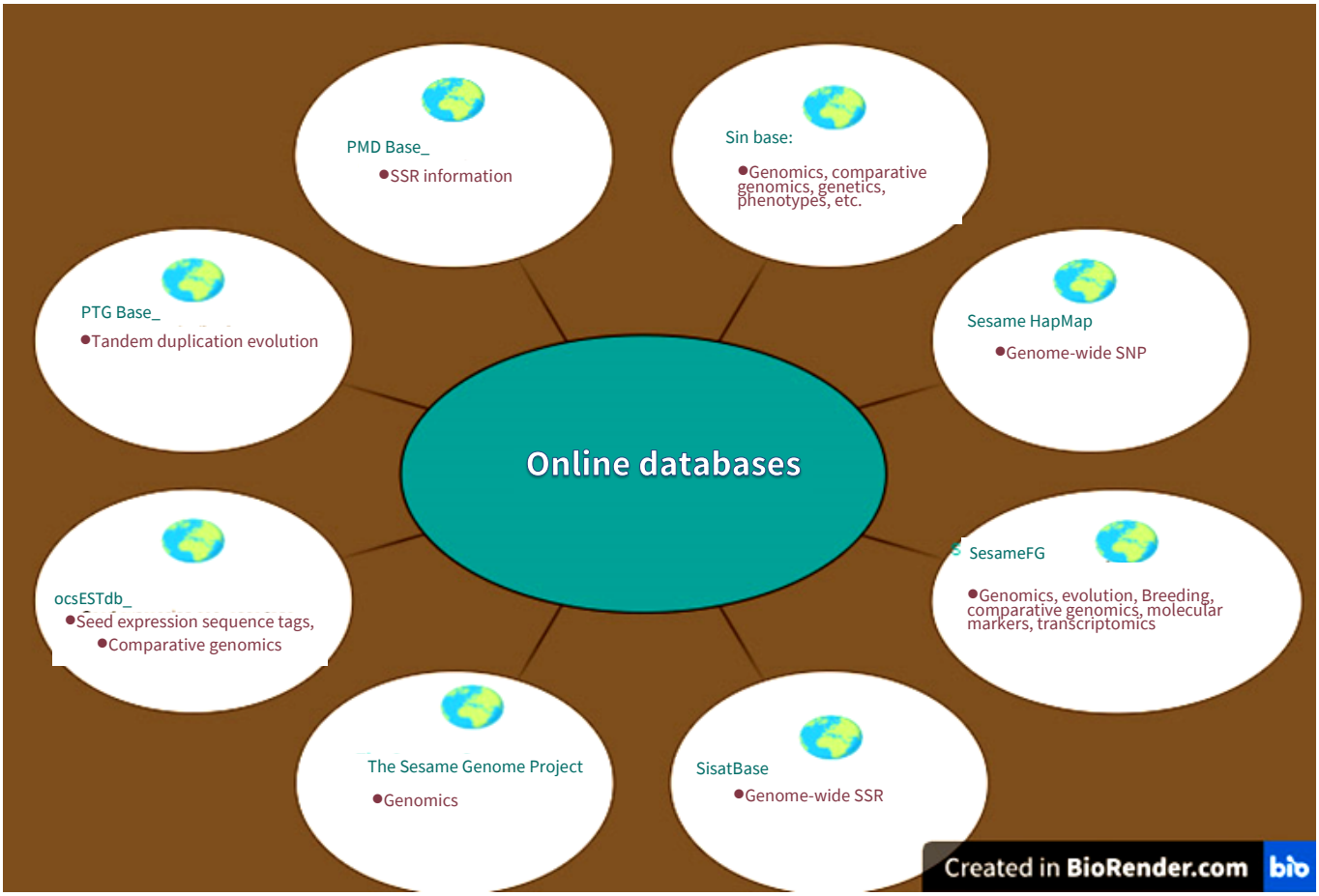

Fig. 4. Sesame online databases.

Table 3. Varieties developed through induced mutation in sesame.

Country	Mutant variety id	Mutant variety	Parent name	Registration year	Mutagens	Improved character	Mutation derived	References
India	1710	Kalika	Binayak	1980	1 % EMS for a period of 6 hrs	Semi-dwarfness, compact growth, number of seeds per capsule and increased yield (15 %)	Yes	
	1714	Uma	Kanak	1990	10 % Arsenic-q	Early and uniform maturity, high oil content		
	1713	Usha	Kanak	1990	10 % Arsenic-q	High yield, uniform maturity and resistance to disease	Yes	
China	2805	Yuzhi11	Yuzhi no. 4	2002	Gamma rays	Yield	Yes	
	2806	Zhengzhi 97C01		2002		Grain and nutritional quality	No	
	2908	Zhongzhi 11		2003	Physical mutagens	High yield, good quality, vigour, resistance to stem blight and fusarium wilt, lodging resistance	Yes	
	2807	Zhengzhi 98N09	Shang 8002 / Zheng H115	2004	Gamma rays	Seed yield and nutritional quality	No	
	2926	Zhongzhi 13		2005		Yield		
Srilanka	1728	ANK_S2	MI-1	1995	Gamma rays, 200 Gy	Resistance to diseases, high yield, vegetation (78-80 d), potential yield (1890 kg/ha) and resistance to *Fusarium*, *Phytophthora* and other plant diseases	Yes	
Iraq	1719	Babil	Local variety	1992	Gamma rays 50 Gy	Early maturity, high oil content and high yield	Yes	
	1717	Eshtar	Local variety	1992	Gamma rays, 40 Gy	Larger capsule size, reduction of branches and high oil content	Yes	
	1718	Rafiden	Local variety	1992	Gamma rays 40 Gy	Early maturity, high oil content and high yield	Yes	
Bangladesh	3160	Binatil-1	S-30	2004	Gamma rays	Tolerance to stem rot (*Macrophomina phaseolina* L.), high seed yield and high oil content	Yes	
	4486	Binatil-2	T-6	2011	Gamma rays, 700 Gy	Higher yields, branched plant architecture and tolerance to temporary waterlogged condition	Yes	
	4487	Binatil-3	Binatil-1	2013	Gamma rays, 700 Gy	Higher yields and branched plant architecture	Yes	
	4488	Binatil-4	T-6	2016	Gamma rays, 700 Gy	Higher yield, less hairy stem, leaves and capsules and tolerance to temporary waterlogged condition	Yes	(71)
Turkey	3431	Birkan		2011		Vigorous growth, taller plant height	Yes	
Egypt	1704	Sinai White 48	Giza 24	1992	200 Gy Gamma rays	White seed color of seeds, increased capsule number, 3-4 branches and wilt resistance	Yes	
	2291	Taka 1	Giza 24	1996	200 Gy Gamma rays	Resistance to wilt	Yes	
	2292	Taka 2	Mutant 2	1996	200 Gy Gamma rays	Resistance to wilt and root rot	Yes	
	2293	Taka 3	Mutant 3	1996	200 Gy Gamma rays	High yield and resistance to diseases (insects)	Yes	
Korea	1721	Ansanggae	Early Russian	1984	Gamma rays, 200 Gy	Resistance to shattering, high yield and resistance to diseases (leaf blight, *Phytophtora* stem rot and *Fusarium* wilt)	Yes	
	1722	Suwonkkae	Early Russian	1992	X-rays, 200 Gy	Good quality, higher protein content, resistance to lodging, resistance to diseases and higher yield	Yes	
	1723	Yangbaeckkae	Danbaeckkae	1995	2 mM sodium azide	Higher *Phytophthora* blight [*P. nicotianae*] resistance and lodging tolerance	Yes	
	1724	Pungsankkae	Hansumkkae	1996		Determinate growth, resistance to shattering of grains and high yield potencial	No	
	1725	Seodunkkae	Danbaeckkae	1997		Resistance to diseases and high yield	Yes	
	1726	Suwon 155		1998	Physical	Improved oil quality and high yield	Yes	
Pakistan	4491	NIAB-Sesame-2016	TS-3	2016	Gamma rays, 100 Gy	Moderately resistant to bacterial blight, phyllody and charcoal-rot diseases	Yes	
	4489	NIAB-Pearl	TS-3	2017	Gamma rays, 100Gy	Higher number of fruiting branches and capsules per plant as compared conventional varieties	Yes	
Yemen	4954	Hazaea-1	Red Locale	2021	Gamma irradiation, 400 Gy	Earliness with higher yields and higher oil content not shattering before and during the harvest	Yes	
	4955	Hazaea-22	Red Locale	2021	Gamma irradiation, 400 Gy	Earliness with seed color (white), higher yield with higher protein content	Yes	
	4956	Hazaea-3	Red Locale	2021	Gamma irradiation, 400 Gy	Earliness with seed color (white) high yield with higher protein content	Yes	

https://nucleus.iaea.org/sites/mvd/SitePages/Search.aspx.

diversity analysis, SSR markers are widely used because of their polymorphic, reproducible and codominant nature (60). Seed coat colour plays an important role; the immense oil quality, sesamin and sesamolin were observed in white-seeded sesame (73). Grain yield per plant is considered to be comprised of the number of capsules per plant, the number of grains per capsule, the grain weight and parameters like plant height, length of capsules, number of capsules per axil and axis height of the first capsule, which are strongly correlated with capsule number per plant in the grain yield of sesame. Though domestication has been done for a long time, the yield per plant is very low (74). The low yield of sesame when compared to other oilseeds is due to its indeterminate growth habit (75). QTLs related to important agronomic traits are mentioned in Table 4.

Table 4. QTLs related to important agronomic traits in sesame.

Trait	Marker type	Name of the QTL / gene	Mapping population	Flanking marker	QTL region (cM) / Chr-space (kb)	References
Growth habit	SNP	*Gene SiDt* (DS899s00170.023)	120 F2	-	-	(72)
Semi dwarf plant type	SNP	*qPH3.3*	430 RILs	SLG3_bin126-SLG3_bin12	-	(73)
Plant height	SNP	*SiDFL1* (SIN_1014512) and*SiILR1* (SIN_1018135)	705 worldwide accessions	-	-	(47)
	EST-SSRs	*Qph-6*	RILs	SBN3089-SBN3112	33.5-33.8	(46)
	InDels	*Qph-12*	RILs	ZM1466-SBI005	13.5-22.3	(46)
Basal branching habit	SLAF	*SiBH*	9378 SLAF markers	Marker129539, Marker41538, Marker31462 Tightly linked markers	-	(71)
Flowering time	SNP	*SiDOG1* (SIN_1022538) and *SiIAA14*	705 worldwide accessions	-	-	(47)
Flowers per leaf axil	SLAF	*SiFA*	9378 SLAF markers	Marker58311, Marker34507 and Marker36337 Tightly linked markers	-	(76)
Capsules per axil	SNP	*SiACS* (SIN_1006338)	705 worldwide accessions	-	-	(47)
First capsule height	EST-SSRs InDels	*Qfch-4* *Qfch-11* *Qfch-12*	RILs	SBN3000-SBN1825 SBN1622-SBN3137 ZM1466-SBI005	60.7-60.8 8.3-17.9 12.0-22.3	(46)
Capsule number per plant	EST-SSRs InDels	*Qcn-11*	RILs	SBN1622-SBN3137	11.3-17.9	(46)
Capsule length	EST-SSRs InDels	*Qcl-3* *Qcl-4* *Qcl-7* *Qcl-8*	RILs	SBN2902-SBN1034 SBN2166-SBN1014 SBN3401-SBN3441 SBN1686-SBN3565	76.1-77.4 64.1-64.2 73.8-79.0 11.0-11.2	(46)
Capsule axis length	EST-SSRs InDels	*Qcl-12* *Qcal-5* *Qcal-9*	RILs	ZM1466-SBI005 SBN3577-SBN3576 SBN3559-SBN2018	14.0-18.0 43.7-44.4 2.1-4.6	(49)
Seed coat colour	SSR	*SiPPO* (SIN_1016759)	500 RILs (F6)			(47)
	SLAF SNP	*qSCa-8.2* *qSCb-4.1* *qSCb-8.1, qSCb-11.1* *qSCl-4.1, qSCl-8.1, qSCl-11.1* *qSCa-4.1* *qSCa-8.1*	430 RILs	SLG8_bin105-SLG8_bin106 SLG4_bin63-SLG4_bin64 SLG8_bin114-SLG8_bin115 SLG11_bin1-SLG11_bin2 SLG4_bin63-SLG4_bin64 SLG8_bin114-SLG8_bin115 SLG11_bin1-SLG11_bin2 SLG4_bin63-SLG4_bin64 SLG8_bin114-SLG8_bin115	575.8 199.9 2518.0 367.8 199.9 2518.0 367.8 199.9 2518.0	(73)
Thousand grain weight	EST-SSRs InDels	*Qtgw-11*	RILs	SBN1798-SBN1765	18.2-20.2	(46)
Grain number per capsule	EST-SSRs InDels	*Qgn-1* *Qgn-6* *Qgn-12*	RILs	SBN1076-SBN2389 SBN1261-SBN1801 SBN1362-SBN3344	29.7-36.0 88.3-92.9 26.0-26.7	(46)
Dominant GMS	SSR	*SBM298* and *GB50*	Novel GMS line W1098A (backcrossing and sib mating); BC2F6	-	-	(77)
Recessive GMS	AFLP	*SiMs1*	-	P06MG04-P12EA14 P01MC08(co-segregated with *SiMs1*)	-	(6)
Waterlogging tolerance	SSR	*qEZ09ZCL13* *qWH09CHL15* *qEZ10ZCL07* *qWH10ZCL09* *qEZ10CHL07* *qWH10CHL09*	RILs	ZM22-ZM92 E16M19-E14M14a E5M12a-ZM351 M20E10-ZM428 E5M12a-ZM351 M20E10-ZM428(ZM428) closely linked to qWH10CHL09	0.0-8.0 0.0-20.0 1.0-11.5 2.0-7.0 0.0-12.5 3.0-7.0	(78)

QTL = quantitative trait loci.

Genome-wide association study (GWAS)

Genome-wide association study (GWAS) in sesame identified 33 single nucleotide polymorphism (SNP) loci for the 4 traits, of which Ch6-39270 and Ch11-142842 were highly environmentally stable and linked with campesterol and stigmasterol content variation. Candidate gene screening identified that *SINPZ1100015*, encoding a region of NAC domain-containing protein 43 in sesame, the major candidate effect gene of phytosterol variation (79).

Genome editing

Genome editing tools will create a huge impact on crop breeding in the 21st century. *Agrobacterium*-mediated sesame genetic transformation is successful and transformation efficiency is found to be nearly 42.66 % (80). Reaching higher efficiency by improving the transformation protocol is found to be difficult in sesame (81). The first successful genome editing in sesame was achieved with the help of the CRISPR/Cas9 tool. Target-induced mutagenesis in sesame for lignan biosynthesis coupled with hairy root transformation mediated by *A. rhizogenes* K599. Two sgRNAs targeting the biosynthetic genes *CYP81Q1* and *CYP92B14* are for sesamin and sesamolin, respectively. InDel mutations at the specific sites, with mutation frequencies of 90.63 % in *CYP81Q1* and 93.33 % in *CYP92B14*. HPLC analysis shows lignan content was affected in *CYP81Q1*-knockout lines; the amount of sesamolin is decreased and sesamin is nearly 1.72-fold increased. CRISPR/Cas9-mediated knockout is a promising strategy for loss-of-function studies in sesame (82).

Future perspectives

The sesame improvement lies in new techniques like the advancement of genomics, precision breeding and climate resilience approaches. With the considerable progress that has been made in identifying QTLs and developing molecular markers for important agronomic traits, these tools must now be efficiently translated into breeding pipelines through marker-assisted selection and genomic selection. The whole genome sequencing and pangenomic analysis offer unpredictable opportunities to explore the allelic variation. Future efforts must also focus on high-throughput phenotyping platforms, transcriptomics and metabolomics to unravel complex trait architectures. Strengthening global collaboration for germplasm exchange and characterizing core collections from gene banks will enrich the breeding base.

Conclusion

Sesame (*S. indicum* L.) is an oilseed crop that is both nutritionally valuable and economically important, but its development is limited by factors such as low yields, seed shattering, indeterminate growth and vulnerability to various stresses. Genetic strategies have been crucial in overcoming these challenges by improving crop productivity and enhancing resistance to both biotic and abiotic stresses, which also supports sustainability. Recent developments, such as genome editing through CRISPR/Cas9, provide precise instruments for targeted trait modification, creating new opportunities in sesame breeding. Furthermore, the creation of genomic databases and functional markers has significantly sped up genetic research. It is vital to combine traditional breeding methods with modern genomic technologies, along with effective conservation and utilisation of genetic resources, for the sustainable enhancement of sesame.

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Authors' contributions

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