

# Sesame Crop: An Underexploited Oilseed Holds Tremendous Potential for Enhanced Food Value

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## Abstract

Sesame, an important oilseed crop, highly valued for its oil quality contains plethora of nutritive substances such as proteins, carbohydrates, polyunsaturated fatty acids (PUFA), lignans (sesamin and sesamol), tocopherol, phytosterols, phytates and other micronutrients. The presence of these substances enhances the keeping quality of oil by preventing oxidative rancidity. Benefits of this underexploited crop include antioxidative, anticancer, antihypersensitive and tumor-suppressive properties. Despite of its high nutritional value, research on this valuable oilseed is meagre due to several biotic and abiotic stresses and absence of non-shattering cultivars. Thus, to explore the potential of sesame as an important oilseed possessing multifarious property, we have tried to provide a detailed overview of the crop and its genetic diversity available throughout the world. Sesame is a promising target oilseed crop for biotechnological applications and marker based studies. The genetic manipulation in the crop along with other strategies would enable development of varieties with high nutritional and functional value. Our aim is to explore the hidden heterogeneity in the crop and provide impetus for valuable oilseed research.

## Keywords

Sesame, Nutraceutical, Breeding, Germplasm, Genetic Diversity

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## 1. Introduction

Oilseed crops are diverse in the plant kingdom and belong to several families. In India, oilseed crops occupy an

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important position in the export earning potential by ranking in billions of dollars every year. However, the slow growth in the domestic production of oilseeds has not been able to keep pace with the increasing demand in the country, leading to more import, and resulting in high inflation rates. Low and unstable yields of most oilseed crops, and uncertainty in returns to investment results from the continued cultivation of oilseeds as rainfed, cover and high stressed environment crops leading to the situation of high demand supply gap. The production of high yielding oilseed cultivars by reconstituting the genetic architecture is of utmost importance to regain the economy returns. Oilseed crops are good sources of oil, protein, sugars, minerals and even vitamins. The oilseeds like groundnut, sesame, soybean and niger are important sources of nutrients and thus are consumed either directly or as ingredients of other food items.

The diverse agro-ecological conditions of India are well suited for several indigenous and naturalised annual oilseed crops. Among the nine oilseed crops grown in the country, seven are of edible oils (soybean, groundnut, rapeseed-mustard, sunflower, sesame, safflower and niger) and two are of non-edible oils (castor and linseed). India is the fourth largest oilseed producing country after USA, China and Brazil. Among the large number of oilseeds grown here, sesame lies at the sixth position of production after soybean, cotton seed, groundnut, sunflower and mustard (National Productive Council, New Delhi). It is predominantly grown in Uttar Pradesh, Rajasthan, Orissa, Gujarat, Andhra Pradesh, Tamil Nadu, Karnataka, West Bengal, Bihar and Assam. The largest producer and exporter of sesame seed in 2011 was Myanmar, secondly India followed by China, Ethiopia, Nigeria and Uganda [1]. China is the world's largest consumer and 70% of world's sesame crop is grown in Asia followed by Africa having a gross share of 26% in the world.

### 1.1. Sesame—An Oilseed Crop

Sesame (*Sesamum indicum* L.) belonging to the order Tubiflorae, family Pedaliaceae, is an important and ancient oil-yielding crop cultivated for its flavorsome, edible seed and high quality oil [2] [3]. Sesame seed contains high oil content (46% - 50%) with 83% - 90% unsaturated fatty acids, 20% proteins and various minor nutrients such as vitamins and minerals, large amount of characteristic lignans (methylenedioxyphenyl compounds) such as sesamin, sesamol, sesamolins and tocopherols [4]. The functional components together impart resistance against oxidative deterioration and provide nutraceutical value to the crop. Therefore, sesame seeds with high amounts of nutritional components are consumed as a traditional health food for its specific antihypertensive effect, anticarcinogenic, anti-inflammatory and antioxidative activity [5]-[8].

### 1.2. Taxonomy

The Indian subcontinent has been reported to be rich in diversity, especially in cultivated sesames. The observable seed colour show range from black to pure white [9] [10]. In India, besides the cultivated species *Sesamum indicum*, six wild species have been reported. These include *S. malabaricum*, closest wild relative of cultivated sesame ( $2n = 26$ ) sharing same chromosome number with the *S. indicum*, an intermediate species complex, *S. mulayanum* ( $2n = 26$ ), *S. prostratum*, *S. laciniatum* ( $2n = 32$ ) and the two introduced African species, *S. radiatum* ( $2n = 64$ ) and *S. alatum* ( $2n = 26$ ). Two species, *S. laciniatum* and *S. prostratum*, grow in Africa and India, while *S. malabaricum* grows only in India. Few wild species are being utilized economically for different purposes. *Sesamum alatum*, *S. angustifolium* and *S. radiatum* are eaten as vegetable in Africa. *Sesamum prostratum* is used as a medicinal plant. *S. angolense*, *S. angustifolium* are used as medicinal plant for skin diseases. *S. radiatum* and *S. angolense* are utilised as ornamental and for soap making or as green manure [11].

### 1.3. Origin and Domestication

Sesame is a very ancient crop, one of the oldest oil crops. Charred sesame seeds about 5000 years old, were found in archaeological excavations in Harappa [12]. Despite the fact that the majority of the wild species of the genus *Sesamum* are native to sub-saharan Africa, the origin of cultivated sesame, its progenitor and its domestication has been a controversial subject since long times as according to some, the progenitor of cultivated sesame is a taxon *Sesamum latifolium*,  $2n = 32$  from African continent [13]. Later studies refuted the concept of African progenitor of sesame and based on interspecific crosses, lignan analyses suggested that cultivated sesame has been derived from wild populations native to Indian subcontinent, the western Indian peninsula and parts of Pakistan [11] [14]-[17]. Researchers have demonstrated that sesame was first domesticated in India and

provided convincing evidences of morphological and cytological affinities between domesticated sesame and the South Indian native *Sesamum malabaricum* [11] [15]. Sesame and the wild form, *S. malabaricum* share the same diploid chromosome number,  $2n = 26$  [18]-[21]. Interspecific crosses have also yielded fertile hybrid products [22]. Molecular studies using RAPD markers have demonstrated close relation of *S. indicum* to this progenitor from Indian subcontinent [2] [23]. Additionally, results from molecular phylogeny analyses, using the two chloroplast DNA regions (ndhF and trnLF), confirmed that *S. indicum* and *S. malabaricum* are most closely related to each other [24]. The biochemical investigation of sesamin and sesamol in sesame germplasm have also revealed high lignan contents in *S. malabaricum* and sesame cultivar from Tamil Nadu, CO-1, indicating close genetic relationship shared by two species [25].

## 2. Wild Relatives as Genetic Resources

Wild relatives of crop plants constitute an increasingly important resource for improving agricultural production and for maintaining agricultural agro-ecosystems. They have contributed many useful genes to crop plants and modern varieties of crops that contain genes from their wild relatives. The conservation and use of crop wild relatives are essential elements for increasing food security, eliminating poverty and maintaining the environment. Wild species have proved useful to crop improvement as source of pest and disease resistance, stress tolerance, in providing valuable information on species relationship revealing crop evolution patterns. Wild sesame species are reported to possess several desirable traits such as high harvest index and other yield components (multilocular capsules per leaf axil, full seed set, large or medium sized seeds etc.), determinate growth habit with uniform ripening, early maturity, photo and thermal insensitivity, high seed retention, high nutritional quality (high oil and protein, high sesamin and sesamol contents, reduced anti-nutritional factors and oxalic acid in seeds). Wild sesame species are likely to exhibit tolerance to different pests and diseases *i.e.* resistance to biotic (*Phytophthora* blight, *Cercospora* spot, *Alternaria* leaf spot, phyllody, leaf curl virus etc. and abiotic (waterlogging, drought and salinity) stresses [26]-[28].

### 2.1. Genetic Wealth of Sesame—Varieties and Gene Diversity

Sesame is believed to have been originated in India where maximum variability in genetic resources is available. Wide diversity is present in the sesame germplasm for the different desirable traits such as plant height, branching pattern, leaf shape, number of capsules per axil, number of seeds per capsule, 1000 seed weight, oil content, seed color, resistance to pest and diseases etc. Sesame samples from different agro-ecological zones of India have been studied using random amplified polymorphic DNA (RAPD) technique [2]. Results showed high level of genetic diversity, indicating the nativity of the crop. Rajasthan and the north eastern states showed maximum genetic diversity. The exploitation of the available sesame diversity from these regions would enable improvement in productivity of existing sesame cultivars.

India is very rich in the genetic variability of wild and cultivated sesame and the crop has been grown under diverse agronomic conditions. Thus, Indian sesame germplasm offer a rich load of genetic variability for breeding. Wide variation in fatty acids and nutritional components found in the Indian sesame germplasm collections offer a great potential for sesame breeding [29] [30]. Moreover, identification and use of wild relatives with desirable genes has become more relevant these days because transfer of genes across species/genera is now feasible using biotechnological tools.

### 2.2. Conservation of Sesame—Core Collections

The purpose of conservation is to conserve plant genetic resources for potential future research, and as such it should support basic study and improvement of crops. The presence of a large number of uncharacterized accessions is a limitation in effective utilization of genetic diversity. Therefore, for meaningful data, the whole collection needs to be reduced to a manageable level. A core collection of germplasm is a representative set of accessions capturing the complete genetic diversity of the entire collection with minimum repetitiveness. The core subset represents a minimum of repetitiveness (about 10% of the entire collection) and provides a good working collection. Core collections of sesame germplasm have been established by the Oil Crop Research Institute of the Chinese Academy of Agricultural Sciences and the National Bureau of Plant Genetic Resources (NBPGR) of India in collaboration with the International Plant Genetic Resources Institute (IPGRI). The NBPGR at the na-

tional level has the main responsibility of sustainable management and safe conservation of diverse germplasm of crop plants and their wild relatives [31]. Large sesame collections are available at National Gene Bank at NBPGR, New Delhi with 9630 accessions stored for long term conservation at  $-20^{\circ}\text{C}$  in the cold modules and 255 *Sesamum* species maintained at cryobank (NBPGR data, 2013, [www.nbpgr.ernet.in](http://www.nbpgr.ernet.in)). Earlier, sesame core has been developed for indigenous sesame comprising of 343 accessions [31]. Recently, characterization of world sesame collection lead to development of new sesame core comprising of 172 accessions [32].

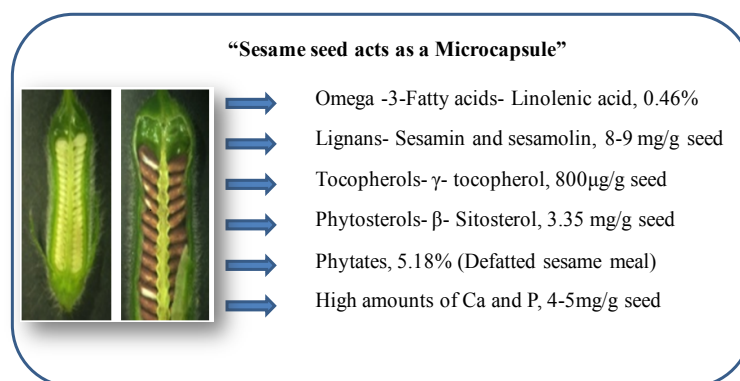
The Gene Bank of Rural Development Administration (RDA) located in Suwon, Korea have collected 7698 sesame accessions, that consist of 3538 exotic collections, 2660 indigenous collections, 1072 improved genetic stocks and 428 others [33]. In addition, conservation efforts of sesame have been done by other organization and gene banks in the world. For example the United States Department of Agriculture (USDA), Agricultural Research Service (ARS), Plant Resources Conservation Unit (PGRCU) has conserved 1226 sesame accessions originating from Europe, Africa, Asia, North America and South America [34].

### 3. Sesame Seed Dietary Components

Sesame seed is rich in oil, contains high amounts of (83% - 90%) unsaturated fatty acids, mainly linoleic acid (37% - 47%), oleic acid (35% - 43%), palmitic (9% - 11%) and stearic acid (5% - 10%) with trace amount of linolenic acid [35]. The seeds are a rich source of antioxidants and bioactive compounds including phenolics, phytosterols, phytates, polyunsaturated fatty acids and short chain peptides. Sesame cake is a rich source of protein, carbohydrate and mineral nutrients. Sesame seeds have special significance for human nutrition on account of its high content of sulphur amino acids and phytosterols. The potential distribution of bioactive components in sesame seed have been presented in **Figure 1**. Sesame seed possess many health promoting effects some of which have been attributed to a group of compounds called lignans (sesamin, sesamol, sesaminol and sesamolol). Sesame seed also contains lignan aglycones in oil and lignan glucosides [36]. The antioxidative agents (sesamin, sesamol, sesamol and sesaminol glucosides along with tocopherol make the oil highly stable and therefore have a long shelf life [37] [38]. Among the vitamins in the sesame seed, the presence of vitamin E is very interesting in relation to the effectiveness of sesame seed as a health food. Sesame seeds are a rich source of phytates and in defatted sesame meal it is 5.18%, compared with 1% in soybean meal and 1.5% in isolated soybean protein [39]. However, the high content of phytic acid and oxalic acid in sesame seed hinders the use of sesame protein as food [40].

### 4. Genetic Diversity and Biotechnological Studies in Sesame

In agriculture, the main objective of plant breeder is to improve the existing cultivars, which are deficient in one or more traits by crossing such cultivars with lines that possess the desired trait. A conventional breeding programme thus involves crossing whole genomes followed by selection of the superior recombinants from among the several segregation products. Indeed, such a procedure is laborious and time consuming, involving several crosses, generations and careful phenotypic selection along with the linkage drag (tight linkage of the undesired loci with the desired loci) may make it further difficult to achieve the desired objective. It is essential to raise the



**Figure 1.** The potential distribution of bioactive components in sesame seed depicting its high food value.

quality of sesame oil by breeding. Marker-assisted selection breeding can provide a dramatic improvement in the efficiency with which breeders can select traits of desirable combination of genes. This can be used to monitor DNA sequence variation in and among the species and create new sources of genetic variation by introducing new and economically important traits from wild relatives, landraces etc.

Genetic diversity of crops holds an important role in sustainable development and food security [41]. The presence of wild relatives, landraces, introgressed lines and elite cultivars enable selection of superior lines for trait enhancement. It is also important for selection of parents that can be used in plant breeding programs. Improvement of a crop species requires good knowledge on genetic diversity. Diversity studies can be carried out by using various methods such as morphological, biochemical and molecular markers. Morphology study has been a primary tool to estimate genetic differences among sesame genotypes. Several studies based on morphological markers have revealed presence of high genetic diversity in sesame populations [31] [42] [43]. Genetic divergence in sesame (*Sesamum indicum* L.) landraces based on qualitative and quantitative traits has also been studied [44]. The study revealed a considerable level of variation in 105 sesame accessions collected from diverse ecologies of Pakistan for a number of morphologic and agronomic traits, while limited diversity was observed among the accessions for characters like stem hairiness, flower color (white with purple shading), seed color and to some extent phyllody disease.

However, morphological markers have limitations in their ability to estimate genetic diversity because of strong influence from environmental factors, which make them highly dependent on the cultivation conditions. Biochemical studies involve study of allelic variants of enzymes known as isozymes. This technique utilizes enzymatic functions and is a powerful method of measuring allele frequencies for specific genes. Isozyme studies have been performed in sesame varieties for genetic diversity studies [45]. However, the major disadvantages shown by biochemical markers include their limited number and influence by environmental factors or the developmental stage of the plant, thus sharing similarity to morphological markers [46].

DNA markers are the most widely used type of marker predominantly due to their abundance and thus these have overcome the limitations shown by morphological and biochemical markers. Molecular markers techniques such as amplified fragment length polymorphism (AFLP), random amplified polymorphic DNA (RAPD), inter simple sequence repeats (ISSR) and simple sequence repeats (SSR) have been widely used in genetic diversity studies in sesame. RAPD study carried out on sesame reported a high genetic diversity of 0.35 among 58 sesame accessions from the Indian subcontinent and other countries [2]. RAPD markers reported a genetic diversity among 38 Turkish sesame accessions ranging from 0.14 to 0.40 [47]. Similarly, high genetic diversity of sesame was reported in Vietnam and Cambodia using RAPD estimated by percent polymorphism (83%) and genetic distance coefficient (0.03 - 0.31) [48]. An ISSR based study on sesame germplasm from Korea and other countries have revealed a low level of polymorphism and genetic distance coefficient between populations (0 to 0.25) [49]. Recently, genetic diversity studies based on ISSR have been carried out in cultivated sesame and related wild species in east Africa [50]. Six reliable ISSR primers generated 51 amplification fragments of which 70.6% were polymorphic.

Low genetic diversity (0.14 - 0.21) among groups was reported in 32 sesame germplasm collections using amplified fragment length polymorphism studies [51]. Additionally, genetic diversity studies based on AFLP have been performed in 96 sesame germplasm collections collected from all over the world [52]. The studies have reported similarity of geographical origin and morphological characteristics of sesame accessions with AFLP pattern and thus demonstrated that for genetic relatedness studies, AFLP is a reliable tool in sesame.

Most recent molecular markers utilized in tagging genes of economic importance include SSR and SNPs. Microsatellites are one of the most commonly used molecular markers to determine the genetic diversity in crop species. However, only a few studies used microsatellites to evaluate genetic diversity in sesame [53]. Study based on ten SSR markers to analyse pattern of genetic variation within and among 50 sesame populations representing the existing Ethiopian collections have been carried out [54]. The workers reported small genetic divergence for between populations than within populations.

Genetic diversity has been evaluated based on phylogenetic relationships and population structure of sesame using microsatellite markers developed from an SSR-enriched genomic DNA library of sesame [55]. A high level of polymorphism was revealed among the accessions. The population structure analysis indicated frequent hybridization and introgression events. Studies based on comparative potential of phenotypic, ISSR and SSR markers for characterization of sesame (*Sesamum indicum* L.) varieties from India have been performed [56]. The morphological clustering suggested that there was no geographical structure discernable and the varieties

were clustered independently of their geographical regions. In contrast, the ISSR- and SSR-based dendrogram analyses showed that all of the genotypes clearly clustered into their respective geographical groups. Studies based on application of microsatellite polymorphisms to evaluate the diversity in seed oil content and fatty acid composition have been performed in Nigerian sesame accessions [57]. The variability in the accessions based on microsatellite markers was closely related to the variation in oil yield and fatty acid composition, which could be potentially beneficial in efforts towards marker assisted selection for these traits.

A variety of molecular markers have been successfully used for detection of their associations with major traits of economic value in several crop plants, amongst which SNP plays an important role [58].

Single nucleotide variations in genome sequence of individuals of a population are known as SNPs. They are the most abundant molecular markers in the genome and are widely dispersed throughout genomes with a variable distribution among species. Several instances of mutations are generally observed in diverse crop species. Sequence variation examined within two lignin biosynthetic genes (cinnamoyl CoA reductase (*CCR*) and cinnamyl alcohol dehydrogenase 2 (*CAD2*) in *Eucalyptus globulus* [59]. Twenty-one single nucleotide polymorphisms (SNPs) were identified in the exons of *CCR*, of which nine were neutral mutations and 12 were missense mutations. DNA sequence variations in coding regions of two lignin genes, Cinnamate 4-hydroxylase (*C4H*) and Cinnamyl alcohol dehydrogenase (*CAD*) from *Acacia mangium* and *Acacia auriculiformis* have been demonstrated [60]. Twenty eight and thirty two SNPs were identified in the coding region of *C4H* and *CAD* region. Thus, variations in the two genes may lead to changes in phenotypic characteristics of the trees.

Recently, genome of sesame crop has been sequenced by a group from China [61]. The valuable information on genome brings in a new era of functional and comparative genomic studies in sesame. The comparative studies on domesticates, *i.e.* *S. indicum* and wild relatives would increase our understanding of limitations posed by domesticated germplasm and potential of utilization of wild relatives in crop improvement programs. In addition, sesame breeding objectives to create new varieties with high oil quality and yield potential, resistance to pathogens, water logging and drought stress would be efficiently fulfilled [62]. With the advent of high-throughput sequencing technology, abundant information on DNA sequences for the genomes of many plant species has been generated. Expressed Sequence Tags (ESTs) of many crop species has been generated and thousands of sequences have been annotated as putative functional genes using powerful bioinformatics tools. The basic objective of effective breeding programs could be achieved by improving the quality of crop plants, a direct function of their metabolite content. In addition, the quality of plant tissues determines their commercial value in relation to its flavour, fragrance, shelf life, physical attributes, etc. [63] [64].

Comparative analyses of ESTs have been studied in *Sesamum indicum* and *Arabidopsis thaliana* developing seeds [65]. They were able to identify genes involved in accumulation of seed storage products and in the biosynthesis of antioxidant lignans. Thus, analysis of ESTs from *Sesamum indicum* and *Arabidopsis thaliana* resulted in similar and different gene expression profiles in the two during seed development and identification of large number of sesame seed specific genes. In addition, full length enriched cDNA library has been generated for developing sesame seeds resulting in 41,248 ESTs [66]. Studies based on identification of homologous genes involved in oil biosynthesis with some conservative transcription factors such as LEC1 (LEAFY COTYLEDON1), PKL (PICKLE), WRI1 (WRINKLED1) regulating oil biosynthesis have been performed. 117 ESTs were possibly found to be involved in sesame lignan biosynthesis.

Molecular markers have been developed to identify morphological traits of sesame such as growth habit and closed capsule trait [67]. Recently, a high-density genetic map was constructed for sesame based on large scale marker development by specific length amplified fragment (SLAF) sequencing [68]. Specific length amplified fragment sequencing (SLAF-seq) is a recently developed high-resolution strategy for large-scale de novo SNP discovery and genotyping. The map was constructed using an F2 population and the SLAF-seq approach, which allowed the efficient development of a large number of polymorphic markers in a short time. The results obtained from the study not only provides a platform for gene/QTL fine mapping, map-based gene isolation, and molecular breeding for sesame, but also serve as a reference for positioning sequence scaffolds on a physical map, to assist in the process of assembling the sesame genome sequence.

Moreover, biotechnology techniques such as *in vitro* regeneration and genetic transformation have also been developed for sesame [69].

## 5. Sesame Breeding Objectives

Even though the sesame crop has high nutritional, medicinal and agricultural value it is losing out as an oilseed.

In spite of being a good source of “healthy oil” in terms of presence of high amounts of PUFA and high antioxidant content, it is not grown on a large extent due to very poor yields [70] [71]. The decreasing crop yield can be attributed to its cultivation in un-irrigated areas, lack of varietal replacement through development of hybrids. Low productivity has been attributed to cultivation of low yielding dehiscent varieties with low harvest index values, significant yield loss during threshing, indeterminate growth, uneven ripening of capsules and lack of improved varieties tolerant to biotic and abiotic stresses like diseases, pests and drought [72]-[74]. For meeting the required yield, advantages of the crop need to be explored such as oil quality, antioxidants, drought tolerance, low cost of production and improvement in soil water percolation **Table 1**. The low seed yield of sesame is a consequence of a lack in breeding attention [72]. Sesame production is also limited by pests, diseases, lack of uniform maturity of capsules, and seed shattering [75]. In spite of huge repertoire of sesame germplasm collections available in India, limited research efforts on the use of conventional and biotechnological methodologies have resulted in minimal success in developing biotic and abiotic stress-tolerant cultivars. The absence of efficient *in vitro* regeneration protocols further provides challenges for development of desired novel sesame genotypes.

Molecular markers are useful for a variety of purposes relevant to crop improvement. The most important of these uses is the indirect marker assisted selection (MAS) exercised during plant breeding. For this purpose, molecular markers need to be amenable to automation and high throughput approaches. The use of molecular markers is based on naturally occurring DNA polymorphism, which forms the basis for designing strategies to exploit for applied purposes. It is essential to raise the quality of sesame oil by breeding. Marker-assisted selection breeding can provide a dramatic improvement in the efficiency with which breeders can select with desirable combination of genes. They can be used to monitor DNA sequence variation in and among the species and create new sources of genetic variation by introducing new and economically important traits from wild relatives, landraces etc.

## 6. Outlook

The breeding efforts in sesame should be targeted on production of white seeded varieties with high returns, short duration of the crop, drought resistance, phyllody resistance, semi-rabi condition, high-temperature tolerance, higher yields, improved plant architecture and indehiscent capsules. The research on sesame breeding has enabled the selection of superior genotypes with high nutritional value. Thorough investigation of genotypes led to detection of lines with increased seed tocopherol, lignan content and high amounts of unsaturated fatty acids [25] [29]. These results have contributed to the identification of the genetic basis underlying the trait, which is a good starting point for future breeding advances in this field. The future research efforts on sesame breeding should be targeted on detection of correlation between oil content and domestication events in sesame as this would be of immense value to the breeders. The great variability for nutritional attributes suggests that these selected accessions may be as useful as parents in hybridization programs to produce sesame with value added traits. In addition, the importance of sesame for value addition of sesame oil has been ignored and thus attention should be given to develop varieties with high amount of unsaturated and polyunsaturated fatty acids. The development of varieties with low or zero anti-nutritional factors like oxalic and phytic acids needs attention for its value addition. In addition, the efforts should also be made to develop low free fatty acid (<2%) sesame varieties.

**Table 1.** Future perspectives of sesame breeding.

Sesame breeding objectives—Future considerations
<b>Growth habit</b> —Determinate with uniform and short flowering period, Synchronous capsule ripening
<b>Capsules</b> —Nonshattering capsules with well filled seeds
<b>Seeds</b> —Uniform shape, well filled, color and size to fetch better market price, Desirable flavour, high oil content, high lignans for prevention of rancidity, high tocopherols, high polyunsaturated fatty acids, high phytosterols.
<b>Yield</b> —High seed yields of good quality adaptable to various environmental conditions.
<b>Resistance to biotic and abiotic stresses</b> —Phyllody disease (Most destructive disease in sesame) resistance. Alternaria leaf spot, Charcoal rot, Fusarium wilt resistance caused by fungi. Development of drought and heat resistant cultivars

Therefore, studies on this valuable oilseed sesame with high antioxidant and nutraceutical value should not be undermined as it possesses potential market niches and it is of utmost importance to unlock the untapped genetic variation hidden in the sesame germplasm. The exploitation of wild sesame germplasm for breeding purposes would enable substantial expansion of gene pool of domesticates and incorporation of novel traits, particularly pest and disease resistance (phyllody disease), high yield and enhanced oil quality.

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