Chapter 15
Advances in Sesame (*Sesamum indicum* L.) Breeding

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Abstract Sesame is a high value and important oilseed crop owing to its dietary uses, health benefits and industrial applications. Sesame oil maintains a balanced fatty acid composition with more or less equal and higher percentages of unsaturated fatty acids. In spite of its several merits, it is behind in genetic improvement as compared to other commercial oilseed crops. Narrow genetic base, less attention to genetic improvement and cultivation in marginal lands with poor management practices are the major constraints for increased yield potential. Sesame has ample scope to breed cultivars with greater yield, as the gap between the potential and realized yields in this crop is enormous. Capsule shattering leads to heavy loss of seed yield and the crop is sensitive to a wide array of biotic and abiotic stresses. Innovative breeding approaches such as mutagenesis, somaclonal variation, interspecific hybridization, somatic hybridization and genetic transformation can be used to restructure the plant's ideotype. In addition, identification of candidate genes/quantitative trait loci (QTL) and their monitoring in succeeding breeding cycles using molecular markers can pave the way for genetic improvement in sesame. In this pursuit, the authors present a detailed outline of the importance of sesame as a potential oilseed crop, its biosystematics, floral biology, genomics, breeding goals, present status of breeding strategies and attention to prospects for sustainable production and productivity in future.

Keywords Achievements · Breeding constraints · Breeding strategies · Future prospects · Importance · Sesame

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15.1 Introduction

Sesame (til or gingelly) (*Sesamum indicum* L.) is recognized as the *queen of oil seeds* owing its high value oil quality and plethora of nutritive substances. Sesame is an important vegetable oil and its consumption is forecast to be 100 million mt by 2030 (Troncoso-Ponce et al. 2011). Traditionally, sesame seeds are used for making confectioneries, cookies, cake, margarine and breads. It is also used in paint formulation due to its unique semidrying property (Bedigian 2003a). It acts as one of the components for the manufacture of soaps, cosmetics, perfumes, insecticides and pharmaceutical products (Warra 2011). The oil is highly resistant to oxidative rancidity due to the presence of antioxidant lignans (Mohamed and Awatif 1998). Moreover, it promotes health and may provide relief from hypertension, oxidative stress and neurodegenerative diseases (Nakano et al. 2002).

Sesame is ranked ninth among the top 13 oilseed crops which make up 90% of the world production of edible oil (Adeola et al. 2010; http://www.statista.com/statistics/267271/worldwide-oilseed-production-since-2008/). India has the largest area under sesame which makes it the largest producer of sesame seeds (15%) in the world with an estimated production of 636,000 mt and productivity of 3419 kg/ha in 2013 (FAOSTAT 2013). India's total edible oil consumption is projected to increase 5.5–6% per annum. Therefore, there is an urgent need for enrichment of oil content in sesame seeds. A gene family comprising 34 lipid transfer protein type 1 (LTP1) genes are confirmed to have a major role in lipid biosynthesis (Wang et al. 2014) by strengthening the transport of fatty acids, acyl-CoAs and other lipid molecules (Kader 1996). Variation and selection are the two basic requirements of genetic improvement in any crop. Without variation, selection becomes ineffective. There exists a wide array of variation in oil content (43.3–51.7%) among the available genotypes (Spandona et al. 2013) and this can be increased by conventional breeding methods. Compared to other edible oil crops, sesame harbors a comparatively higher oil content (up to 55% of dry seed), and is thus an attractive potential model for studying lipid biosynthesis (Ke et al. 2010). However, the pattern of inheritance of oil content in sesame is not clear. Sesame oil is more variable in terms of quantity of oil than quality (fatty acid composition) (Baydar et al. 1999a). Erucic acid content remained unaltered while stearic, linolenic and arachidic acid contents were reported to be least affected over changing environments (Were et al. 2006a, b). There is no conclusive information on the number of genes controlling oil content and the exact nature of the gene (s) meant for biosynthesis of lipids although many researchers (Aladji Abatchoua et al. 2015; Vekaria et al. 2015) have addressed this problem using different base materials. In this pursuit, the authors reviewed the present status of breeding and suggested future prospects to increase yield potential and oil quality in sesame.

15.1.1 Cultivation Area, Production and Productivity

The major cultivated areas of sesame (90%) are in Asia and Africa. World sesame production was estimated at 6.1 million mt in 2016, with Tanzania, Myanmar, India, China and Sudan as the largest producers (https://www.tridge.com/intelligence) and FAOSTAT 2017) (Fig. 15.1). India ranked third in sesame production (866 million mt) with the largest area (1947 million ha) among different countries in 2015–2016 (http://agritech.tnau.ac.in/demic/pdf/2016/Price%20Forecasting%20for%20sesame-english.pdf). Despite its unique position, productivity in India is extremely low (413 kg/ha), below the world average yield (535 kg/ha), and about one-third the productivity of China (1234 kg/ha) (Figs. 15.2 and 15.3).

15.1.2 Uses and Nutritional Composition

Sesame seeds and their high quality oil are traditionally used as key ingredients in food products, salad preparation, pharmaceuticals and for making margarine, confectioneries, cookies, cake, breads, cosmetics (skin softener and in massage), antibacterial mouthwash and perfume (Bedigian 2003a). Nutrient-rich sesame seeds are mixed with cereals, rice, noodles and other dishes at mealtime as condiments. The seeds are often mixed with warm jaggery and sugar to make sweet balls eaten as a snack.

Low-grade oil is used locally in soaps, paints, varnishes, insecticides, lubricants (Blal et al. 2013), and as source of illuminants and biodiesel (Ahmed et al. 2010). The meal after oil extraction contains 30–35% protein that makes a rich feed for poultry and livestock. Sesame oil has both dietary (edible oil) and therapeutic applications. Sesame oil is also used as laxative, a solvent for intramuscular injections and as an ingredient in Ayurvedic medicine. In addition, sesame oil is used as a coating on stored grains to prevent weevil attacks.

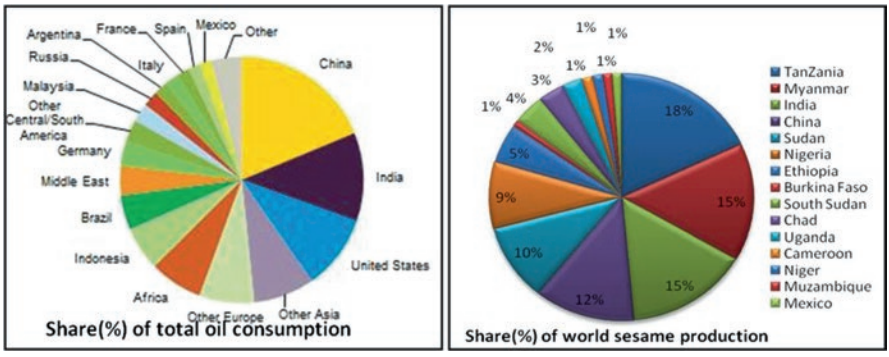

Fig. 15.1 Global scenario of total oil consumption and sesame production (2016). (Sources: https://ihsmarkit.com/products/fats-and-oils-industry-chemical-economics-handbook.html; https://www.tridge.com/intelligence)

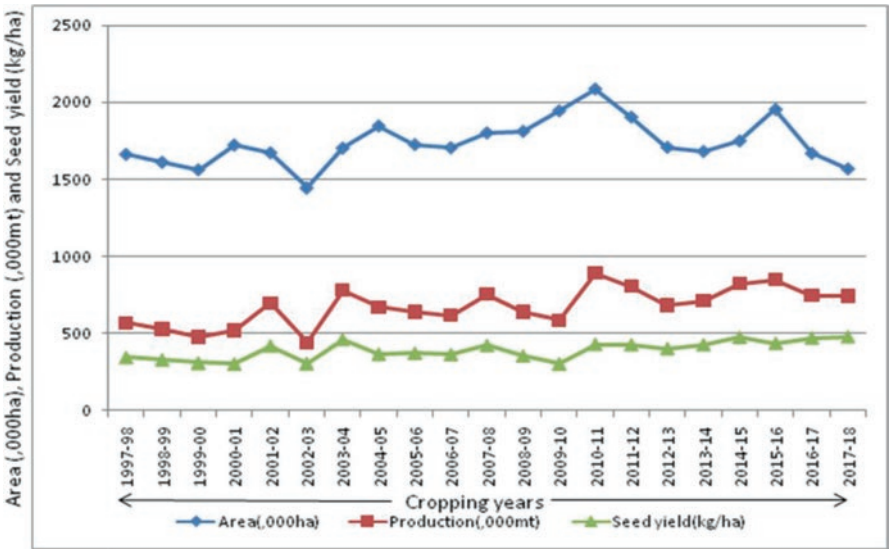

Fig. 15.2 Area, production and productivity of sesame in India. (Source: Ministry of Agriculture, Govt. of India)

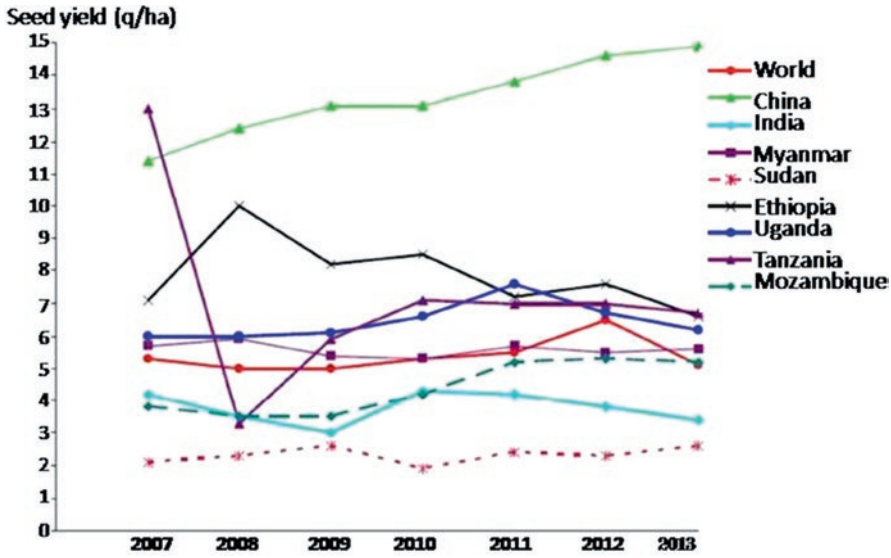

Fig. 15.3 Productivity of sesame in leading countries. (Source: FAOSTAT 2015)

Table 15.1 Nutritional value per 100 g dried sesame seeds

Constituents	Content
Moisture	4.7 g
Energy	573 kcal (2400 kJ)
Carbohydrate	23.4 g
Sugar	0.3 g
Dietary fiber	11 g
Protein	17.7 g
Fat	49.7 g
Saturated	7 g
Mono-unsaturated	18.8 g
Poly-unsaturated	21.8 g
Minerals	
Calcium	975 mg
Phosphorous	629 mg
Iron	14.6 mg
Zinc	7.8 mg
Magnesium	351 mg
Sodium	11 mg
Potassium	468 mg
Vitamins	
Vitamin A	9 IU
Thiamine (B1)	0.79 mg
Riboflavin (B2)	0.25 mg
Niacin (B3)	4.52 mg
Pyridoxin (B6)	0.79 mg
Folate (B9)	97 μg
Vitamin C	0.00 mg
Vitamin E	0.25 mg

Source: Link to Full USDA Database Entry (https://ndb.nal.usda.gov/ndb/foods/show/3620)

Sesame seeds are rich in oil and protein, and have high dietary energy value 5730 kcal/kg. Chemical composition of seed reveals that it contains 49.7% oil (fat), 17.7% protein and 23.4% carbohydrate (Table 15.1). Oleic acid (43%), linoleic acid (35%), palmitic acid (11%) and stearic acid (7%) are the most abundant fatty acids present in sesame oil, which together contribute 96% of total fatty acid content (Elleuch et al. 2007). Seeds are rich in iron, magnesium, manganese, copper and calcium, and important vitamins B_1 (thiamine) and E (tocopherol). Sesame fat is preferred in the food industry due to its delicate flavor and stability as well as high-quality cooking value. The nonglycerol fraction of sesame oil contains sesamin and sesaminol lignans that contribute to its oxidative stability and antioxidative property (Wu 2007). These antioxidants restrict oxidative damage to cells by detoxifying oxidative radicals. In addition, the above lignans serve as dietary supplements purported to prevent cancer and heart disease.

Sesame serves as the cheap source of high content dietary protein; vitamin B-complex which helps to improve the metabolism and nervous system, organs, eyes, muscles, skin and hair; magnesium, calcium, iron and copper – useful for red blood cell production, bone mineralization, enzyme synthesis and hormone production; high fiber content and high in mono-unsaturated fatty acid, oleic acid, lower bad cholesterol and increased good cholesterol in the blood and purported prevention of coronary artery disease and strokes. In addition, sesame proteins are rich in lysine, tryptophan and methionine.

15.1.3 Quality Features of Sesame Oil

Sesame seeds harbor oil in the cotyledons regarded as one of the highest oil content (up to 55%) among oil crops. It is used as edible oil and also in the pharmaceutical and chemical industries (Blal et al. 2013). The oil is colorless with distinct sweet flavor and quality is similar to olive oil (Kapoor 1990). It harbors a wide array of phytochemicals with antioxidant, antifungal, hypolipidaemic and hypoglycemic properties. Oil content and its chemical composition vary with genotype, color and size of the seed. Oil content in sesame varies from 35% to 63% among the available world collection of germplasm lines. Sesame oil maintains a balanced fatty acid composition with more or less equal or higher proportion of unsaturated fatty acids e.g., oleic acid (up to 39%) and linoleic acids (up to 46.26%) (Liu et al. 1992). The major saturated fatty acids are palmitic acid (7.9–12%) and stearic acid (4.8–6.1%) along with small quantities of vaccenic, linoleic, arachidic, behenic and eicosenoic acids. Cultivars with exceptionally high oleic or linoleic acid are rare. The stearic, oleic and linoleic acid contents differs between determinate and indeterminate cultivars. Determinate cultivars generally have higher stearic and oleic acids, and lower linoleic acid compared to indeterminate ones. Capsule position on the plant also affects the relative quantities of the fatty acids. Palmitic, stearic and oleic acids tend to increase up the stem while linoleic acid decreases. The fatty acid composition is strongly influenced by environmental factors (year, season). Among fatty acids, erucic acid content does not vary with the year, while stearic, linolenic and arachidic acid are least affected. Linoleic acid content has been reported to increase under cool growing conditions. The peroxide value and free acidity increases during storage over 5 weeks. The iodine value of the sesame oil decreases over a period of storage suggesting the loss of unsaturation in the fatty acids. Sesame oil is rich in essential fatty acids needed for normal growth and development.

Sesame oil is high quality semi-drying oil suitable for use in paint formulation (Bedigian 2003a). The presence of natural antioxidants such as sesamin, sesamolin, gamma tocopherol and sesamol, prevent rancidity of oil and, therefore, sesame oil is blended with less stable vegetable oils to improve their stability and longevity.

Usually, light colored and thin-coated seeds are higher in quality and content of oil than dark-colored seeds. In contrast, black sesame seeds are abundant in fiber, calcium, zinc, iron and vitamin B (Saha 2017).

Sesamin has bactericide and insecticide properties, but sesamolin has only insecticidal properties for which it is used as a synergist for pyrethrum insecticides. The oil elicits formation of higher concentration of lecithin, a phospholipid that acts as a powerful emulsifier (facilitating the dissolution of saturated fatty acids in an aqueous medium) to control blood pressure.

15.1.4 Health Benefits

Sesame is used for many reputed health promoting and anti-ageing benefits. The seeds and oils are widely used around the globe for the following health benefits. Sesame seeds are rich in magnesium which regulates the insulin and glucose levels in blood, lessening the chances of hypertension by reducing blood pressure and to manage diabetes effectively (Miyahara et al. 2001). High fiber content, phytosterol content and polyunsaturated fatty acids in seed also displace blood cholesterol. Fermented sesame often exerts anti-allergic effects (Jung et al. 2018). In addition, high zinc, calcium and phosphorus content in sesame purportedly prevent osteoporosis (Onsaard 2012). It also said to reduce inflammation due to the high copper content in sesame seeds. Intake of sesame seeds in the form of various food products is reported to clear up worms in the intestinal tract and also improve digestion due to its high fiber content (helps in making food ball up and move through the digestive tract) and hence, reduces constipation and diarrhea. Sesame seeds are rich in antioxidants and reduce the effects of free radicals (Nupur et al. 2010). This purportedly reduces the chances of colon cancer.

Sesame oil is also used as carrier oil for many cosmetic products. It serves as a good moisturizer and massage oil (making the skin soft), and is said to improve blood circulation and joint pains. Sesame oil may improve blood circulation due to high copper content required to produce red blood cells. It is an anti-aging of skin due to sesamol (an antioxidant) and vitamin E (gamma-tocopherol-an isomer of vitamin E) that prevent the skin cells from oxidation, repairs damaged skin cells and is claimed to avoid the appearances of wrinkles (Weldemichael and Juhar 2018). Antibacterial properties of linoleic acid and palmitic acids of sesame oil prevent bacterial infections of skin wounds. The high magnesium and phytate content of sesame oil makes it a natural sunscreen as it serves as a natural UV protector.

High zinc, copper and calcium content in sesame oil may improve bone growth. In addition, high iron content in sesame oil may act as a natural cure of anaemia. Nutritionally, it is rich in vitamin B-complex and vitamin D; while high zinc and magnesium content may boost metabolism. Sesame oil purportedly prevents diabetes by stabilizing blood glucose level (Miyahara et al. 2001) and may keep hepatitis and migraines at bay. In addition, use of sesame oil may help in treating premature graying of hair and boost dental health. Consumed as part of a balanced diet, sesame may have health benefits; however, there is scant scientific evidence to substantiate the various claims of its medicinal properties.

15.2 Biosystematics

15.2.1 Origin and Distribution

Sesame is one of the oldest oilseed crops in the world. It belongs to the genus *Sesamum* and the family Pedaliaceae, which contains more than 38 species (Kobayashi 1991). Most of these species are distributed in the tropics and subtropics of Africa and some are common in both Asia and Africa. Archaeological surveys demonstrate domestication of sesame in South India about 1500 years ago and the sesame trade with other countries (Mesopotamia) dates back to 2000 BC (Fuller 2003). There exists high morphological and cytogenetic homology (Bedigian 2003a, b) and close molecular affinity (Nanthakumar et al. 2000) between cultivated sesame (*S. indicum* L.) and the south Indian native species *S. mulayanum* (progenitor). In addition, genetic variation is enormous among the cultivated forms of Indian origin (Ganeshan 2001). Uncu et al. (2015) revealed a common pattern of gene flow between *S. indicum* and *S. mulayanum.* Therefore, it is believed that the wild form *S. mulayanum* is the progenitor and the Indian subcontinent the origin of sesame (Ganeshan 2001).

15.2.2 Taxonomy and Cytogenetic Elucidation of Sesame Evolution

Taxonomically, *Sesamum* is related to *Utricularia gibba* as revealed by high throughput genome sequencing; it is estimated to have diverged from *U. gibba* approximately 98 million years ago. The 38 species are classified into three groups on the basis of chromosome numbers. A few important species are indicated below (Table 15.2).

Table 15.2 Important *Sesame* species with chromosome number variation

Group	Species	Chromosome number	References
1	*Sesamum indicum* *S. latum* *S. capense* *S. malabaricum* *S. mulayanum* *S. schenckii* *S. africanum*	2n = 26	Ram (2011)
2	*S. prostratum* *S. laciniatum* *S. angolence* *S. angustifolium*	2n = 32	Ram (2011)
3	*S. radiatum* *S. occidentale* *S. schinzianum*	2n = 64	Ram (2011)

The basic chromosome number in sesame is x = 8 and 13. Giemsa banding allows identification of all the 13 chromosomes. The most closely related genera *Cerathotheca* and *Pedalium* contain the basic chromosome number x = 8; while chromosome number of the wild form *Sesamum mulayanum* (progenitor) is the same (x = 13) as the cultivated species *S. indicum*. A number of researchers have reviewed the evolutionary relationship within and among the chromosome number groups (2n = 26, 32 and 64) (Nayar and Mehra 1970; Prabhakaran 1996). The detailed taxonomic hierarchy of the present-day cultivated sesame (*Sesamum indicum* L.) is as follows:

Kingdom: Plantae – Plant kingdom
Sub-kingdom: Viridiplantae
Infrakingdom: Streptophyta
Superdivision: Embryophyta
Division: Tracheophyta
Sub-division: Spermatophytina
Class: Magnoliopsida
Superorder: Asteranae
Order: Lamiales
Family: Pedaliaceae
Genus: *Sesamum*

15.3 Botany, Floral Biology and Crossing Techniques

15.3.1 Botany

Sesame plants are generally tall and branched with an indeterminate growth habit. Some nonbranching/shy branching types are also found. Plants are annual or biannual herbs, the stems bear ridges, the leaves are sessile at the bottom and petiolate from middle to top, with entire margins; sometimes with lobed leaves. Leaves are arranged in opposite phyllotaxy and carry oil glands on the dorsal side. Flower color is mostly white, but pink, purple or various shades of purple-white flowers also occur.

15.3.2 Floral Biology

Flowers are solitary, axillary, shortly pedicilate and zygomorphic with pendulous tubular corollas 3–4 mm in length (Fig. 15.4). They are hermaphrodite and borne (singly or in groups) in the leaf axils. Each flower bears 4 stamens in didynamous condition (2 long and 2 short), filaments are dorsifixed, epipetalous and anthers dehise longitudinally. The gynoecium is multicarpelar with a superior ovary (hypogynous) with a long style and bifid stigma. The flower produces nectar in a nectary

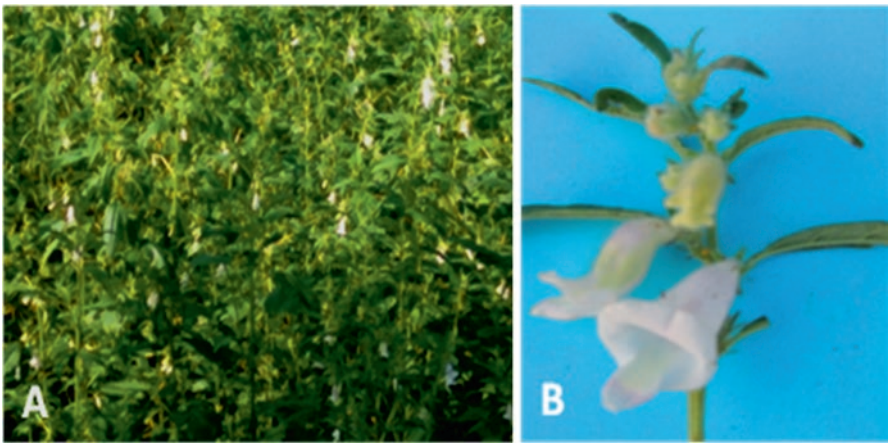

Fig. 15.4 Sesame: (**a**) Field view, (**b**) Floral morphology

disk-like structure surrounding the ovary. The calyx bears 5 fused sepals. The corolla is tubular with a lobe upwards. One of the petals is extended and serves as a landing platform for the visiting insects.

Stigma receptivity varies with genotype (Langham 2007) and it usually lasts 24 h after flower opening (Abdel et al. 1976), although loss of viability within 14 h is also reported (Yermanos 1980). In addition, some reports state that the start of stigma receptivity is from 2 h after anthesis (Free 1993) and duration of pollen viability for 24 h at 24–27 °C after dehiscence of the anther (Yermanos 1980).

15.3.3 Mode of Pollination

Sesame is predominantly a self-pollinated crop although outcrossing occurs and may vary from 5% (Langham 1944) to as high as 68% (Ashiri 2007) in field-grown crops under tropical condition. Therefore, required isolation distance is approximately 180–360 m. Flowers open at morning; anthers dehisce very shortly and stigma remain viable for about 24 h. Pollination must occur between 7 and 11 am to ensure a greater fruit set; the flower withers after 4–6 h of anthesis.

15.3.4 Selfing and Crossing Techniques

Crossing between parent varieties differing in flowering and maturity duration are staggered and sown thrice at 10-days interval. The varieties are grown in 3 rows each of 4 m length on every sowing. Any off-types are rouged out. Hybridization is initiated as soon as about 50% of plants of a variety start flowering.

Selfing in sesame can be ensured by tying the corolla tips of mature flower buds with threads in the evening. For emasculation, the epipetalous corolla is pulled out

leaving the gynaecium intact before the opening of the flower. A plastic straw with one side bent, is used to cover the emasculated flower bud at evening. Pollination is carried out the following morning and the plastic straw is placed in position. Alternatively, the corolla (with stamens intact) of the desired male parent, which is about to open is placed on to the emasculated flower using a speck of fevicol (Das 1990) for pollination and follow-up fertilization. A speck of fevicol is to be placed on the top of the corolla in late afternoon hours to prevent its opening.

15.4 Factors Affecting Sustainable Production and Quality of Sesame

Genotype Farmers prefer high yielding stable sesame cultivars with inherent resistance to major pests and diseases, good end use quality, and exportable quality (white seed color, large seed size and good flavor). The cultivar must be resistant to bacterial blight in high rainfall areas, early maturing in low rainfall areas and resistant to phyllody under irrigated condition.

Adaptability The cultivars and breeding lines so developed have poor adaptability to production systems in the area of cultivation. Selective mid-early genotypes with tolerance to biotic and abiotic stresses can cope best with the changing environments across different locations.

Yield Potential Important components traits e.g. number of capsules per plant, seeds/capsule and 1000-seed weight are the important consideration for improvement of productivity. Eight-loculed plants have more seeds per capsule but they are not necessarily the highest yielding cultivars as they bear a comparatively fewer number of capsules.

Harvest Index Modification of plant architecture is needed to improved the harvest index. This can be achieved by selection of medium plant height (around 1.0 m) with high density capsule bearing starting from 15 to 20 cm above the ground.

Crop Management Sesame is mostly grown under low-input conditions. Global average productivity of the crop is around 340 kg per ha, but it may go up to 2250 kg per ha using advanced management practices (Brigham 1987). Selective sesame genotypes with a specific ideotype and wider adaptability can endure in diverse environments and respond better to intensive management practices.

Biotic Stress Resistance Sesame is sensitive to bacterial blight, *Fusarium* wilt (*Fusarium oxysporum* Schlecht. emend. Snyder & Hansen) and charcoal rot (*Macrophomina phaseolina* (Tassi) Goid.) in high rainfall areas and phyllody (caused by *Phytoplasma*) under irrigated condition (Ojiambo et al. 1999). Similarly, the crop may be drastically affected by major insect pests such as the leaf webber/roller and capsule borer (*Antigastra catalaunalis* Duponchel), sphinx moth

(*Acherontia styx* Westwood), aphids (*Aphis gossypii* Glover) and gall-midge/gall fly (*Asphondylia sesami* Felt). There is a need to develop cultivars with multiple resistance to the above biotic factors.

Abiotic Resistance Sesame is generally cultivated in marginal lands. Therefore, cultivars with inherent tolerance to drought stress and better water use efficiency are mostly preferred. In addition, sesame is sensitive to salinity, waterlogging and chilling which limit sustainable production.

Shattering Resistance Almost all cultivars are of the shattering type and 99% of the fields are harvested manually, leading to 60–70% yield loss under dry weather (Georgiev and Stamatov 2005). There is a need to reorient breeding strategy to alleviate the high costs of manual harvesting and yield loss due to shattering. Development of new high-yielding cultivars with semi-indehiscent capsules is a possible option to fit mechanized farming.

Oil Content and Fatty Acid Composition Sesame is a high value high yielding oil crop. Oil yield can be increased by improving mature seed yield and oil content (˃50%). Light seed color cultivars harbor higher oil content than the dark seeded cultivars. A balanced fatty acid composition with proportionately higher percentages of unsaturated fatty acid (linoleic and oleic acids) as compared to saturated fatty acid (stearic and palmitic acids) together with higher amounts of antioxidants (sesamol, sesaminol) and tocopherols is needed for high quality export value.

Confectionery Quality For confectionery uses, the breeding lines should have favorable seed color, size and shape (Fig. 15.5). White-seeded types are most preferred for export. In addition, these should be screened for desirable texture and seed coat thickness, and oil flavor using specific descriptors. The seeds should be readily dehulled by processors for use in sweets, halva and bakery products or milled to produce high-grade sesame oil.

Fig. 15.5 Seed color development at physiological maturity. (**a**) White seed, (**b**) biscuit color seed, (**c**) black color seed

15.5 Genetics

15.5.1 Genetics of Qualitative Traits

The knowledge of inheritance pattern of various traits is a priori to any genetic improvement in sesame. Pioneering works on sesame genetics date back to Langham (1945–1947). Thereafter, a number of studies were published on the mode of inheritance of various traits using diverse sesame germplasm resources. Subsequently, these were reviewed by Joshi (1961), Weiss (1983) and Ram (2011) in detail. The information is summarized in Table 15.3.

Table 15.3 Inheritance pattern of qualitative traits in sesame

Traits	Mode of inheritance
Growth habit	Branched dominant over unbranched (Nb, nb)
Stem characteristics	Normal vs fasciated stem – single or duplicate genes involved (F_1, f_1; F_2, f_2)
Flowering trait	Solitary is dominant over multiple (2–3) flowers and capsules/ leaf axil (T, t)
	Indeterminate is monogenic dominant over determinate habit (Dt, dt) (Cagirgan et al. 2009)
Capsule trait	Bicarpellate is dominant over quadricarpellate (Tc, tc)
Male sterility	Fertility is dominant over male sterility (Ms, ms)
Capsule dehiscence	Dehiscent vs indehiscent are monogenic with pleiotropic effect (Id, id) or two genes with complementary gene action
Capsule hairiness	Capsule hairiness is dominant over hairless
Capsule number per leaf axil	One capsule/leaf axil is dominant over three capsules/axil
Phyllody resistance	Single dominant gene (Singh et al. 2007), or two dominant genes with complementary gene action (Vanishree et al. 2013)
Powdery mildew	Susceptibility is dominant over tolerance and is controlled by two independent recessive genes with complementary epistasis (Rao et al. 2011)
Alternaria leaf spot	Polygenic inheritance with significant additive effect
Stem rot	Polygenic inheritance with equal proportion of positive and negative alleles in the parents
Fusarium wilt	Polygenic inheritance with equal proportion of dominant and recessive genes in the parents
Seed coat color	Brownish black is monogenic dominant over white seed color. In some crosses, F_2 plants segregated into black, brownish white, brown and white-seeded types indicating complex nature of inheritance (Falusi 2007). Zhang et al. (2013) identified two major genes with additive-dominant – epistatic effects; and four QTLs (QTL1-1, QTL11-1, QTL11-2, QTL13-1) with additive-dominant-epistatic effects

15.5.2 Genetics of Agro-economic Quantitative Traits

Gene action for agro-economic quantitative traits has been studied by different researchers. Some also reported the importance of both additive and nonadditive components of variation. Usually these follow the inheritance pattern as below, although they may vary depending upon different sets of materials. They include the traits listed in Table 15.4.

The presence of both additive and nonadditive gene action operates for all morpho-economic traits (Mungala et al. 2017) although their magnitudes proportionately differ. Singh (2004) reported higher variance due to general combining ability (GCA) than specific combining ability (SCA) effects for days to maturity, plant height and 1000-seed weight, indicating a greater role of additive gene action in the inheritance of these characters. In contrast, Solanki and Gupta (2003) analyzed combining ability for yield and its components in a 6-parent half diallel cross and reported that GCA and SCA effects were similar in magnitude for seed yield indicating equal importance of both additive and nonadditive gene action for productivity. In another set of materials, variance due to the SCA effect was greater than that of GCA for number of capsules per plant and seed yield indicating greater role of nonadditive gene action in the inheritance of these traits (Saravannan and Nadarajan 2003; Singh 2004). Preponderance of nonadditive gene action was also revealed for days to maturity, plant height, number of primary branches per plant, capsule length, seeds per capsule, 1000-seed weight, yield and oil content except days to flowering where GCA was greater than SCA (Prajapati et al. 2006). Balaram et al. (2018) reported the preponderance of additive effects for days to flowering, seeds/capsule and oil content. Differential magnitudes of GCA and SCA effects for above various traits could be due to different composition of experimental materials used. Mishra et al. (2016) reported additive gene action for days to maturity, number

Table 15.4 Inheritance pattern of agro-economic quantitative traits in sesame

Traits	Mode of inheritance
Flowering duration	Additive gene action
Leaf chlorophyll content	Nonadditive
Capsule length	Both additive and nonadditive
Seeds per capsule	Both additive and nonadditive
Capsule bearing nodes	Additive gene action
Main fruiting stem length	Both additive and nonadditive
Number of capsules/plant	Both additive and nonadditive
Photoperiod response	Polygenic inheritance
Photosynthesis rate	Additive gene action
Leaf area index	Nonadditive
Height to first branch	Nonadditive
Effective branches/plant	Nonadditive
Harvest index	Additive
Seed yield	Both additive and nonadditive

of primary branches/plant and capsule breadth for which pedigree selection would be an appropriate method to have higher selection response for these traits. In contrast, heterosis breeding may be exercised for period of flowering, number of capsules/plant, oil content and seed yield/plant owing to their greater magnitude of nonadditive variance. However, number of days to cessation of flowering and seeds/capsule exhibit more or less equivalent GCA and SCA effects. In this context, diallel selective mating along with recurrent selection would be useful for recovery of desirable homozygotes in later generations. Tripathy et al. (2016a) reported that a number of groups of genes or loci having recessive alleles with increasing effect might be involved in realization of high seed yield and involvement of modifiers in the background genotype could not be ruled out. Pratap x RT103, CST785 x E8 and BS 5-18-6 x Phule Til-1 revealed high SCA effect for seed yield in which at least one parent in each case was reported to have high GCA (Tripathy et al. 2016b). On the other hand, a few of the crosses e.g. B67xE8, B67xRT 103 and RT 103xT13 being good specific combiner for oil content, did not involve any parent with high GCA indicating role of dominance and epistatic gene interaction in these crosses. Such above crosses are likely to be useful for genetic improvement of seed yield and oil content. Balaram et al. (2018) reported a preponderance of additive effects for days to flowering, seeds/capsule and oil content.

15.5.3 Genetic Basis of Oil Content and Fatty Acid Composition

Comparative genomic and transcriptomic analyses have revealed the mechanisms of lipid biosynthesis in sesame. Lipid biosynthesis is associated with tandem duplication in Type 1 lipid transfer genes, truncation of genes related to lipid degradation and tissue specific expression of genes in the triacylglycerol biosynthesis pathway during early stage of seed development (https://phys.org/news/2014-03-genome-sesame-oil biosynthesis.html). Thus, most of the candidate genes related to lipid biosynthesis are involved in one of the three pathways: (a) fatty acid and TAG (triacylglycerol) synthesis and elongation, (b) TAG degradation or (c) fatty acid dehydrogenation (e.g. Stearoyl-ACP desaturase, determining the ratio of saturated and unsaturated fatty acids). Li et al. (2014) performed the association mapping of oil content and found it varied from 27.9% to 58.7% and protein content from 16.7% to 27.8% among 369 worldwide germplasm accessions under 5 environments using 112 polymorphic SSR markers. Among these, 19 and 22 SSR markers were linked with oil content and protein content, respectively, with high phenotypic variation. In addition, a genome wide association study revealed a total of 13 significant associations for oil content (Wei et al. 2015).

Usually, oil content maintains a weak positive correlation with oilseed yield but, negatively with the protein content in sesame. Modern cultivars more or less show lower nucleotide diversity than landraces. However, there exist no significant asso-

ciations between the allelic variation for the seed oil content and the yield traits, suggesting that it would be possible to generate sesame cultivars with both high yield and oil content.

Fatty acid composition displays less genetic variability among cultivars than the oil content. The genetics of oil content indicated importance of both dominant and additive gene action. A group of genes with *dominant* and *increasing* alleles and some modifying genes are likely to be involved in the biosynthesis of oil in seeds. Whole genome scanning can help to gain insight into the oil biosynthesis to understand oil content in the seed. Recently, a gene family consisting of 34 lipid transfer protein type 1 (LTP1) genes was identified to have key role in lipid biosynthesis. LTP1 family help in oil accumulation by strengthening the transport of fatty acids, acyl-CoAs and other lipid molecules. However, until now, there is no conclusive information on the number of genes controlling oil content and fatty acid composition. As many as 46 candidate causative genes encode the enzymes involved in fatty acid biosynthesis and oil content. Lignification and black pigmentation in the seed coat are controlled by two major candidate genes and these are also associated with large variation in oil content. SNP analysis using genome wide scanning revealed a 100 bp 'A' in the low-oil allele of cv. Mishuozhima. This allelic variant has a very high expression level in seeds 8 days after pollination. The genes strongly associated with oil content in sesame also have a major role for sesamin and sesamolin content. Fortunately, such allelic variation for the seed oil content is not linked to yield traits, suggesting the possibility to breed high yielding sesame varieties with high oil content. Weak negative correlation exists for oil content with palmitic and linoleic acids, and feeble positive association with stearic and oleic acids. This indicates no overlap(s) between the associated loci for the traits. However, the content of different fatty acids is often correlated and the shared associations are possibly due to common candidate genes (*SiACNA, SiDGAT2, SiFATA, SiFATB, SiSAD*) being involved.

15.6 Genomics of Sesame

The sesame genome size is about 350 Mb and it is largely unexplored. The phenotypic and genome sequence information is available from the data base SesameFG (http://ncgr.ac.cn/SesameFG/) which can serve as an important tool for functional genomic research and molecular breeding of sesame (Wei et al. 2017). Dossa et al. (2017) developed a SSR marker-based sesame genome map. As many as 27,148 genes have been annotated in a sesame reference genome which has a relatively low proportion of repetitive sequences (28.5%) (Wang et al. 2014). Dinucleotide repeat motifs are the most common (84.24%), followed by 13.53% trinucleotide, 1.65% tetranucleotide, 0.3% pentanucleotide and 0.28% hexanucleotide motifs in the ses-

ame genome sequence (Wei et al. 2014). Candidate genes represent loci that encode components of metabolic or signaling pathways known to be related to the corresponding phenotypes or based on expression profile. Using whole sesame genome analysis, Supriya and Bhat (2018) revealed 8244 functional genes, 58 transcription factors and 25,069 transposable elements in the sesame genome. Multiple loci that related to several agronomic traits such as plant height (Ding et al. 2013), disease resistance (Zhang et al. 2012), drought tolerance (Li et al. 2013), waterlogging tolerance (Zhang et al. 2014), seed coat color (Zhang et al. 2013) and oil and protein content (Li et al. 2014) had been identified in sesame land races (cvs. Baizhima and Mishuozhima). Next generation sequencing (NGS) revealed a total 1,332,025 SNPs (single nucleotide polymorphisms) and 506,245 indels (insertion-deletions) by genome comparison with Zhongzhi 13 (white seeded). Indels are more polymorphic than SSRs but these are comparable in terms of deciphering genetic diversity (Wu et al. 2014). Seed color varies from black, intermediate colors to white. Black-seeded types usually harbor less oil but more protein and lignin content (Zhang et al. 2013) than black-coated seeds. The polyphenol oxidase (PPO) gene produces black pigments is the key regulatory gene of sesame seed coat color (Wei et al. 2017). Sesame was domesticated 5000 years ago, then dispersed to quite different environment along trade routes and thereby underwent natural selection to adapt to new conditions (Bedigian 2003b). During the domestication of land races, some of the variations (indels) may have come from the natural selection. Rare SNPs and indels can serve as useful markers to assist genetic improvement and delineate status of variation across genomes (Ohmido et al. 2000). The regions saturated with high SNPs and indels contain genes with elevated localized mutation rates or recombination hot spots (Lercher and Hurst 2002). High stringency filtering resulted in the identification of 420 SNPs distributed among 13 linkage groups. These markers will be useful to tag QTLs of metabolic and agronomic traits (Uncu et al. 2016).

15.7 Genetic Diversity

In any crop breeding program, the existence of adequate genetic variability is the prerequisite for selection to be effective to create the desired genotype. In general, the genetic variability in available *Sesamum* germplasm is limited. Sesame has a long history of domestication. Owing to continuous cultivation in marginal lands under rainfed situation, some plant types have adapted to survival through natural selection. Therefore, in the course of sesame evolution, most of the valuable genes associated with high yield have been eroded. In addition, modern plant breeding with limited use of land races (as parents), has presumably narrowed the genetic basis of cultivated sesame. Genetic variation was subsequently reduced by genetic drift and selection. Therefore, broad-based genetic resources have become more

important for genetic improvement in sesame. A complete array of sesame germplasm consists of: (a) wild distant relatives and closely-related species, (b) local land races, (c) obsolete breeding lines including mutants and (d) newly developed improved varieties.

Knowledge of genetic variation, inheritance pattern and interrelationship of plant traits is a priori for effective use of germplasm in any genetic improvement program (Ganesh and Thangavelu 1995). Germplasm banks are reservoirs of the valuable genes essential for improvement of crop species. Despite high nutritional value, sesame is still lagging behind in the achievement of breeding perspective. No international agency has yet come forward to work on sesame (Bedigian 2003a, b). Centers for sesame genetic diversity are found in India, China, Central Asia and Ethiopia (Hawkes 1983). However, information on their genetic diversity is not explicitly documented. Such a stock of information is of immense importance for planning genetic conservation strategies and for use of elite germplasm lines in breeding programs.

Crop genetic diversity can be determined with the aid of morphological, biochemical and molecular markers (Stuber 1992) or in combination. Several studies have exploited the morphological genetic diversity in sesame populations (Arriel et al. 2007; Bisht et al. 1998). However, characterization of cultivars for genetic diversity by molecular markers is of great value to assist phylogenetic relationships, parental line selection, population structure and allele distribution among germplasm lines and to design breeding strategies. Presently, molecular techniques including isozymes (Isshiki and Umezaki 1997) and DNA profiles based on amplified fragment length polymorphism (AFLP), simple sequence repeats (SSRs), intersimple sequence repeats (ISSRs) and random amplified polymorphic DNA (RAPD), all widely used to study genetic diversity in sesame (Abdellatef et al. 2008; Erkan et al. 2004; Kim et al. 2002; Kumar et al. 2012; Pham et al. 2009; Salazar et al. 2006; Uncu et al. 2015). Dossa et al. (2016) studied the genetic relatedness among 96 sesame accessions collected from 22 countries and found that the genetic diversity observed in African accessions was lower than that in Asian accessions. Indels are more polymorphic than SSRs; hence, they can comparatively reveal maximum degree of allele diversity in a set of genotypes. Wu et al. (2014) detected 325 alleles including some unique alleles among 130 Chinese sesame accessions. Morphological and molecular markers help scientists and plant breeders in screening and selection (Pham et al. 2011) of germplasm and their use in breeding program. However, little progress has been made in this regard in sesame (Bhat et al. 1999). Development of genetic maps (Dossa et al. 2017) and availability of few closely-linked molecular markers (using the AFLP technique) have made it possible for reliable screening of sesame germplasm. Uzun et al. (2003) detected closely-linked molecular marker for the closed-capsule mutant trait and it helped to introgress shattering resistance in sesame.

15.8 Germplasm Conservation

Germplasm serves as the source of valuable genes. Conservation of genetic resources has had an impact on today's cultivated crops (Ishaq and Falusi 2008). Wild related species and local land races are primary sources of genetic variation due to the evolution of the crop over time. The preservation and protection of genetic resources may be done in their natural habitat (in situ) e.g. national parks and government reserves (Ford-Lloyd and Jackson 1986). However, ex situ conservation (collection and maintenance by research institutes/universities) ensures safety, proper characterization, documentation and ready accessibility of materials. Genetic stocks are also preserved in sealed test tubes over nutrient media in the form of cells in a culture room, calli or tissue (in vitro conservation) or cryopreserved for more than 10 years at ultra low temperature (cryopreservation). In addition, DNA banks are most preferred for those species that do not produce seeds and are not possible to conserve in situ due to high risk factors.

India has a rich diversity of sesame and a large collection of landraces maintained at the National Bureau of Plant Genetic Resources (NBPGR). The Ethiopian Institute of Agricultural Research collected 221 germplasm lines during 2002–2004 and preserved these lines at the Werer Agricultural Research Center (Teshome et al. 2015). A core collection of world sesame germplasm accessions (over 2100) is held in Israel, and now also maintained in gene banks in Kenya, Korea and India. These were developed to facilitate efficient germplasm management and effective use in crop improvement (Mahajan et al. 2007).

15.9 Breeding Goals

Sesame breeding objectives are primarily focused on improved seed retention in the capsule, increased oil content, uniform maturity and disease resistance. For more clarity, the following breeding goals deserve special mention:

(a) Ideal plant type: Determinate plant type, higher numbers of leaf axils for more capsule bearing/plant, high yield and stability of performance;
(b) High oil content, improved fatty acid composition and other quality traits;
(c) Low or zero antinutritional factors (oxalic and phytic acids) for value addition;
(d) Development of CMS lines for ease in hybrid seed production;
(e) Resistance to biotic stress: insect pests (leaf eating caterpillar, gall fly) and diseases such as phyllody (virus, mycoplasma), bacterial leaf spot (*Pseudomonas sesami*), powdery mildew, wilt and leaf curl;
(f) Semi-indehiscence of capsules;
(g) Resistance to abiotic stresses: drought, waterlogging and salinity, particularly under the scenario of global climate change.

15.10 Distinctness, Uniformity, Stability Characterization and Prebreeding

It is in vogue to characterize cultivars for DUS (distinctness, uniformity, stability), characteristics based on morphological expressions (Goodrich et al. 1985). However, often the morphological markers are not quite enough to reveal the genetic diversity between the morphological overlap cultivars and the morphological identical accessions. DNA and seed storage protein profiling of genotypes can provide an analytical tool for genome probing and reliable cultivar identification (Gilliand 1989). In addition, this serves as a useful tool to eliminate duplicates and/or very similar genotypes resulting in a core germplasm stock (prebreeding) without reducing the existing genetic diversity.

Sesame displays contrasting genetic variation in morpho-economic traits, oil content, quality features (seed shape, color, length) and resistance to biotic and abiotic stresses. This helps to identify segregants in a crossing program and accelerate crop improvement (Weiss 1983). Mathur et al. (2016) characterized 16 *Sesamum* cultivars for DUS testing. Similarly, Singh et al. (2017) carried out DUS testing of 83 cultivars of sesame using 18 morphological descriptors. They revealed maximum variation in seed coat color, capsule shape, leaf lobe, leaf size, leaf serration, capsule hairiness, capsule arrangement, stem hairiness, petal color, seed size, days to 50% flowering, branching pattern and petal hairiness. The standard evaluation system using DUS characteristics as per the Protection of Plant Varieties and Farmer's Rights (PPV & FR), Govt. of India for sesame are given in Table 15.5.

15.11 Breeding Approaches

Creation or existence of genetic variability is a prerequisite for selection of better plant types and follow-up establishment of a pure breeding line in sesame. A general scheme of different breeding approaches followed in sesame breeding is shown in Fig. 15.6.

15.11.1 Plant Introduction

Useful new sesame seed are in vogue, introduced from their place of origin to new areas of cultivation across geographical boundaries and as such used directly or recommended for release for commercial cultivation after minimum selection. Two new outstanding cultivars, cv. Dangur (EW 013) and cv. Chalasa (EW023), in Ethiopia are such introductions. The Mexican cv. Yori 77 was introduced to Northern Australia where it has performed well. The Venezuelan cv. Morada was a selection from introduced materials from Republic of Congo and also performed well in Tanzania. Similarly, cv. Early Russian was introduced from Texas and released directly in South Korea (https://books.google.co.in/books?isbn=1420005367). In

Table 15.5 Distinctness, uniformity, and stability (DUS) characteristics of sesame

Characteristics	States	Score (1–9)	Example cvs.	Observation stage	Assessment type
Days to 50% flowering	Early <36 Medium 36–45 Late >45	3 5 7	RT 125,RT 54 TKG 21, JCS94 Rajeswari	45	VG
Flower petal color	White Light purple Dark purple	1 2 3	Kalika RT 54 RT 103	45	VS
Flower petal hairiness	Absence Sparse Dense	1 3 5	– RT 125 Rajeswari	45	VS
Plant height of main stem (cm)	Short <75 Medium 75–125 Tall >125	3 5 7	RT 125, JTS 8 GT 1, N 32 Rajeswari	65	MS
Plant branching	Absent Few 1–2 Medium 2.1–4.0 Profuse branching >4	1 3 5 7	N32 GT 1, JCS 94 TKG 55, RT-T25,T13, RT 46	65	VS
Plant branching pattern	Basal branching Top branching	1 2	RT 127 AKT 64	65	VS
Stem hairiness	Absent Sparse Dense	1 3 5	Rajeswari T 12 B67, RT 46	65	VS
Leaf lobes	Slight lobed Deeply lobed	1 2	GT 10, N 32 Rajeswari	65	VG
Leaf size	Small Medium Large	3 5 7	VRI 1, Gauri TKG 22 Rajeswari	65	VG
Leaf margin serration	Weak Strong	3 5	TKG 21 Sweta Til	65	VG
Capsule hairiness	Absent Sparse Dense	1 3 5	Rama, T 78, Chandana JCS 94, GT 2	65	VS
Capsule locule number	4 6 8	3 5 7	TKG 22 – Adarsh 8	75	VS
Capsule shape	Tapered Narrow Oblong Broad oblong	1 2 3 4	GT 10 TKG 21 Phule Til-1 –	100	VG
Capsule number per leaf axil	1 More than 1	1 9	Thilak G.Til-1, GT 2	100	VG

(continued)

Table 15.5 (continued)

Characteristics	States	Score (1–9)	Example cvs.	Observation stage	Assessment type
Capsule arrangement	Alternate Opposite Cluster	1 2 3	RT 46 TKG 22, N32 G.Til-1, GT 2	100	VG
Capsule length (cm)	Short <1.5 Medium 1.5–2.5 Long >2.5	3 5 7	– Adarsh 8, GT 2 AKT 64	100	MS
Days to maturity	Early <75 Medium 76–85 Late 86–95 Very late >95	3 5 7 9	RT 54 RT 125 Swetha Til Rajeswari	100	VG
Seed coat color	White Grey Light brown Dark brown Black	1 2 3 4 5	TKG 21 Uma Rama Thilak Krishna	100	VS
Seed:1000 seed weight (g)	Low <2.5 Medium 2.5–3	3 5	Kalika TKG 55	100	MG
Seed oil content (%)	Low <45 Medium 45–50 High >50	3 5 7	Tilottama Krishna TKG 21	100	MG

Source: Guidelines for DUS testing on sesame, PPV&FR Authority, Govt. of India
VS & VG: Visual assessment of individual and group of plants, respectively
MS & MG: Measurement of individual plants and group of plants, respectively
Growth stage code: 45–50% flowering, 65% complete flowering, 75% complete capsule formation, 100% maturity stage

addition, the new introduced cultivars/breeding lines serve as valuable starting material for intensive breeding programs.

15.11.2 Mass and Pureline Selection

Mass and pureline selection is the most ancient and basic breeding approach in which desired plants are selected from genetically variable populations. Local land races are the target for such a selection process. A land race may be a domesticated, locally adapted or genetically heterogeneous traditional variety cultivated over time in a certain ecogeographical area (Casanas et al. 2017). At times, farmers and breeders made unconscious or conscious selection of similar looking plants (mass selection) to improve the locally adapted genetic stocks. Alternatively, a few plants distinctly different from the local land race are often selected and grown plant on a row basis to assess their merit based on progeny performance (pureline selection). In

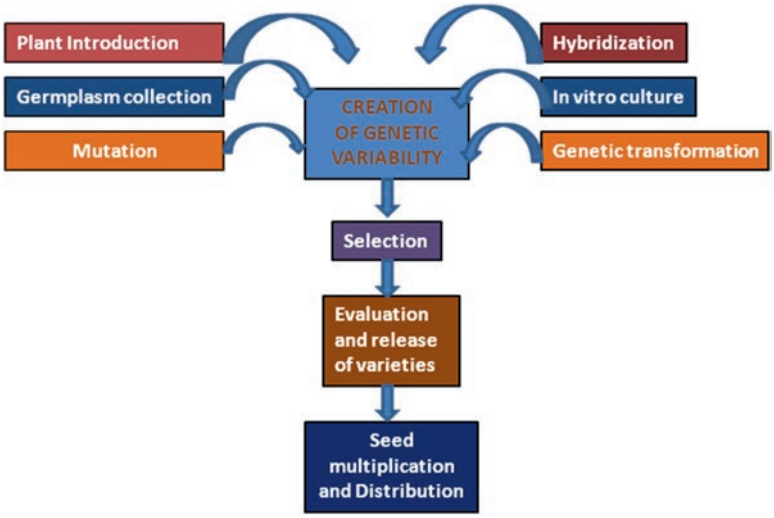

Fig. 15.6 Breeding approaches in sesame

self-pollinated crops, varieties developed through mass selection are in fact composed of a mixture of purelines (https://www.britannica.com/science/plant-breeding/Breeding-self-pollinated-species). Hence, these cultivars show wider adaptability and stability of performance over environments than individual purelines. A number of sesame varieties have been developed using the above selection process.

15.11.3 Hybridization

Most of the national production of sesame comes from landraces which are less productive than exotic genotypes due to a low level of resistance to biotic and abiotic stresses. Therefore, it is often necessary to combine desirable traits from different parental lines into a single plant by hybridization. Selection of desirable segregants with suitable gene combinations is of practical value for development of new varieties. Bisht et al. (2004) successfully recovered high-yielding sesame plants from progeny of 103 crosses. Pungsankkae is an example of a high-yield mutant variety (Islam et al. 2016), which was released in Korea by crossing a Korean variety with the Israeli determinate mutant dr-45.

15.11.4 Mutation Breeding

Well-adapted, high-yielding varieties which are popular in a locality but lack one or two important quality traits are selected for mutation induction. Low doses of mutagens (gamma-rays 150–800 Gy and fast neutrons 30–80 Gy) are more suitable for

inducing desirable mutations (Ashri and van Zanten 1994). For chemical mutagenesis, seeds are first pre-soaked in water for 24 h at 4 °C and then treated with chemical mutagens such as ethyl methane sulfonate (EMS: 0.4–1.0% v/v) solutions with phosphate buffer (pH = 7) for 2–4 h or sodium azide (NaN_3) solution (4–6 mM) with phosphate buffer (pH = 3) for 4–6 h at 18–24 °C (Ullah et al. 2012).

15.12 Breeding Strategies

15.12.1 Breeding for Ideal Plant Type

15.12.1.1 Determinate Type

Ashri (2007) identified the first determinate sesame mutant dt-45 from a M_2 population of Israeli cv. No-45 irradiated with gamma-rays (500 Gy). In addition, three true-breeding determinate mutants (dt-1, dt-2, dt-3) were derived from cv. Muganl 1-57 and another three such mutants (dt-4, dt-5, dt-6) were isolated in the Çamdibi cv. following irradiation of seeds with gamma rays (150–750 Gy) Cagirgan (2006).

15.12.1.2 Formation of Increased Number of Leaf Axils

In sesame, flowers are produced in the leaf axils and later develop into capsules. Therefore, the extent of capsule bearing depends upon the number of leaf axils per plant (Fig. 15.7). Theoretically, a greater number of leaf axils and capsules/leaf axil per plant would result in higher seed yield. This can be achieved by a plant type with short internodes and determinate flowering.

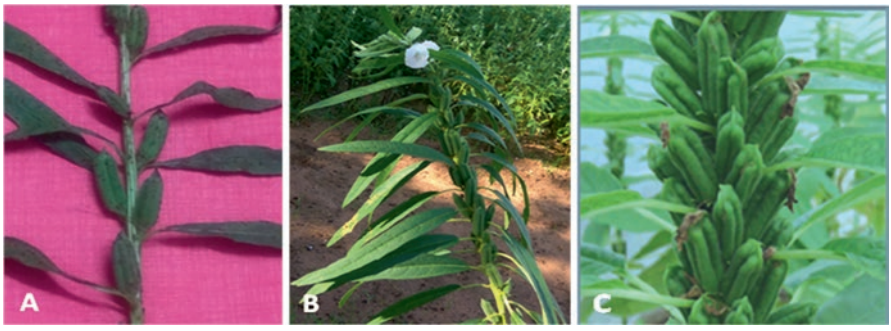

Fig. 15.7 Capsule bearing in sesame. (**a**) Poor capsule density, (**b**) Medium capsule density, (**c**) Very high capsule density per leaf axil

15.12.1.3 High Yield and Wide Adaptability

Tall-stature plant types with longer duration are not suitable for crop rotation; the ideal plant type of sesame for rice-fallow would be: (a) short stature and profuse fruit set, (b) short duration and high seed set and (c) moderate basal branching and high productivity (Ganeshan 2001).

Preferably, genotypes that exhibit medium plant height, moderate branching, determinate habit, high capsule density with moderately long capsule bearing starting from 15 to 20 cm above the ground, reach physiological maturity before the first few capsules dry, release seeds upon sun drying after harvest and are expected to yield better over environments. The number of capsules and dry-weight per plant are reported to have a significant positive correlation with seed yield and these also exert a higher magnitude of direct effects on seed yield (Abdalla 2017). In addition, increased initial vigor, a deep rooting system, non-lodging and lanceolate hairy leaves are favorable for plant establishment and higher seed yield. A monogenic recessive determinate growth habit mutant, termed dt45, with a very unique plant architecture and with clustered capsules was induced by gamma rays (500 Gy) in the Israeli cv. No. 45 (Ashri 1988, 1995). Also, short flowering period mutations (synchronous maturity) were induced by EMS and gamma rays in Thailand (Wongyai et al. 1997).

15.12.2 Breeding for Oil Content and Fatty Acid Composition

Sesame oil is highly preferred due to its exceptional quality. Sesame seeds harbor 44–57% oil (Borchani et al. 2010), but Baydar et al. (1999a, b) claimed oil content can vary from 34% to as high as 63%. Estimation of oil content of African sesame showed also wide variability of oil (29–51%) (Were et al. 2006a, b). In addition, Azeez and Morakinyo (2011) reported wide variation in fatty acid composition among Nigerian sesame accessions. This envisaged enough scope for improvement of oil content and fatty acid composition in sesame. Higher proportion of linoleic and linolenic acid content in seeds drastically affects oil stability and other quality features. Conventional breeding methods in vogue are effectively used to increase oil content in sesame and, successively, have produced sesame varieties with high oil content (Baydar et al. 1999b). In addition, genetic modification can be an alternative way to achieve high oleic acid and low linoleic and linolenic acids content.

15.12.3 Induction of Novel Variants

The induction of novel variants involves induction of novel sesame plant types by treatment with mutagens (chemical/physical) and thereby avoids the use of wild/related species for genetic improvement. The mutants induced include higher yield

(Wongyai et al. 2001), improved seed retention, determinate habit, modified plant architecture (Cagirgan 2006), synchronous maturity, earliness, resistance to diseases, genic male sterility, larger seed and changes in seed coat color (Hoballah 2001), higher oil content and modified fatty acid composition (Arslan et al. 2007). Mutation breeding has been practiced to induce a number of useful morphological and physiological mutants (Ashri 1985; Micke et al. 1987). A number of mutants (Kalika, Uma, Usha) have been released as improved cultivars in India. Some mutants are useful in physiological, genetic and molecular studies.

15.12.3.1 Disease Resistance

Currently, sesame breeding for disease resistance is the main focus in several countries. An induced mutation with moderate resistance to *Fusarium* and *Rhizoctonia* and resistance to *Corynespora* and *Phytophthora* has been reported (Lee and Choi 1985); it was released in South Korea as cv. Ahnsan. Similarly, Pathirana (1992) successfully isolated induced mutations for resistance to *Phytophthora* following irradiation with gamma rays; and one of these mutant lines was released as cv. ANK-82 in Sri Lanka.

15.12.3.2 Pest Resistance

Thus far, no efforts have been made to induce mutations for pest resistance, but identifying lines with tolerance or resistance to devastating pests in sesame such as webworm/leaf webber and capsule borer (*Antigastra catalaunalis*), sphinx moth (*Acherontia styx*), aphids (*Aphis gossypii*) and gall-midge/gall fly (*Asphondylia sesami*) would be very helpful.

15.12.3.3 Shattering Resistance

A spontaneous indehiscent mutant (id) was recovered by Langham (1946), but could not be exploited due to low yield and other undesirable side effects. Van Zanten (2001) reported eight gamma ray (300–750 Gy) induced closed capsule (indehiscent) mutants from four different Turkish cultivars. Three shattering resistant mutants, all out yielding their respective parent varieties were induced by gamma ray (500 Gy) in two Thailand local landraces. In addition, seven delayed shattering and shattering resistant mutant lines were obtained following treatments with EMS (0.5–1.0%, 4 h) in Thailand. Wongyai et al. (1997) reported a delayed shattering mutant and Maneekao et al. (1997) found semi-shattering mutants in sesame.

15.12.3.4 Hairy Capsule Mutants

The hairy capsule mutant trait is dominant over smooth capsules; the hairy trait may be related to drought tolerance (Cagirgan 2001).

15.12.3.5 Oil Yield and Fatty Acid Composition

Baydar (2005) found the highest oil content in low-yielding types, while the reverse is the case in the high-yielding types. The lowest content of oleic acid (41.3%) and the highest content of linoleic acid (43.1%) are associated with low-yielding types, while the best high-yielding type harbor a lower amount of tocopherol. However, induced mutations can bring about changes in the fatty acid composition in sesame lines, with high oil content (>50%). Variation for fatty acids content was induced by gamma-rays (Murty and Bhatia 1990) and by dodium azide (Kang 1997) in South Korea.

15.12.3.6 Antioxidants

Induction of mutations could be attempted for increased content of lignans such as sesamin, sesamolin and similar products. These substances have a wide applications in the production of pharmaceuticals, pesticides and other industrial products. In addition, total tocopherol content has been reported to vary from 175.6 to 368.9 mg/kg in the seed oil of sesame pedigree mutant lines (Baydar 2005).

15.12.3.7 Morphological Marker Traits

Marker mutant traits are always useful in genetics and breeding. Some of these display distinctive traits such as narrow, elongated, thick leaf types, ovate, ternate elongated petiole types and white, pigmented flower types. Out of these, the thick leaf mutants are most preferred. They possesses superior agronomic traits such as plant height, primary and total branches per plant, number of capsules on main axis, distance from base to first branching, total capsules per plant, seed yield and seed protein content, than the parent variety (Najeeb et al. 2012). Similarly, Mary and Jayabalan (1995) reported EMS induced mutations affecting leaf morphology in sesame at M_2.

15.12.4 Breeding for Disease and Insect Resistance

Plants inheriting the resistance (r) gene express a defense response as soon as a pathogen having the corresponding avirulence (avr) gene invades and express the gene (avr) in the plant tissue (Flor 1971). Disease resistance is usually pathogen species-specific or pathogen strain-specific. Pathogens evolve continuously and natural selection in the pathogenic population may lead to emergence of more virulent strain(s) leading to resistance breakdown (boom & bust cycle).

Biotic stresses such as diseases and insect pests affect sesame crops adversely resulting in huge losses in productivity and production. Thus, improved cultivars need to be resistant to diseases and insect pests to attain sustainable production. Sesame yield is drastically reduced by diseases such as, *Alternaria*, *Cercospora* leaf spot (Nahunnaro and Tunwari 2012), stem rot, bacterial diseases, powdery mildew and wilts (Nyanapah et al. 1995; Ojiambo et al. 1999). Farmers typically control these diseases through fungicide application and location-specific cultivation techniques. However, breeding a cultivar resistant to diseases and insect pests seems to be cost effective. Natural genetic variation for disease resistance in a core germplasm does exist. A varying degree of resistance to white and angular leaf spot has been observed in Kenyan sesame cultivars. SIK 031 and SIK 013 have shown resistance to white leaf spot, while SIK 031 and SPS 045 have been reported to have field resistance to angular leaf spot (Nyanapah et al. 1995).

In general, disease infestation is controlled by additive gene action with appreciably high heritability estimates, and consequently it becomes easy to effectively select disease-free sesame plants. But, there exists no cultivar with absolute resistance to bacterial leaf spot, stem rot, wilt and phyllody in sesame (Naqvi et al. 2012), although a number of Indian and Nigerian wild species are resistant to the above biotic stresses. Efforts to incorporate these traits into commercial cultivars is scanty. A few crosses involving *Sesamum indicum* with wild sesame species resulted in recovery of resistant lines to root rot. El-Bramawy and Abd Al-Wahid (2009) claimed resistance of S2 and H4 cvs. to *Fusarium* wilt out of 28 sesame genotypes screened under field conditions. In addition, Sanliurfa-63,189 was also identified to be the most resistant genotype (Kavak and Boydak 2006) for the disease. Wang et al. (2014) constructed a SSR based genetic linkage map and identified QTLs for charcoal rot resistance in sesame.

Different researchers attempted intra- and inter-specific crosses in sesame for phyllody-resistance and it revealed that disease resistance is governed by one dominant (wild species) and one recessive (cultivated species) gene (Singh et al. 2007). Naqvi et al. (2012) identified a few elite bacterial blight (*Xanthomonas campestris*) resistant germplasm lines (SG 22, SG 55, SG 72, SG 33) for use as donors in breeding program.

15.12.5 Breeding for Abiotic Tolerance

Cultivated sesame is sensitive to salinity (Koca et al. (2007), drought (Boureima et al. 2011), waterlogging (Ucan et al. 2007) and chilling (Levitt 1980). Koca et al. (2007) found that cv. Cumhuriyet was relatively more salt tolerant (at 50 and 100 mM salinity stress) than cv. Orhangazi which was linked to high-proline level. Proline plays a crucial role in plants by stabilizing proteins, regulating cytosolic pH, and scavenging hydroxyl radicals by superoxide dismutase, ascorbate peroxidise, catalase, peroxidise (Matysik et al. 2002). In addition, the growth parameters, lipid peroxidation and proline accumulation are reported to be positively correlated with the salt tolerance in sesame (Matysik et al. 2002).

Sesame cultivated in marginal uplands becomes drastically affected by drought stress which hinders plant metabolism, growth and seed yield (due to decreased seed setting and reduced seed weight) (Kim et al. 2007). A sesame cultivar with an extensive rooting system is able to sustain drought stress. Development of drought tolerant cultivars with enhanced water use efficiency will benefit both sesame cultivation and production.

Sesame is highly sensitive to chilling stress (0–5 °C). Its growth is considerably reduced below 20 °C, while seed germination and growth is completely inhibited below 10 °C (Oplinger et al. 1990). Low temperature reduces the efficiency of ROS (reactive oxygen species) scavenging enzymes produced in response to chilling stress (Beroza and Kinman 1955). Cold stress causes cellular injury, plant senescence and degrades oil quality by reducing the lignin content of seeds (Beroza and Kinman 1955). Progress towards breeding for cold tolerance in sesame is indeed limited. Understanding the pathway for cold acclimation and searching for molecular changes (Dong et al. 2006) can help to achieve success.

Sesame experiences a reduction in growth and yield after 2–3 days of submergence in water or under excessive irrigation. In fact, stagnate water considerably reduces plant growth, leaf axils per plant, biomass, seed yield and net photosynthesis at various stages of growth (Sun et al. 2009). A number of genes involved in energy metabolism and those related to flavone and flavonol biosynthesis, steroid biosynthesis, photosynthesis, are reported to be down-regulated under standing water in the field (Wang et al. 2012).

15.12.6 Heterosis Breeding and Development of Heterotic Hybrids

Despite many efforts, classical breeding methods of selection, pedigree breeding, backcross and induced mutations have not achieved a major yield breakthrough in sesame seed yield. Heterosis breeding exploits the advantage of heterozygotic performance. In addition, it exploits a greater extent of instant genetic variation as

compared to conventional breeding techniques. Recently, a number of research reports have indicated significant heterosis in certain hybrid combinations. Therefore, there is a need to intensify hybrid development programs to maximize sesame yield and it may be remunerative, as in case of other autogamous crops and as such may be profitable for oil production.

Male sterile lines provide an opportunity to facilitate the cross-pollination process for hybrid seed production, and to exploit sesame heterotic vigor. A naturally-occurring *split corolla* recessive genic male sterile mutant (msms) was first found in Venezuela (Langham 1947) and it was induced later with gamma rays by Murty and Oropeza (1989). In addition, male sterile mutants were induced by Rangaswamy and Rathinam (1982), and Ramanathan et al. (1992) with lower gamma-ray doses and with fast neutrons by Murty and Bhatia (1990) in India. Liu et al. (2013) recovered two spontaneous male-sterile plants in a Chinese sesame cv. Zhuzhi 4 in 2006. They developed a new high yielding GMS line, D248A, by consecutive sib mating with fertile plants from Zhuzhi 4. Its yield potential was higher than other GMS lines (95 ms-2A, 95 ms-5A). GMS is maintained by hybridizing male sterile lines (ms/ms) with isogenic heterozygous plants (Ms/ms) which segregate into 1 male fertile: 1 male sterile. This would require early rouging of the fertile Ms./ms progenies which is labor intensive and not cost effective. This becomes a major hindrance for production of commercial hybrid using GMS.

Fortunately, it was possible to develop cytoplasmic male sterile (CMS) lines in sesame by transferring the male sterility factor from the wild relative *Sesamum malabaricum* to the cultivated sesame *S. indicum* (Bhuyan et al. 1997). This CMS system was later used to develop 36 hybrid combinations of diverse origin (Bhuyan and Sharma 2003). Many of these experimental hybrids exhibited high heterotic performance for capsule number per plant, seed yield and oil content. Cultivars in suitable cross combination resulted in high-yielding sesame hybrids that exhibited 77–540% heterotic effect (Yadav et al. 2005). Similarly, heterosis in sesame hybrids for seed yield may be as high as 100–500% (Uzun et al. 2003). Mubashir et al. (2009) reported 40.3–255.1% heterosis in yield-contributing components in a set of ten crosses comprising of five diverse parental lines. However, Pandey et al. (2018) revealed a weak association of genetic distance based on SSR markers with F_1 performance.

Popular sesame hybrids show fast growth rates and a high leaf area index (LAI). Banerjee and Kole (2006) also showed that increased LAI in sesame plays a crucial role in oil production. However, Banerjee and Kole (2011) opined that the increased oil content in sesame hybrids is the result of the combined heterosis effects of different physiological traits. This demonstrates the great potential of hybrid sesame plants for higher oil yield. China is the first country to develop sesame hybrids for commercial cultivation. In India, seven experimental hybrids (AHY TIL 5, AHY TIL 12, RTH 1, AHYT 13, RTH 3, TKG-HY 5, TKG-HY 4) have been developed which exhibited superiority of 31.0–44.3% in seed yield and 13–48% in oil yield over cv. TKG 22.

15.12.7 Breeding for Mechanized Farming

Seed shattering in sesame before and during the harvest causes considerable losses (30–40% or even more) (Fig. 15.8). Recently, sesame with an indehiscent trait became a breeding target to produce high-yielding cultivars and to achieve profitability (reduced labor cost) and sustainability in production (Langham and Wiemers 2002). In fact, capsules with a thinner endocarp layer retain seeds better, as the tension built up between the mesocarp and endocarp during capsule drying would decrease leading to less shattering of capsules.

Medium plant height of at least 25–30 cm to the first branch, upright stem with a limited number of branches, strong and lodging resistant stem, determinate flowering habit, synchronous maturity, senescence and/or drop of leaves before maturity and maturity of seed before capsule opening, placenta attachment of seeds (better seed retention), capsule constriction (better seed retention) and closed capsule at the time of harvesting are all desirable for mechanized harvesting. The capsules should open easily by slight pressure during threshing and release all seeds without visible damage. This would prevent a deterioration of product quality and decrease in germination of seeds. Georgiev (2002) developed 22 indehiscent lines from 6 crosses. The total number of capsules/plant correlated positively with the capsule number on the branches, but negatively with capsules on the main stem. In addition, plant height was shown to be negatively correlated with branch number. In order for the capsules to be more densely positioned on the stem, the stem top should be shorter. This means that tall plant types are usually sensitive to lodging, associated with shy branching and show less fruiting density which is unwanted in mechanized harvesting, as well as undesirable for high yield. Therefore, restructuring of plant architecture is needed for its complete adaptation to the requirements of mechanized harvesting (Georgiev et al. 2008). The extent of shattering may be scored, as shown in Table 15.6, to assist the selection process in different breeding cycles.

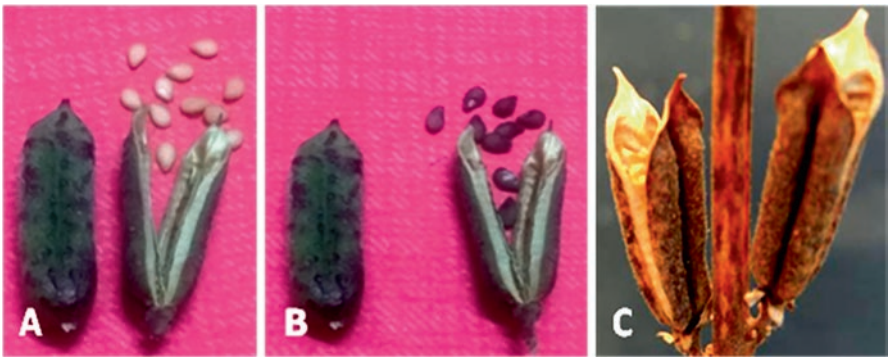

Fig. 15.8 Capsule shattering in sesame. (**a**) and (**b**) Green capsule before physiological maturity (left) and capsule shattered at maturity stage (right), (**c**) Capsule severely shattered due to overmaturity

Table 15.6 Shattering types based on percentage of seed retention

Shattering types	Percentage of seed retention
Super-shattering (SUS)	Less than 10% seed retention
Shattering (SHA)	10–50% seed retention
Non-shattering (NSH)	50–80% seed retention
Direct combine (DC)	Greater than 80% seed retention
Indehiscent (ID)	Id/id genotype, retains all seeds

15.12.8 Innovative Breeding Strategy

In certain instances, conventional plant breeding fails to achieve desired success and requires working in conjunction with biotechnological approaches. With the advancements in biotechnology, sesame breeding can be hastened with reliable selection of desired plant types. A few possible avenues worth mentioning are discussed below.

15.12.8.1 In Vitro Screening

Somaclonal variation among regenerants and their progeny is the result of hereditary changes, mostly induced in the process of callus induction and proliferation (Hoffman et al. 1982). A repeated and prolonged period of subculture of calli increases the frequency of gene mutations and gross chromosomal aberrations (Sanal and Mathur 2008). Regenerants derived from such long-term callus cultures are most likely to bear one or more heritable changes (Bairu et al. 2006). In addition, in vitro mutagenesis due to a mutagen added to the medium can be a step forward to enhance genetic variability. In vitro screening of cell lines, somaclonal variants and somatic mutants is possible using various selection agents such as pathogenic fungal toxins, antinutritional factors (phytate, trypsin inhibitor, tannins), herbicides, PEG (polyethelene glycol) and minerals (Abd El-Himed and El-Bramawy 2011; Maluszynski et al. 1995; Tripathy 2015).

In vitro culture has been extensively studied in sesame, but with limited progress toward genetic improvement primarily due to inefficient selection of induced variants. In sesame, response to callus induction and plantlet regeneration was reported to be better using cotyledon (Yadav et al. 2010) and hypocotyl and shoot tips (Baskaran and Jayabalan 2006) as explants. Nutrient media supplemented with 6-BAP (6-benzylaminopurine) elicited rapid shoot induction and plantlet regeneration (Yadav et al. 2010). Baskaran and Jayabalan (2006) studied the effects of plant growth regulators on callus induction in hypocotyls and cotyledon explants of sesame. Good callusing was achieved at 2, 4-D (2,4-dichlorophenoxyacetic acid) (3 mg/l) with 100 ml of coconut milk followed by 2, 4-D (3 mg/l) with casein hydrosylate (0.1 mg/l). However, MS media (Murashige and Skoog 1962) supplemented with 1 mg/l IAA (indole-3- acetic acid), 1–1.5 mg/l BAP and 1.25 mg/l Kn (Kinetin) resulted in significantly higher shoot multiplication ratio. Callus cultures derived

from cotyledons and hypocotyl segments produced somatic embryos and plants regenerated from such cultures showed morphological variations for seedling growth, vigor, placental thickness, capsule dehiscence, seed size, seed dormancy, yield, oil content and oil quality (Ram et al. 1990).

15.12.8.2 Genetic Transformation

Sesame plants regenerated from primary cultures via somatic embryogenesis or direct regeneration from shoot apical meristems and hypocotyl segments (George et al. 1987) reveal minimal or no genetic variability and such regeneration systems provide an opportunity for *Agrobacterium*-mediated gene transfer (Xu et al. 2009).

Some wild species of sesame are resistant to biotic and abiotic stresses, but post-fertilization barriers restrict transfer of their resistance genes to cultivated *Sesamum indicum* through conventional breeding. However, Were et al. (2006a, b) devised the protocols for gene transfer of sesame by optimizing hormonal concentration and macronutrients for plant regeneration. Application of 20 mM TDZ (Thiodizuron) along with 2.5 mM IAA was the best for successful plant regeneration. The major drawback is that sesame is sensitive to *Agrobacterium tumefaciens* infection (Taskin et al. 1999). However, Yadav et al. (2010) successfully produced fertile trasformants by using cotyledon explants for plant regeneration via multiple shoot organogenesis on MS basal medium containing 25 mM BAP, 25 mg/l kanamycin and 400 mg/l cefotaxime.

15.12.8.3 Interspecific Hybridization

Tissue culture methods can be used to facilitate interspecific crosses using embryo and ovule culture techniques. Crossing was unsuccessful between cultivated *Sesamum indicum* (2n = 26) with either of the wild species *S. alatum* Thonn (2n = 26) or *S. radiatum* (2n = 64). However, there was normal fruit development and seed setting for crosses involving cultivars of *S. indicum* with *S. malabaricum* (2n = 26) indicating high genomic homology of sesame with such wild species (Kumara and Ganesamurthy 2015). Kulkarni (2006) revealed poor pollen tube growth finally reaching to the micropylar end in case of cross *S. indicum* × *S. prostratum* using aniline blue fluorescent microscopy. In contrast, there was good pollen tube growth having micropylar penetration in two crosses e.g. *S. radiatum* × *S. indicum* and *S. occidentale* × *S. indicum*. However, none of the above crosses produced any viable seed, confirming the presence of post-fertilization barriers. However, a standardized ovule culture protocol recovered the above interspecific hybrids. In another study, Kulkarni et al. (2017) also confirmed non-existence of pre-fertilization barrier between wild (*S. mulayanum* and *S. malabaricum)* with cultivated species of sesame. Rajeswari (2001) observed cessation of pollen tube growth in the mid-stylar region in the direct crosses of *S. indicum* and *S. alatum*. The reciprocal cross combinations (*S. alatum* × *S. indicum*) resulted in fertilized embryos, but such

embryos degenerated after 48 h of pollination. However, ovule culture of the crosses made it possible to recover plantlets through direct organogenesis in MS medium supplemented with growth regulators such as BAP (2 mg/l) + IAA (0.5 mg/l) + glutamine (250 mg/l).

In vitro culture and plant regeneration was optimized for wild species of genus *Sesamum* by Dasharath et al. (2007a, b). This paved the way for recovery of successful interspecific hybrids between cultivated *S. indicum* and its wild relatives *S. radiatum* and *S. occidentale* through ovary and ovule culture. Use of 8 mg/l Kn along with BAP was shown to the best combination among different levels of BAP and Kn applied. Ram et al. (1990) cultured zygotic embryos at various developmental stages, and plants were regenerated from 15-day-old embryos after pollination. MinMin et al. (2017) attempted interspecific hybridization of cultivated sesame with *S. indicatum* to introgress charcoal rot (*Macrophomina phaseolina*) resistance from the later using the immature embryo culture technique. Rajeswari et al. (2010) produced interspecific hybrids between *S. alatum* and *S. indicum* through ovule culture to introgress phyllody disease resistance.

15.12.8.4 Doubled-Haploid Breeding

Sesame being self-pollinated, doubled haploid (DH) breeding offers a rapid method of genetic improvement as it significantly reduces the breeding period due to early fixation of homozygosity. Callus induction and androgenic plantlet regeneration from F_1s have been successful (Fig. 15.9). At present, more than 200 crop varieties have been developed by utilizing the doubled-haploid approach (Thomas et al. 2003). Variation among anther culture derived DHs is due to unlocking new genetic variation. It ensures production of stable desirable recombinants with high efficiency stacking of specific target genes (without masking effects) in a homozygous state.

Production of DHs using anther culture of intervarietal/interspecific heterotic hybrids has been reported in rice (Baisakh et al. 2001), wheat (Chaudhary et al. 2015), barley (Weyen 2009) and *Brassica* species (Alam et al. 2009). In sesame, anther-derived callus induction was first reported in Korean cultivars using MS with 25 mg/l 2,4-D and 1 mg/l BAP (Anonymous 1986). Ranaweera and Rathirana (1992) reported better callusing response of anthers from flower buds collected 36–48 h before anthesis and pre-treated at 8 °C for 24 h in the dark. MS media with

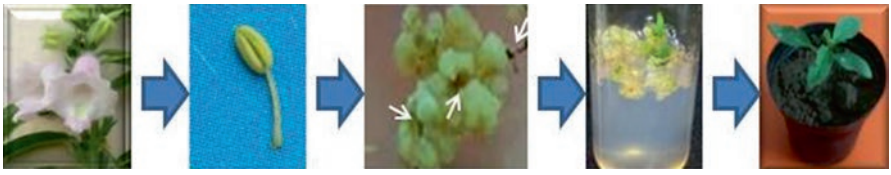

Fig. 15.9 Callus induction and androgenic plantlet formation derived from a sesame cross: Vinayak (reddish brown seed) × TC 25 (white seed). (Source: authors' unpublished research)

10 mg/l 2,4-D, 2 mg/l IAA and 2 mg/l BAP induced calli (46%) after 2–3 weeks of inoculation and the above medium with 5 m/l IAA and 3 mg/l BAP resulted in better response in sub-culturing. In addition, Yifter et al. (2009) were successful to induce anther derived calli in MS media with 2 mg/l 2,4-D + 1 mg/l BAP and recovered regenerants in MS with 1 mg/l NAA + 2 mg/l BAP in four Ethiopian varieties of sesame. The plantlets were rooted in MS with 0.25 mg/l IBA + 0.5 mg NAA. After hardening, the survival percentage of plantlets was as high as 66.7% and 50% in coco peat and soil mixture, respectively.

15.12.8.5 Marker-Assisted Selection (MAS)

Sesame is a promising target oilseed crop for marker-based studies. Its genetic improvement relies on the search for and utilization of desirable alleles present in the gene pool. Use of MAS seems to be an appropriate option to detect the presence of allelic variation in the genes underlying the agronomical important traits (shattering, abiotic and biotic resistance). Precise phenotyping coupled with high throughput next generation sequence information in the form of web-based database SesameFG (http://ncgr.ac.cn/SesameFG/) is now available.

Construction of genetic maps is the foundation of the genome research in any crop. The first comprehensive genetic linkage map in sesame was developed on a F_2 population using EST-SSR (expressed sequence tags-simple sequence repeat), AFLP (amplified fragment length polymorphism) and RSAMPL (random selective amplification of microsatellite polymorphic loci) markers (Wei et al. 2009). It serves as a starting point to tag traits of breeding interest and further aid in sesame molecular breeding. In this context, marker-aided selection allows rapid introgression of a target trait into the recurrent parent by identifying plants carrying the target allele even at early vegetative stages.

Molecular markers are in vogue and used in genetic diversity analysis (Fig. 15.10), construction of genetic maps, gene mapping and cloning and marker-aided selection in crop improvement. Molecular markers have been applied for the study of genetic

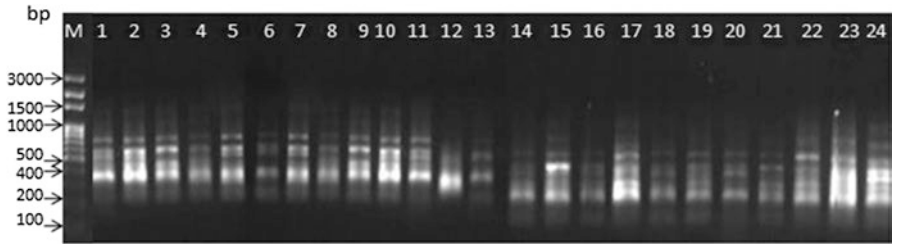

Fig. 15.10 ISSR profile of 24 genotypes of sesame amplified with primer OUAT 10. M = DNA ladder, Lane 1-24: Vinayak, TC 25, B67, CST 785, Pratap, BS 5-18-3, BS 5-18-5, BS 5-18-6, BS 5-18-10, T 46, RT 103, RT 346, RT 351, TMV 5, Phule Til 1, T13, Madhabi, E8, B7-11, IS 309, RT 54, TKG 22, Kanpur local Sel. 1 and Kanpur local sel. 2. (Source: authors' unpublished research)

diversity by using diverse *Sesamum indicum* accessions and Abdellatef et al. (2008) suggested the usefulness of the RAPD (random amplified polymorphic DNA) technique in sesame breeding, conservation and maintenance of germplasm banks and in efficient parental line selection. A limited number of reports are available on molecular markers such as isozymes (Isshiki and Umezaki 1997), ISSR (Kim et al. 2002), AFLP (Ali et al. 2007), SSR (Dixit et al. 2005) and SNP markers (Libins et al. 2014) for sesame improvement and study of genetic variability. Only a few studies are available for tagging of desired genes to assist in the selection process for genetic improvement (Wei et al. 2009). Using marker assisted selection, Uzun and Cagirgan (2009) identified two ISSR markers linked to the dt gene regulating determinate growth habit in sesame using bulk segregant analysis (BSA) in F_2 population of a determinate mutant line (dt1) x indeterminate (cv. Muganlı-57) cross. Yield loss due to capsule shuttering may be greater than 50%. Uzun et al. (2003) reported an AFLP marker linked to closed capsule mutant trait in a cross of cc3 x Muganly-57 using BSA. SSR molecular markers (ZMM0913, ZMM3752, ZMM5636, ZMM5775) closely linked to the major candidate gene/locus for sesame stem rot resistance are now available (https://patents.google.com/patent/CN107058518A/en) which can be suitably used in sesame breeding. The primer sequences of the above molecular markers are:

(a) ZMM0913 (F: 5′-ctcatgtggaacgaggcata-3′, R:5′-atggccaccacctaacattc-3′),
(b) ZMM3752 (F: 5′-caacgatgagatggctttga-3′, R:5′-tcttgcacgcacagtagtcc-3′)
(c) ZMM5636 (F: 5′-ctgctcatcacctctggaaag3′, R:5’tgacctatgatgtgataacagttgg-3′)
(d) ZMM5775 (F:5′-ttcactttgcttttgttgcc-3′, R:5′-gcccattccatgagtttttg-3′).

Wang et al. (2017) identified 14 QTLs for charcoal rot resistance using SSR markers. Yan-Xin et al. (2014) detected an effective SSR marker ZM 428 closely linked with the major QTL qWH10CHL09 for waterlogging resistance in sesame. A SNP survey in the sesame genome revealed 30 SNP markers associated to three important fatty acid (oleic, linoleic, linolenic acids) compositions (Mondal and Bhat 2015) which can be used to enrich unsaturated fatty acid composition in sesame.

15.13 Achievements

A large number of sesame cultivars have been released and reported from time to time for commercial cultivation in different states of India. A state wise list of these cultivars with specific features is provided in Table 15.7. In addition, a detailed list of sesame genetic resources arranged by specific traits and cultivars developed through international sesame breeding is presented in Appendix II.

Table 15.7 Sesame varieties released and notified for different states of India

Variety	Year of notification	Duration (days)	Seed yield (q/ha)	Oil content (%)	Salient features
Andhra Pradesh					
Gouri	1974	85–90	675	43–49	Biscuit color seed, MR to major diseases and pest, MT to water stress and lodging
Madhavi	1978	70–75	700	50–53	Pale white seed, MR to stem/root rot, leaf spot, phyllody, PM, *Antigastra* MT to water stress
Rajeswari	1988	85–90	Kh– 450, Rabi 750	50.5	White seeded, few branches, T to *Macrophomina*, stem rot and powdery mildew, for late kharif (autumn) and rabi (winter)
Varaha	1993	80–85	950	53.0	Dark brown seeded, uniform maturity for kharif and rabi-summer
Gautama	1993	75–80	925	53.0	Light brown seeded, uniform maturity, tolerant to *Alternaria* leaf spot, kharif and rabi-summer
Sweta Til	2014	75–80	900	44–49	Determinate white seeded, tolerant to gall fly, capsule borer, phyllody, leaf curl and powdery mildew for kharif
Bihar					
Kanke White	1965	85–90	550	50.0	Dull white seeded, for kharif
Krishna	1986	85–90	775	46.0	Black seeded, tolerant to *Alternaria* leaf spot and capsule borer, for kharif
Gujrat					
Gujurat Til 1	1979	85	630	49.2	White seeded, branched, smooth green stem, pink flower, multicapsule for kharif
Gujurat Til 2	1994	85	790	50.2	White seeded, branched, multicapsule for kharif
Gujurat Til 3	2009	86	1200	47.3	White bold seeded suitable for export
Gujurat Til 4	2012	85	770	50.8	White bold seeded, resistant to gall fly, capsule borer and mites,suitable for export, kharif
GJT–5	2015	93	1000	46.9	High yielding, summer irrigated condition

(continued)

Table 15.7 (continued)

Variety	Year of notification	Duration (days)	Seed yield (q/ha)	Oil content (%)	Salient features
Gujurat Til 10	2004	92	807	50.0	Black seeded, good for export, kharif
Haryana					
Haryana Til 1	1978	80–85	500	52.0	White seeded, early maturing, resistant to major diseases, tolerant to phyllody and leaf curl
RT 46	1990	76–85	500	49.2	White and bold seeded, for kharif
RT 125	1994	71–83	500	49.0	Seed with brown tinge for kharif
HT–9713 (HT–2)	2013	–	700	48.2	White seeded, T to phyllody and leaf curl
Karnataka					
E 8	1991	100–110	550	53.0	White bold seeded, MR to powdery mildew, R to bacterial leaf spot
DS 1	1997	85–90	450	51.0	White seeded, non–branching, T to bacterial blight and *Alternaria* leaf spot
DSS–9	2009	85–90	625	48–50	White bold seed, early maturing
DS–5	2012	–	650	49–51	White bold seed, kharif
Kerala					
Kayamkulum1	1980	90–100	550	50.0	MT to phyllody, for summer rice fallows.
Thilothama	1982	80–85	650	50.0	Brownish black seeded, for summer rice fallows.
Soma	1985	80–85	750	51.2	Black seeded for kharif
Surya	1985	87–90	750	51.4	Gray seeded, T to leaf spot and phyllody disease, eight loculed, small capsules for semi-rabi
Thilak	1998	80–85	650	51.0	Dark brown bold seeded
Thilathar	1999	78–85	850	51.5	Brown bold seeded
Madhya Pradesh					
N 32	1970	100	770	53.0	White seeded, MR to leaf spot, R to gall fly and capsule borer, kharif
Kanchan	1981	85	880	54.0	Medium sized white seeded, for kharif
JT 21	1993	78	600	55.9	White seeded, T to *Antigastra*, bacterial and *Cercospora* leaf spot, for kharif

(continued)

Table 15.7 (continued)

Variety	Year of notification	Duration (days)	Seed yield (q/ha)	Oil content (%)	Salient features
TKG 22	1994	76–81	800	53.3	White seeded, T to *Phytopthora* blight, for kharif
TKG 55	1998	76–78	630	52.6	White seeded, T to *Phytopthora* blight, R to Macrophomina stem rot for kharif
Jawahar Til −12	2004	82–85	775	48–52	White seed, MR to *Macrophomina* stem/root rot
TKG–306	2007	86–90	750–800	49–52	White seeded, R to *Phytophthora* blight and MR to *Macrophomina*, *Cercospora*, powdery mildew, *Alternaria* leaf spot
Jawahar Til −14	2008	82–85	700–750	50–52	For summer
TKG–308	2010		700–750	48–50	MR to *Macrophomina*, *Cercospora*, bacteria leaf spot, leaf curl, T to capsule borer, kharif
Maharashtra					
Phule Til1	1978	85	500	50.0	White and bold seeded, for kharif
N–8	1982	130	500	50.5	Seed with brown tinge for kharif
Tapi	1987	85	600	50.0	White and bold, early maturing, for kharif
Padma	1991	75	700	50.0	White seeded, early maturing, for kharif
RT 54	1992	83	800	44.1	Brown seeded, R to leaf blight, *Macrophomina* stem rot, tolerant to *Antigastra*, kharif
RT 103	1994	88	900	48.0	White seeded, T to *Macrophomina* stem rot, *Alternaria*, bacterial leaf blight and phyllody and R to insect pest, for kharif
PKV–NT–11	2009	88–92	800–850	50–53	White seed, MR to root rot, bacterial blight, summer
JLT–408	2010	80–85	700–800	51–53	High yielding, moderately tolerant to major diseases & pests

(continued)

Table 15.7 (continued)

Variety	Year of notification	Duration (days)	Seed yield (q/ha)	Oil content (%)	Salient features
Odisha					
Vinayak (Sel–14)	1989	90	500–600	47–48	Light brown seed MR to major diseases and pest
Kanak (BS–6–1)	1979	80–85	600–650	46–48	Deep brown color seed, MR to leaf spot resistant to lodging
Kalika (BM–3–7)	1985	85–90	600–650	45–48	Dark brown seed, less S to CLS, stem/root rot R to lodging
Usha (OMT–11–6–5)	1992	85–90	650–700	43–49	Biscuit color seed, MR to major diseases and pest, MT to water stress and lodging
Uma (OMT–11–6–3)	1992	70–75	650–750	50–53	Pale white seed, MR to stem/root rot, leaf spot, phyllody, PM, *Antigastra* MT to water stress
Nirmala (OS–Sel–164)	2003	80–85	750–800	42–44	Gray white seed T to phyllody, wilt, BLS, PM MR to stem/root rot and ALS
Prachi (ORM 17)	2004	85	700–750	42–45	Black seed, MT to leaf spot, PM, stem/root rot and *Antigastra*, T to water stress and lodging
Amrit	2007	75–80	750–850	43–46	Light brown seed, T to leaf spot, PM, stem/root rot, R to lodging
Smarak	2014	75–80	800–1000	44–49	Golden yellow seed, MR to major diseases and pest
Shubhra	2014	75–90	900–1000	46–52	White seed MR to major diseases and pest, R to water stress
Punjab					
Punjab Til 1	1966	85	700	50	White seeded, T to phyllody, for kharif
TC 25	1978	85	700	48.4	White seeded, MT to disease insect pest, for kharif
TC 289	1986	100	600	51.6	White seeded, kharif
TH–6	2008	105	700	50	Edible bold seed, R to charcoal rot and phyllody
Rajasthan					
RT 46	1990	85	700	49.2	White seeded, R to oozing complex, T to *Macrophomina* stem rot, capsule borer and gall fly, for kharif

(continued)

Table 15.7 (continued)

Variety	Year of notification	Duration (days)	Seed yield (q/ha)	Oil content (%)	Salient features
RT 54	1992	83	800	41	Brown seeded, R to leaf blight, *Macrophomina* stem rot, T to *Antigastra*, kharif
RT 125	1994	83	700	49	White seeded, T to *Macrophomina* stem rot, *Alternaria, Cercospora* and bacterial leaf spot and phyllody, for kharif
RT 103	1994	88	750	48	White seeded, T to *Macrophomina* stem rot, *Alternaria*, bacterial leaf blight and phyllody and R to insect pest, for kharif
RT 127	1999	85	800	50.6	Bold, white seeded, drought, hardy, T to *Macrophomina* stem rot, phyllody, bacterial leaf spot, powdery mildew, gall fly and mites, for kharif
RT 346	2009	84	629	50	White seed, R to leaf curl, MR to *Macrophomina*, *Alternaria*, *Cercospora*
RT 351	2011	85	650	49.7	White seeded, T to *Macrophomina*, root rot, *Cercospora*, phyllody
Tamil Nadu					
TMV 1	1939	85	300 (rainfed) 600 (irrigated)	50	Erect, fairly bushy with moderate branching, 4-loculed reddish brown to black seeds
TMV 2	1942	80	300 (rainfed)	52	Open, moderate branching 6–8 loculed, cylindrical big sized capsules dark brown to black seeds. Suitable for rabi
TMV 3	1948	82.5	600	52	T to leaf miner
TMV 4	1977	87.5	650	50	Light brown seeded for summer
TMV 5	1978	80	750	51	Erect with moderate branching, 4 locule, brown seeds.
TMV 6	1979	87.5	700	54	Brown seeded, T to drought, for kharif
Co. 1	1983	87.5	730	50	Black seeded for kharif
SVPR 1	1992	80	800	50	White seed, 4locule, high yield, suitable for irrigated condition

(continued)

Table 15.7 (continued)

Variety	Year of notification	Duration (days)	Seed yield (q/ha)	Oil content (%)	Salient features
TSS 6	1994	77.5	800–900	54	White seeded, T to phyllody, *Alternaria* leaf spot, 4 loculed capsules, for kharif
Paiyur 1	1997	92.5	600–700	50	Black seeded, bushy, capsules 4 loculed, for kharif
VRI 1	1997	72.5	600–700	51	Dark brown seeded, short erect, 4 loculed capsules, for kharif
VRISV2	2005	82.5	750	51.9	MR to shoot webber, suitable for both rainfed and irrigated condition
TMV (SV7)	2009	85.0	800	51	Suitable for kharif
VRI 3	2017	77.5	700	49	High yielding, moderately tolerant to major diseases & pests
Uttar Pradesh					
T 12	1963	87.5	600	47	White seeded, T to phyllody and leaf curl, kharif
T 13	1968	92.5	600	47	White seeded, T to lodging, for kharif
Sekhar (T78)	1994	82.5	700	50	White seeded, R to lodging, T to phyllody and leaf curl, kharif
West Bengal					
Tilottama (B 67)	1981	77.5	900	40	Blackish brown seeded, R to *Macrophomina* stem rot, phyllody and Bihar hairy caterpillar, for rabi/summer
Rama	1989	87.5	1200	45	Reddish brown seeded, R to *Macrophomina* stem rot, phyllody and Bihar hairy caterpillar, for rabi
SWB–32–10–1	2008	86.0	1200–1500	50	Light brown seed, T to *Macrophomina* stem rot

Sources: Ram HH (2011) and URL: https://sites.google.com/a/tnau.ac.in/cpbg/oilseeds/sesame-cultivars

R resistant, *MR* Mod. resistant, *T* tolerant, *MT* Mod. tolerant, *S* susceptible

15.14 Limitations and Challenges

Sesame is a highly valued oilseed crop owing to its high percentage of oil recovery of superior quality. A large number of cultivars have been developed using conventional breeding. However, productivity (325 kg/ha) in India is far below the world average (535 kg/ha), primarily due to poor adaptability, high capsule shattering and sensitivity to salinity, waterlogging, low temperature and biotic stresses including phyllody, stem rot, *Cercospora* leaf spot, bacterial leaf blight, powdery mildew and wilts. The progress of genetic improvement in sesame has been inadequate as much attention is directed toward food crops (rice, wheat, maize). Fertile plain lands are the choice for food crops while; the left-out, undulating and marginal lands are in vogue and diverted to sesame cultivation with minimal input use. In addition, the narrow genetic base of the sesame gene pool may be an explaining factor for the slow pace of genetic improvement. A number of reports on novel induced variants for agro-economic traits are available. However, in most of cases, research initiatives become stalled at some midpoint without carrying forward materials to establish new cultivars. Similar is the case for breeding materials generated through innovative breeding approaches such as in vitro culture, genetic transformation, protoplast fusion and marker-aided backcrossing.

15.15 Conclusion and Prospects

Among the oilseed crops, sesame offers a range of dietary and purported health benefits, as well as industrial applications. A genotype with a higher number of capsule bearing leaf axils, longer capsules, determinate and semi-shattering habit, resistant to major diseases and having good end use exportable quality (white color, large seed size and good aroma/taste) are preferred. This can be achieved by harnessing genes present in novel mutants and locally-adapted cultivars through crossing programs. In vitro induced variation (somaclonal variation), in vitro mutagenesis (somatic mutation), interspecific hybridization (embryo rescue), wide hybridization between distant species (somatic cell hybridization) may be adequately attempted to re-structure the sesame ideotype. In addition, development of doubled haploids (DH) has immense potential in sesame improvement to short-cut breeding cycles without sacrificing the success rate expected in pedigree selection. Identification of candidate genes/QTLs underlying tolerance to drought, salinity, chilling, waterlogging and heavy metal stresses using molecular markers and pyramiding the genetic

factors for the above abiotic stresses using MAGIC (multi-parent advanced generation inter-crosses) populations seems to be a possible option to adjust against vagaries of environmental conditions.

A variety of targeted gene editing methods such as RNA interference (RNAi), site directed mutagenesis, zinc finger nucleases (ZFNs), transcription activator like effector nucleases (TALENs) and clustered regularly interspaced short palindromic repeats/Cas9(CRISPR/Cas9) are available that bring about knock-outs (deletions) or knock-ins (insertions) for a gene of interest to generate altered phenotypes in vitro. The most popular and current précised gene editing technique is the CRISPR/Cas9 system where, gRNA sequences (about 20 bases long) direct the Cas9 protein to induce a site-specific double strand break in the genomic DNA. However, none of the currently available editing platforms is foolproof to guarantee a pure population of cells. For gene knock-outs, single cell cloning will typically require a few hundred cells to be plated. For knock-ins, these occur at further lower frequencies, and may need over 1000 target cells per edit. The desired gene edit event can be identified by a typical amplified product by PCR or absence of the protein due to gene knock-outs and such gene edited clones can be maintained in vitro. This is a most versatile and precise method of genetic manipulation and it can be extended to sesame genome editing to offer disease resistance.

Oil content is a very complex trait which varies depending upon genetic background and environmental conditions. Therefore, identification of wide adaptable sesame genotypes maintaining high oil content is warranted. A number of candidate genes/QTLs determine the oil content and its fatty acid composition. Little information is available about the number of such genetic factors and their mode of action. There is an urgent need to explore candidate genes underlying biosynthesis of sesame oil for selection of suitable parents for convergent breeding to improve oil content and/or its quality. The study of molecular marker-trait association is still at infancy in this crop as compared to other commercial oilseed crops (peanut, mustard). Identification of QTLs and their monitoring in succeeding breeding cycles using molecular markers can pave the way for increase in seed oil content.

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Appendices

Appendix I: Research Institutes Relevant to Sesame

Institute	Specialization and research activities in sesame	Contact information and website
Bose Institute, Kolkata	Genetic diversity	Ranjana Prasad https://www.researchgate.net/profile/Ranjana_Prasad
C. S. Azad University of Agriculture & Technology, Kanpur, India	Screening for phytoplasma disease	Prabhakaran Kumar Singh, CSAUAT, Kanpur, India http://csauk.ac.in/
Chinese Academy of Agricultural Sciences, China	Sinbase and ssr based-genome mapping	Wang Linhai http://www.sesamebioinfo.org/PMDBase.
Crane Global Solutions Ltd, India	New approaches for crop improvement	Raghav Ram https://www.zoominfo.com
Henan Academy of Agricultural Sciences, Nanjing Agricultural University, China	Association mapping of seed oil and protein content	Chun Li Email:zhy@hnagri.org.cn http://www.caas.cn/en/index.shtml
Indian Agricultural Research Institute, New Delhi	Breeding for disease resistance	Sajadun Nabi https://www.researchgate.net/publication/284097386
Indian Institute of Oil-seeds Research (IIOR), Hyderabad-30, India	Oil seeds research including sesame breeding	A. Vishnuvardhan Reddy email: director.iior@icar.gov.in http://www.icar-iior.org.in/
Institute of Plant Genetic Resource, Bulgaria	Mechanized harvesting	St. Georgiev, IPGR, BG – 4122 Sadovo, Plovdiv, Bulgaria http://ipgrbg.com/en/
Izmir Institute of Technology, Turkey Georg-August-Univ., Germany	SNP identification for GBS analysis	Sami Doganlar, Ayse Ozgur Uncu Email: samidoganlar@iyte.edu.tr http://www.iyte.edu.tr/AnaSayfa.aspx?d=ENG
JNKVV, Jabalpur, India	DUS testing	Rajani Bisen Email: rajanitomar20@gmail.com http://jnkvv.org/
Joint FAO/IAEA Divi-sion of Nuclear Techniques in Food and Agriculture	Sesame improvement by induced mutations	IAEA-TECDOC-1195 https://www.iaea.org/
Louisiana State University, USA	Powdery mildew resistance	P. Venkata Ramana Rao https://www.facebook.com/public/P-Venkataramana-Rao

(continued)

Institute	Specialization and research activities in sesame	Contact information and website
Modibbo Adama University of Technology, Nigeria	Disease resistance	H. Nahunnaro Email: hycenth.nahunnaro@yahoo.com. http://mautech.edu.ng/new/index.php/en/
Nanjing Agricultural University, China	Genetic linkage map construction	Li-Bin Wei Email: moelab@njau.edu.cn, http://english.njau.edu.cn/
National Bureau of Plant Genetic Resources, India	SNP markers for study of functional polymorphism	Nupur Mondal Email: nupur.mondal84@gmail.com http://www.nbpgr.ernet.in/
National Crop Experiment Station, Korea	Disease and Shatter resistance	C.W.KANG, https://www.researchgate.net/profile/Cw_Kang
Odisha Univ. of Agril. & Tech, Odisha, India	Gene action, heterosis, combining ability	Swapan K Tripathy Email: swapankumartripathy@mail.com http://www.ouat.nic.in/
Oil Crops Research Institute of Chinese Academy of Agricultural Sciences	Interspecific hybridization	Yang MinMin E.mail: nc.saac@nimnimgnay; moc.361@mmgnaybh http://en.oilcrops.com.cn/
Oil Crops Research Institute, China	Sesame genomics	Linghai Wang E.mail: wangnuo@dlmu.edu.cn http://en.oilcrops.com.cn/
Pir Mehr Ali Shah Arid Agriculture University, Pakistan	Bacterial blight resistance	S. Farah Naqvi Email: dr.inam@uaar.edu.pk http://www.uaar.edu.pk/
PPV & FRA, Govt. of India	Guidelines for DUS Testing	PPV & FRA, Govt. of India http://plantauthority.gov.in/
Punjab Agricultural. University, India	Genetic diversity using ISSR markers	Hitesh Kumar Email: hiteshkmr25@gmail.com http://www.pau.edu/
Suez Canal Univ., 41522 Ismailia, Egypt	Nature of gene action, screening for antinutritional factors	M.A.S. El-Bramawy Email: el_bramawy71@hotmail.com http://scuegypt.edu.eg/en/
Tamil Nadu Agricultural University, India	Interspecific hybridization	S. Rajeswari Email: rajisundar93@gmail.com http://www.tnau.ac.in/
Universidade Federal do Ceará, Brazil	Floral biology	Patrícia Barreto de Andrade Universidade Federal do Ceará, Brazil http://www.ufc.br/

(continued)

Institute	Specialization and research activities in sesame	Contact information and website
University Goettingen, Germany	Relationship between metabolic and genomic diversity	Petr Karlovsky Email: pkarlov@gwdg.de http://www.uni-goettingen.de/en/1.html
University of Agricultural Sciences, Dharwad, India	Mechanized harvesting	Vikas V. Kulkarni Email: VikasVKulkarni@VikasVKulkarni3 http://www.uasd.edu/
University of Ruhuna, Sri Lanka	Selection procedure for breeding	Ranjith Pathirana ranjith.patirana@plantandfood.co.cn http://www.ruh.ac.lk/ruh/
University of Suleyman Demirel, Turkey	Breeding for ideal plant type	H, Baydar Email:baydar@ziraat,sdu,edu,tr https://w3.sdu.edu.tr/international
Izmir Institute of Tech., Turkey	Genome sequencing and SNP based characterization of the high oil crop	Ayse Ozgur Uncu Email: samidoganlar@iyte.edu.tr http://www.iyte.edu.tr/AnaSayfa.aspx?d=ENG

Appendix II: Sesame Genetic Resources and Varieties Developed Through International Sesame Breeding

Cultivar	Important traits	Cultivation location
Zhongzhi13	High oil content, improved variety	China
Baizhima and Mishuozhima	Land races and both contain multiple loci for several agronomic traits	China
Morada	Moderate branching	Venezuela
dr-45	Determinate, mutant of 'No. 45'	Israel
dt-4, dt-5 and dt-6	Determinate, mutants of Çamdibi	Israel
dt-1, dt-2 and dt-3	Determinate, mutants of Muganl 1-57	Israel
SIK 031 and SIK 013	Resistance to white leaf spot,	China
SIK 031 and SPS 045	Resistance to angular leaf spot	China
'S2' and 'H4'	Stable resistant to *Fusarium* wilt.	Egypt
Sanliurfa-63189	Resistant to *Fusarium* wilt	Turkey
SG 22, SG 55, SG 72 and SG 33	Resistant to bacterial blight	Pakistan
Zhuzhi 4"	High yielding	China
D248A	High yielding MS line	China
95 ms-2A and 95 ms-5A	GMS lines	China

(continued)

Cultivar	Important traits	Cultivation location
Zhonghi 11,12,14	High yielding	China
Ezhi 1, 2, 4	High yielding	China
Zhu 0J3, 9-4155, Hangzhi 2, 98-6204, Zhonghi 18 and 01-2658	High yielding restorer lines	China
AHY TIL 5, AHY TIL 12, RTH 1, AHYT 13, RTH 3, TKG-HY 5 and TKG-HY 4	All are experimental hybrids, 31.0–44.3% in seed yield and 13–48% in oil yield over TKG 22(Check).	India
IC-204078	Moderate branching, very early maturing, low plant height, small capsules, low yield potential	Andhra Pradesh, India
IC-204099	Less branched, early maturing, moderate	Andhra Pradesh, India
C-204337	Less branched, early maturity, medium tall, bold seeds, moderate yield potential, susceptible to phyllody	Rajasthan, India
C-204524	Moderate branching, medium maturity, relatively longer capsules, low yield potential, susceptible to phyllody	Gujrat, India
C-204628	Highly branched, medium tall, medium to late maturity, moderate yield potential	Karnataka, India
C-204653	Highly branched, medium to late maturity, tall and moderate to high yield potential	Kerala, India
C-204681	Highly branched, multilocular (6–8), early maturity, moderate yield potential	West Bengal, India
IC-204773	Highly branched bushy type, late maturity, photosensitive, resistance to phyllody and leaf roller	Nagaland, India
C-204814	Highly branched, medium to late maturity	Mizoram, India
C-204843	Medium branching, multilocular capsules, early	Bihar, India
C-205000	Highly branched bushy type, late maturity	Assam, India
C-205209	Moderate branching, late maturity,	Andhra Pradesh, India
IC-205314	Moderate branching, relatively long capsule	Uttar Pradesh, India
IC-205479	Less branched, early maturity, bold seeds	Himachal Pradesh, India

(continued)

Cultivar	Important traits	Cultivation location
C-205509	Moderate branching, medium maturity	Odisha, India
C-205595	Moderate branching, late maturity, tall, low yield potential	Odisha, India
IC-205730	Unbranched, medium maturity, relatively long capsules	Rajasthan, India
IC-205817	Moderately branched, relatively long capsules	Tamil Nadu, India
EC-346125-1	Moderately branched, tall, medium-sized capsules, early	Greece
EC-346489	Late maturity, small capsules, white seeds	Afghanistan
EC-346987	Moderately branched, medium-sized capsules	Unknown
EC-377025	Unbranched, glabrous stem, long capsules, low yield potential	Somalia
DLH-2 (S. mulayanum)	Branched, thin glabrous stem, tall, purple flower, black seeds, low susceptibility to phyllody	Delhi, India
SVPR 1	White seed, selection from Western Ghats White	Srivilliputhur, India
VRI 1	Brown seed, Pureline selection from Tirukattupali local	Vridhachalam, India
VRI 2	Reddish brown seed	Vridhachalam, India
VS07023	Landraces, brown seed	Vridhachalam, India
MD 1	Landraces, white seed	Madurai, India
MD 2	Landraces, white seed	Madurai, India
MD 3	Landraces, white seed	Madurai, India
MD 4	Landraces, white seed	Madurai, India
MD 5	Landraces, white seed	Madurai, India
NIC-7943	Shy branching	India
SP-41, VOSI-5846, VOSI-8458, NIC-8202, IS-101,IS-92-2,SI-3265-5	Moderate branching	India
TKG-22, SI-2973, GRT-83125, IS-56, NIC-16268, IS-355	Moderate branching	India
SI-2940, IC-382-2, GT-10, DSK-1, 49-E-SPS-6, ES-29, NIC-8559	Moderate branching	India
KANPUR LOCAL, KMR-77, ES-28, MT-6262, SI-2174, B-7-11	Moderate branching	India
KIS-357-A, KIS-297-2, RJS-29, EC-14121, EC-334952, IC-132408	Profuse branching	India

(continued)

Cultivar	Important traits	Cultivation location
IS-172, IS-136, IS-750-1-84, IS -184-1, IS-146, SI-44, SI-3275, PjCU-36	Profuse branching	India
S-0448, IC-14160-1, S-0337, KMR-17, C-96128, S-0434,NIC-16236	Profuse branching	India
KIS-357-A, KIS-297-2, VOSI-5846, VOSI-8458, EC-14121, EC-334952,	Basal branching	India
IC-132408, NIC-8202, IS-101, IS-136, IS-146	Basal branching	India
NIC-8984, MT-67-25, MIC-8526,NAL/28/27/31/4, IC-14093, IS-351-2	Basal branching	India
SI-199-2-84, SI-3275, SI-982, PCU-37, PCU-38	Basal branching	India
IS-750-1-84, IS -184-1, IS-92-2, RJS-29, SP-41	Top branching	India
13,598, NIC-8559, NIC-8202, NIC-10622	Top branching	
KIS-297-2, KIS-357-A, VOSI-5846, VOSI-8458, SP-41, EC-334952, IC-132408, NIC-8202	Dense hairiness of flower petal	India
EC-14121, RJS-29, MT-6262, NIC-8984	Sparse hairiness of flower petal	India
GT-10, TKG-22, RT-54	Light purple petal of flower	India

In addition, a detailed list of Indian sesame improved varieties with specific traits has been mentioned in Table 15.7

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