Chapter 5
Sesame

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Abstract Sesame (*Sesamum indicum* L.) is one of the oldest domesticated oilseed crops. Due to the presence of high oil, protein and other nutritional elements, its seed has become an important ingredient of food and feed. However, lack of information about sesame yield structure has restricted the process of crop improvement through breeding. Sesame breeding methods vary from plant selection and hybridization to molecular breeding. Genetic variability in a species is the basic requirement of any breeding program. Available genetic diversity is either directly used for evaluation and selection or desired traits are combined into a single plant via hybridization and backcrossing. Sesame germplasm evaluation and selection for high-yielding varieties are based on genetic heritability estimates of yield-related traits including higher number of capsules, branches and plant biomass, etc. Mutational techniques are employed for broadening genetic diversity of sesame breeding material. Concentrations and application time of any mutagen were found critical for mutation-breeding program. Large number of sesame varieties possessing desirable traits for higher yield and better quality has been developed through mutagenesis. Application of innovative breeding methods helps to reduce our dependence on existence of genetic variability within a species and overcome the limitations of conventional breeding. For this purpose biotechnological techniques have been introduced to sesame breeding programs. Protocols for sesame in vitro culturing and genetic transformation are optimized by using appropriate concentration of hormones and nutrients. Various marker-assisted selection (MAS) techniques such as isozymes, random amplified polymorphic DNA (RAPD) and inter-simple sequence repeats (ISSR), etc. are also used in sesame breeding to study genetic variability of sesame to increase selection efficiency.

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S.K. Gupta (ed.), *Technological Innovations in Major World Oil Crops, Volume 1: Breeding*, DOI 10.1007/978-1-4614-0356-2_5,
© Springer Science+Business Media, LLC 2012

Keywords Sesame (*Sesamum indicum* L.) • Genetic variability • Mutational techniques • Biotechnological techniques • MAS • RAPD • ISSR

1 Introduction

Sesame (*Sesamum indicum* L.) is pioneer among the domesticated oilseed crops being still cultivated throughout the world in about 70 countries, out of which 26 are located in Africa and 24 in Asia. It is grown worldwide over an area of 75 million hectares producing 60,000 t seed (FAOSTAT 2008). Myanmar, Sudan, China and India are the leading sesame-producing countries of the world. The crop is generally adapted to tropical regions of world, where it is mainly grown for edible seeds and oil (Weiss 2000). Despite its ideal adaptation to dry climates, sesame can also be grown in humid, tropical and subtropical regions. Traditionally, it is cultivated between latitudes 6 and 10°N (Agboola 1979) with the highest yield-producing countries in Asia and Africa (FAOSTAT 2008). *Sesamum orientale* and *Sesamum indicum* are the alternatively used scientific names of sesame (Bedigian 2003). However, Nicolson and Wieserma (2004) proposed *S. indicum* name against *S. orientale*, which was conserved against *S. orientale* and is in use since 2005.

1.1 Botany

Sesame plant is an annual in habit, with indeterminate growth and possesses diploid chromosome number of $2n = 26$. Plants are erect to semi-erect depending on branching types; ovate to lanceolate leaves with pointed apices, the leaf margins are entire to serrate, and stem is round or square type. Flowers range in size containing small-sized tubular calyx and five-lobed corollas and color, e.g., white, violet, red or maroon. Corolla is campanulate having lower corolla lobe longer than the upper one with one sterile and four functional epipetalous stamens.

1.2 Nutritional Composition

Sesame seeds are rich in oil and protein with high dietary energy value of 6,355 kcal kg^{-1}. Chemical composition of seed shows that it contains 57–63% oil, 23–25% protein, 13.5% carbohydrate and 5% ash (Tunde-Akintunde and Akintunde 2004; Elleuch et al. 2007). It is rich source of various nutritional elements including iron, magnesium, manganese, copper and calcium, and important vitamins B_1 (thiamine) and E (tocopherol). Due to its flavor and stability as well as high-quality cooking value, sesame fat is of great significance in the food industry. The presence of sesamin and sesaminol lignans in its nonglycerol fraction contributed to oxidative stability and antioxidative activity of sesame oil (Wu 2007). These antioxidative agents terminate the process of oxidative damage in cells by capturing oxidative radicals. Antioxidants are also used as dietary supplements to cure cancer and heart diseases. The most abundant fatty acids present in sesame oil include: oleic acid (43%), linoleic acid (35%), palmitic acid (11%) and stearic acid (7%) contributing toward 96% of total fatty acids (Elleuch et al. 2007).

1.3 Origin and History

Most of sesame wild relatives are found in sub-Saharan Africa (Bedigian 2003), but these are also present in India in small numbers (Desai 2004). Its archeological evidences are documented in Pakistan (2250 and 1750 BC) at Harappa in the Indus valley. Major development and differentiation of genus *Sesamum* has been documented in Africa (about 30 species) although most of them are synonyms of just 20 species (Ihlenfeldt and Grabow-Seidensticker 1979). These species have spread from African to Asian and South American countries.

There have been contradictions about the exact origin of sesame for a long time. In the beginning, it was believed to be domesticated in Africa; later evidence from inter-specific hybridization and molecular analysis confirmed its domestication in the Indian subcontinent (Bedigian 2004). Domesticated sesame showed morphological and cytogenetic affinities with the south Indian native *Sesamum mulayanum* (Bedigian 2003), which also contains same number of chromosomes (Annapurna-Kishore-Kumar and Hiremath 2008). Further, Nanthakumar et al. (2000) confirmed proximity between cultivated sesame and its progenitor through RAPD markers.

1.4 Classification

Sesame also known as Till or Gingelly belongs to genus *Sesamum* and family *Pedaliaceae*. More than 38 species have been described in this genus, which are classified into different groups on the basis of their geographic distribution, morphologic and cytogenetic information (Kobayashi 1991).

1.5 Culinary Aspects, Processing and Medicinal Use

Sesame seed is used as an ingredient in several food products and animal feed, whereas its oil is medicinally important for application in pharmaceutical industry. Williamson et al. (2007) reported high sesamin (0.67–6.35 mg g^{-1}) and gamma tocopherol (56.9–99.3 μg g^{-1}) levels among various sesame accessions, which help in the prevention of hypertension and stroke (Noguchi et al. 2004). The antioxidant lignans in sesame seed viz., sesamolin and sesamin are active ingredients of various antiseptics, bactericides, vermicides, disinfectants, moth repellants, anti-tubercular agents, etc., and proved beneficial for animal and human health (Ashakumary et al. 1999). In addition, neuroprotective effects of sesamin cause hypoxia-induced cell death of cortical cells present in culture (Hou et al. 2003). Sesame oil can also be used as alternative diesel fuel by mixing with methanol and sodium hydroxide (Saydut et al. 2008).

1.6 Genetic Variability

Broad-based plant germplasm resources are imperative for sole and successful crop improvement. Genetic diversity has become more important as cropping intensity and monoculture continue to increase in all the major crop-producing regions of the world. A complete array of sesame germplasm consists of

1. wild relatives, weed races and local races
2. obsolete lines and cultivars
3. improved varieties.

Proper understanding of genetic variability, heritability and correlation studies of plant traits is vital for effective use of germplasm in any breeding program (Ganesh and Thangavelu 1995). Germplasm banks are source of genetic variability and are essential for improvement of crop species. Crop variability is characterized by genetic and phenotypic parameters used for identification and selection of desirable parents for breeding program. Despite the high nutritional value, historic and cultural significance of sesame, there has been little focus on sesame research. No international agency (CGIAR, Consultative Group on International Agricultural Research) is assigned work on sesame crop (Bedigian 2003). Similarly, limited information regarding its genetic diversity is available. Centers for sesame genetic diversity are found in India, China, Central Asia and Abyssinia (Hawkes 1983). Large genetic diversity of sesame should be considered, while planning conservation strategies or exploiting it for breeding programs. Presently, molecular techniques including isozymes (Isshiki and Umezaki 1997a), random amplified polymorphic DNA (RAPD) and inter-simple sequence repeats (ISSR) are being employed to study genetic variability in sesame (Abdellatef et al. 2008; Kim et al. 2002).

1.7 Breeding Objectives

There are various objectives for sesame breeding.

- High seed yields
- Superior plant architecture (ideotype)
- Indehiscent capsules
- Improved oil quality
- Resistance to diseases and pests

Crop improvement has resulted in rapid replacement of old races, wild and weedy species and cultivars. These materials are excellent source of genes for adoptability and resistance to biotic and abiotic stresses. The genetic resource management includes collections, conservation, evaluation characterization, classification and cataloging of germplasm. Lack of specific research and understanding of yield-related attributes limited production and extension process of sesame (Ashri 1989). Yield is an important but complex parameter of crop that is affected by various factors. Development of high-yielding varieties is the ultimate goal of any plant breeder. For efficient crop breeding and improvement, it is of utmost importance to ascertain the contribution of each yield-related trait toward yield, and to select components maximizing yield. Such studies are helpful in determining the model plant type for species.

Indeterminate plant growth habit of sesame and seed shattering at maturity resulted in poor adaptation of plant architecture to modern farming techniques (mechanized harvesting) (Çağırgan 2006). Due to indeterminate sesame growth habit, flowering continues for long time, this heterogeneous capsule maturation causes harvesting problem and yield losses. Development of sesame varieties with improved architecture and determinate habit can assist sesame yield improvement programs. Sesame yield potential is negatively affected by its early senescence and susceptibility to biotic and abiotic stresses (Rao et al. 2002). Sesame is susceptible to phyllody disease caused by phytoplasma, resulting stunted plant growth and yield losses (Singh et al. 2007). Development of phyllody-resistant varieties is one of the important objectives in sesame breeding program. Sesame wild species possess genes for resistance to biotic and abiotic stresses, which can be introduced into cultivated varieties either through backcrossing or genetic engineering.

2 Breeding Methods

Plant breeding is a combination of both science and art for effective management of available genetic variability and creation of new ones to attain desired goals. It is the process to identify and select plants possessing desirable traits, and/or to develop an ideal type plant by combining these desired traits into single plant. Breeding methods used for sesame genetic improvement are simple varying from plant selection to hybrid development and molecular breeding. Application of biotechnology and molecular breeding methods can boost the breeding process for development of superior sesame varieties.

2.1 Conventional Breeding

Conventional breeding is under the control of human for choice of parental lines, and selection of their offspring to direct the evolution process for crop production according to their desires. Although low percentage of cross pollination is reported, the sesame is predominantly regarded as a self-pollinated plant (Ashri 2007). Development of sesame types with desirable characters is achieved through pedigree selection from segregating generations of different crosses. In conventional plant breeding these traits are manipulated to get desired genetic combination through various procedures.

There are several advantages of conventional breeding, it is technically simple, convenient and need no sophisticated tools. It is suitable for improvement of many traits or polygenic or traits with unidentified genes at one time. However, there are certain disadvantages of conventional methods including incompatibility in crosses, limitation of genetic variation within crop gene-pool and time consuming. Selection of plants with desirable traits from segregating generations is a time-consuming process, and sexual breeding methods are not useful for improving sexually sterile crops.

2.1.1 Pure Line and Mass Selection

Evaluation and consequent selection of improved lines are the first step in breeding process that largely depends on the knowledge of plant genetic diversity and heritability. Selection is regarded as the most ancient and basic procedure in plant breeding in which desired plants are selected from genetically variable population. These lines are evaluated against existing commercial varieties for yield and other traits for making justified plant selection.

Information about relationship between yield and yield-contributing attributes is very important for a successful breeding program (Ganesh and Sakila 1999). Plant selection with appropriate type sesame is essential for increasing seed yield and developing novel sesame varieties. It is considered that breeding based on additively controlled characters helps improving sesame yield (Mubashir et al. 2007). Since seed yield is a polygenic character, it is essential to identify yield-contributing attributes for selecting high-yielding sesame cultivars. Various physiological traits are useful for determining selection criteria including higher number of capsules, branching and biomass, harvest index, which exhibit significantly positive correlation with seed yield in sesame (Sarwar and Hussain 2010). Large numbers of sesame cultivars and lines have been classified on the basis of diagnostic morphological and genetic traits such as flower characters including phyllotaxis, number of nectar, flower or capsule per axil and carpel number per capsule (Sarwar et al. 2005). These classifications provide foundation for development of high-yielding sesame varieties.

High genetic advance and heritability for yield-related parameters including seed yield, capsule number and branches per plant were documented by Sarwar and Haq (2006), who evaluated 106 sesame genotypes from different parts of the world. They concluded that selection of sesame elite genotypes for seed yield is possible on the basis of these characters. On the basis of these phenotypic and genotypic marker traits, various high-yielding sesame varieties have been selected, and a positive correlation of these traits with seed yield was confirmed (Sarwar et al. 2005). Plant characteristics such as bicarpels, monocapsule, branch and tricapsules have been used as marker in pedigree selection method by Baydar (2005) to obtain high-yielding sesame varieties.

High heritability estimates of disease infestation are under additive gene action control, and consequently help in the selection of disease-free sesame plants. El-Bramawy and Abd Al-Wahid (2009) screened 28 sesame genotypes for resistance to *Fusarium oxysporum* under field conditions for two successive seasons. Two genotypes “S2” originated from a selection and “H4” from hybridization demonstrated stable resistant to *Fusarium* wilt throughout the evaluation. Some other genotypes including Mutants-8, A-130, H-1 and S-1 also maintained their resistance classes during the two successive seasons. In another study, Arslan et al. (2007) evaluated 29 gamma rays (γ-rays) induced mutants and selected sesame plants exhibiting high level of resistance to *Fusarium* blight.

2.1.2 Hybridization

In conventional plant breeding, hybridization is the most frequently used technique. It helps to combine the desirable traits from different plant lines into a single plant through cross pollination. Desired traits such as disease resistance and improved oil quality can be transferred from wild relatives of a crop species to the cultivated forms. Heritability estimates and combining ability studies assist in predicting genetic improvement of different types and are useful in hybrid selection program.

In sesame, emasculation is the simplest and most commonly used technique for producing F_1 hybrids through cross pollination. Additively control characters can be effectively transferred through hybridization process. In sesame high heritability for yield-related parameters, i.e., the number of branches per plant, the number of capsules per plant, seed yield per plant and seed yield per square meter, shows that additive gene action governs these characters (Sarwar and Haq 2006). Bisht et al. (2004) made crosses among 24 diverse and un-adapted parental lines in various combinations and selected high-yielding sesame plants from a progeny of 103 crosses. Phyllody-resistant sesame cultivars were developed through intra- and inter-specific crosses among different sesame cultivated and wild species, and it was revealed that disease resistance is governed by one dominant (wild species) and one recessive (cultivated species) gene (Singh et al. 2007).

Production of male sterile lines provides an opportunity to facilitate cross pollination process for hybrid seed production, and to exploit sesame heterotic vigor. Sesame cytoplasmic male sterile (CMS) lines were developed by hybridizing *S. indicum* with its wild relative *S. malabaricum* (Bhuyan et al. 1997). Later using CMS system, Bhuyan and Sarma (2003) obtained 36 hybrid combinations of diverse origin. Out of which many hybrids exhibited high heterosis for seed yield, oil content and capsules number per plant. Heterosis, a phenomenon of increased vigor, is obtained by hybridization of inbred lines. Heterosis breeding is a common technique for developing high-yielding sesame varieties that may exhibit 77–540% heterotic effect (Yadav et al. 2005). Mubashir et al. (2009) conducted an experiment comprising of five parental lines and their ten crosses, recording 40.35–255.12% heterosis in yield-contributing components.

2.2 Mutation Breeding

Mutation breeding involves induction of new genetic variability through spontaneous or artificial mutagens (chemicals or physical). It minimizes our dependence on the use of wild species or species from other cultivars. Induced mutants are evaluated and selected for desired traits. However, development of large number of mutants with undesirable traits limits its wide application in the breeding programs.

Mutagenic techniques are successfully employed in sesame to induce genetic variability. Applications of appropriate doses of physical mutagen or concentration of chemical mutagen are important to get adequate mutations that could benefit sesame breeding program. Researchers at FAO/IAEA have initiated coordinated research project for genetic improvement in sesame, and developed 142 mutants having agronomically useful characters by using both physical and chemical mutagens and devised method for mutation breeding for sesame (Van Zanten 2001). Following were the recommendations for mutagen treatment.

Well-adapted, homozygous and uniform varieties should be selected for mutation induction for improvement of one or two characters at a time. Lower dose ranges of mutagens are more suitable for inducing desirable mutations, i.e., γ-rays 150–800 Gy, fast neutrons' irradiation 30–80 Gy. For chemical mutagenesis, first seeds are pre-soaked in water for 24 h (4°C). Then soaking into chemical mutagen, e.g., in ethyl methane sulfonate (EMS) solution (0.4–1.0% v/v) with phosphate buffer ($pH=7$) for 2–4 h or in sodium azide (NaN_3) solution (4–6 mM) with Sörenson phosphate buffer ($pH=3$) for 4–6 h at 18–24°C.

Sesame mutants have been selected for desirable traits of higher yield and quality (Wongyai et al. 2001), improved plant architecture (Çağırgan 2006), seed retention, larger seed size and seed color (Hoballah 2001). A research program on radiation-induced mutagenesis has been initiated to induce genetic variations and to screen desirable "plant type" (Chowdhury and Datta 2008). Sengupta and Datta (2005) identified a narrow leaf mutant in sesame through nitrous acid and hydrogen peroxide treatments in different doses, and the mutant yielded higher number of capsule per plant on the main axis than control.

Early maturing and high-yielding sesame mutants have been developed by using NaN_3 and colchicines, and Mensah et al. (2007) found that 0.0625% NaN_3 and 0.125% colchicine were the most efficient concentration for inducing mutations in sesame. The γ-ray-induced mutants with improved plant architecture were developed having closed capsule, determinate growth habit, resistance to *Fusarium* blight, etc. These mutants had improved oil quality with considerably higher oleic acid and low linoleic acid contents (Arslan et al. 2007).

Indeterminate sesame habit is a challenge for sesame breeders, and mutagenic breeding approach is applied to solve this problem (Çağırgan 2006). A spontaneous indehiscent mutant "id" was discovered in 1942 in Venezuela by Langham (1946). However, due to its low yield and other undesirable side effects it was not used in commercial varieties. The first determinate sesame mutant (dt-45) was selected by Ashri (1981) from an M2 population by irradiating Israeli variety "No-45" with γ-rays (500 Gy). Çağırgan (2006) irradiated seeds of four sesame cultivars with γ-rays (150–750 Gy) and found three true botanical determinate mutants (dt-1, dt-2 and dt-3) of cultivar Muganlı-57 and dt-4, dt-5 and dt-6 of cultivar Çamdibi. They also proved that selection of determinate growth habit mutants depends upon population size, cultivar response to mutagenic treatment and careful screening.

Marker traits are always useful in genetics and breeding as they are easily scorable and selectable in field conditions. Cytogenetical and agronomical aspects of some morphological (leaf and pollen related) marker mutants were induced following different doses of X-rays and γ-rays (Chowdhury et al. 2009). These morphological sesame mutants exhibited distinctive traits viz., narrow, elongated, thick leaf types, ovate, ternate elongated petiole type and white, pigmented flower type. Out of different mutants, thick leaf mutants were the most desirable plant types possessing superior agronomic traits such as plant height, primary and total branches per plant, capsule on main axis, distance from base to first branching, total capsule per plant, seed yield and seed protein content than control. Mary and Jayabalan (1995) induced mutation-affecting leaf morphology in sesame at M2 following EMS treatments to seeds.

2.3 Innovative Breeding

Shortcomings in the conventional breeding (sexual reproduction) are overcome by genetic engineering techniques that introduces desirable genes directly into the target crop making gene pool unbounded. Only desirable traits are improved in this method, therefore, large populations and multiple generations are not required for selection of plants. In addition, there are no limitations for application of this technique to sterile and vegetatively propagated crops.

Likewise, these techniques also have certain drawbacks; only simple and monogenic traits are transferred most of the time, they are relatively expensive and technically demanding and they are controlled by government organizations. Various innovative approaches are used for sesame breeding viz., in vitro culture, genetic transformation and molecular breeding as described below.

2.3.1 In Vitro Culture and Screening

Somatic plant cells are used for in vitro culturing on nutrient media and new plants are generated from these explants. Plant regeneration through tissue culture is a source of creating genetic variations, heritable variants with desirable agronomic traits are selected, and used in further breeding programs. Plants can also be selected for resistance traits at early stage by exposing cells of calli to pathogens, or isolated pathotoxins by eliminating unwanted plants from the large population. Three factors affect plant regeneration process, viz., genotype, explant source and culture conditions.

Tissue culture and regeneration through in vitro culturing can speed up breeding process by producing a number of stable regenerants via callus or somatic embryogenesis in a short span of time. In sesame in vitro culturing, cotyledon (Yadav et al. 2010) hypocotyl and shoot tips (Baskaran and Jayabalan 2006) have been reported to be more responsive to callus induction and plant regeneration. Appropriate concentrations of plant growth regulators and their combinations are very important to achieve successful plant regeneration from cultured cells and tissues, and were optimized in different studies. Application of BAP (benzylaminopurine) in the nutrient media was reported essential and the most effective cytokinin for shoot induction and plant regeneration in *S. indicum* (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, and reported callus induction on media containing 2.2–22.6 μM 2, 4-D and 2.6–26.8-μM NAA (α-naphthalene acetic acid), increased shoot proliferation on BAP and Kn (kinetin), whereas rooting took place on NAA (8.0 μM).

In another study, Saravanan and Nadarajan (2005) investigated in vitro response of four sesame varieties on different media components for callus induction, multiplication, shooting and rooting. The highest callusing frequency was recorded at 2, 4-D (3 mg L^{-1}) with 100 mL of coconut milk followed by 2, 4-D (3 mg L^{-1}) with casein hydrosylate (0.1 mg L^{-1}). Significantly higher shoot multiplication ratio was achieved in MS media (Murashige and Skoog 1962) supplemented with 1-mg L^{-1} indole acetic acid (IAA), 1–1.5-mg L^{-1} BAP and 1.25-mg L^{-1} Kn. Tissue culture and plant regeneration protocol for wild species of genus *Sesamum* was also optimized by Dasharath et al. (2007a, b). They used *Sesamum occidentale* and *Sesamum radiatum* and found 8-mg L^{-1} Kn along with BAP as the best combination among different levels of BAP and Kn applied.

2.3.2 Somatic Hybridization

Sesame is a self-pollinated crop; however, conventional crosses between cultivated sesame and its wild relatives have been attempted, the hybrids were difficult to produce. Use of wild relatives in hybridization program is restricted due to cross incompatibility and low hybrid frequency through embryo culture. Hybrid plants can also be developed through fusion of somatic plant cells. Protoplast fusion is helpful to overcome sexual incompatibility as distantly related species can be fused. In vitro culturing system can help to multiply F_1 plants in the lab first and then to transfer them into the field (Dasharath et al. 2007a).

In sesame, Dasharath et al. (2007b) successfully developed inter-specific hybrids between cultivated *S. indicum* and its wild relatives *S. radiatum* and *S. occidentale* through ovary and ovule culture. In another study, a simple and efficient protocol for production of hybrids of a cross between *Sesamum alatum* and *S. indicum* were optimized through ovule culture (Rajeswari et al. 2010). For this purpose, capsule retention without embryo abortion was delayed by spraying mixture of growth regulators 289-μM gibberellic acid (GA_3), 80.6-μM NAA and 23.3-μM Kn. The plants were regenerated through direct organogenesis of 7-day-old capsules by culturing them on MS medium containing 8.8-μM BAP, 2.8-μM IAA and 1,712.3-μM glutamine. The developed hybrids were screened for phyllody resistance which exhibited moderate resistance.

2.3.3 Genetic Manipulation

Sexual incompatibility among plants limits the application of conventional breeding. In genetic engineering techniques, specific genes from any organism (plants, bacteria, fungi, animals and viruses) coding for desired traits are introduced into the genome of any plant. Various techniques are used to obtain transgenic plants viz., DNA transfer through *Agrobacterium* or direct DNA transfer via bombardment, electroporation and polyethylenglycol permeabilization.

The *Agrobacterium*-mediated DNA transformation is the most commonly used techniques in plants (Xu et al. 2009). Desired genes are first transferred to plasmid DNA of *Agrobacterium* and then allowed to transmit into individual plant cells for their expression. This method is suitable for *Agrobacterium* susceptible plants. However, it cannot be used for many economically important plants including cereals; therefore, direct DNA uptake method is applied.

Sesame yield is limited due to different biotic and abiotic stresses (Rao et al. 2002). Some wild sesame species possess resistance genes, but post-fertilization barriers restrict their transfer to cultivated crops through conventional breeding. Establishment of in vitro plant regeneration is a prerequisite of any genetic transformation system that is already optimized (Were et al. 2006). Sesame has been reported as susceptible to *Agrobactarium tumefaciens* infection (Taskin et al. 1999). Protocol for genetic transformation and plant regeneration of sesame were optimized by Were et al. (2006). A significant interaction between hormonal concentration and macronutrients for plant regeneration was recorded, and application of 20-μM TDZ along with 2.5-μM IAA was found the best for successful plant regeneration. Yadav et al. (2010) optimized an *A. tumefaciens*-mediated transformation protocol to generate fertile transgenic sesame plants. In this method, cotyledon explants were used for plant regeneration via multiple shoot organogenesis. They recovered plants on MS basal medium containing 25.0-μM BAP, 25.0-mg L^{-1} kanamycin and 400.0-mg L^{-1} cefotaxime.

2.3.4 Marker-Assisted Selection

Marker-assisted selection (MAS) process has revolutionized plant breeding disciplines by increasing selection efficiency at early stages of development and characterization in later generations (Cahill and Schmidt 2004). The MAS program has been widely applied tool in commercial crop breeding and product development in a variety of agriculturally important economic crops, including cereal, oilseeds, vegetables and ornamentals.

Various morphological plant traits, their geographical origins and genotype-specific bands developed through molecular markers provide useful information about economic importance of crop, and help in further classification (Ali et al. 2007). Molecular markers have been applied for studying genetic diversity by using various *S. indicum* accessions (Abdellatef et al. 2008) and suggested the usefulness of RAPD technique in sesame breeding and conservation programs, for proper maintenance of germplasm banks and efficient parental line selection.

However, in spite of high economic value, a limited number of reports are available regarding the application of molecular markers for sesame improvement and studying genetic variability viz., isozymes (Isshiki and Umezaki 1997b), ISSR (Kim et al. 2002), amplified fragment length polymorphism (AFLP) (Ali et al. 2007) and simple sequence repeat (SSR) markers (Dixit et al. 2005). The application of MAS is generally limited to exploration of genetic variability and germplasm evaluation. Only few studies are conducted for tagging desired genes to facilitate the process of plant selection for genetic improvement. Construction of genetic linkage maps is a useful technique for tagging of the desired traits in sesame molecular breeding (Wei et al. 2009). Using MAS, Uzun and Çağırgan (2009) tagged *dt* gene, which regulates determinate growth habit in sesame. Development of molecular markers could assist sesame plant identification and selection for breeding programs, and facilitate integration of these genes into improved cultivars.

3 Conclusion

Conventional and innovative breeding methods are complementary to each other for improving crops. Depending on breeding objectives, their application can be appropriate or inappropriate; however, none of the improvement strategies alone is totally perfect. Sesame breeding objectives can be achieved by devising breeding programs with specific targets for crop improvement. Application of biotechnology along with conventional breeding methods is a useful approach for breeding superior varieties in a short time. In addition, the construction of molecular genetics maps, tagging-desired traits for marker-assisted selection and positional cloning could be more reliable tools in genetic studies than morphological traits. Similarly, physiological and pathological studies offer deeper understanding and effective ways to identify plant traits useful for solving particular problems. Co-ordination of breeding, physiology, pathology and biotechnology will be very helpful for increasing the productivity and production of sesame, and will provide a model for other crops.

Acknowledgement We are highly grateful for the support from scientific officers of Oilseed Program of National Agriculture Research Centre, Islamabad, Pakistan; PMAS Arid Agriculture University, Rawalpindi, Pakistan; College of Agriculture and Biotechnology, Zhejiang University, Hangzhou, China.

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