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REVIEW ARTICLE

GENETIC AND GENOMIC INTERVENTION TO UPSURGE NUTRITIVE VALUES OF SESAME (*SESAMUM INDICUM* L.)

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ABSTRACT

Recent years witnessed an interest from the industrial sector in sesame for production of superior quality oil augmented with sound antioxidants. However, despite its economic significance being widely felt, breeding programmes of sesame has not been complemented adequately with the innovative breeding and biotechnological tools. The crop has enormous variability and several molecular marker systems have been used to increase selection efficiency for genotyping of several traits as well. Rich genetic diversity is available to ease the genomic advancements in the crop through comparative mapping and also in the study of lipid biosynthesis. The framework genetic map of sesame is now available in public domain. Wild species constitute a rich repertoire of genes for biotic and abiotic stresses besides oil quality traits and need to be utilized. Resequencing data in various sesame accessions from diverse sources suggested that the high genetic diversity of lipid-related genes might be associated with the wide variation in oil content. *In vitro* manipulations and genetic transformation protocols through vector mediated gene transfer in sesame crop are in place providing scope for development of transgenic for desirable traits. This article reviews the benchmark interventions in the field of genetics as well as genomics of the crop and highlights further research thrust for promoting the same in an international arena.

INTRODUCTION

Sesame (*Sesamum indicum* L.), a species of the family Pedaliaceae, cherishes the longest history of cultivation. Archeological remains of sesame dating back to 5500 BC have been found in the Harappa valley in the Indian subcontinent (Bedigian and Harlan, 1986). It used to be a highly prized oilseed crop in ancient world not only because of its extremely stable oil content but also its resistance to draught (Langham and Wiemers, 2002). The exact origin of sesame is a contentious issue; however, mounting evidence has shown that sesame originated either in India (Bedigian, 2004) or in Africa (Kobayashi, 1986). Genetic, morphological, and phytochemical evidence support the hypothesis that domesticated sesame originated on the Indian subcontinent (Bedigian, 2004). On the other hand, the assumption of Africa being the primary centre gets a valid support through the presence of a wide genetic diversity of sesame in African continent (Hiltebrandt, 1932). Sesame is grown principally for its nutritious seed that is rich in linoleic acid, protein, and calcium as well as vitamin E, and small quantities of vitamins A, B1, and B2.

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Nearly 70% of the world`s sesame seed is processed into oil and meal while the remainder is channeled to food and confectionery industries (Morris, 2002). The oil has very diversified role from cooking and salad on one hand, while for making margarine, in cosmetic preparations, pharmaceutical products, paints, soaps and insecticides (Asri, 1989) on the other. Small uses of sesame oil consist of pharmaceutical and skin care products (Morris, 2002). The antioxidant sesamin is used as a synergist for pyrethrum or rotenone insecticides and increases the toxicity of insecticides when spayed against flies (Haller *et al.*, 1942). Mucilaginous leaves or leaf of sesame sap are used to treat fever, as a remedy for cough and sore eyes and to kill head lice; the sap is taken to facilitate childbirth, to treat dysentery and gonorrhea and is used in dressings after circumcision (Akbar *et al.,* 2012). The meal left after oil extraction contains 35-50% protein and makes a rich feed for poultry and livestock. The sesame crop is currently cultivated throughout the world in about 70 countries of Africa, Asia and Australia. It is grown worldwide over an area of 79 million hectares producing 63,000 tonnes seeds (FAOSTAT 2012). India, China Myanmar, and Sudan are the leading sesame-producing countries of the world. Current world production is estimated at about 610 thousand metric tons annually, placing sesame behind soybean, peanut, cottonseed, sunflower, linseed and rapeseed, in the quantity of world oilseed production

(FAOSTAT 2012). India ranks second in the world only after Myanmar with 18.20 Lac ha area and 6.10 Lakh tonnes production with Rs. 1510.4 Crore export. The Average yield of sesame on global scale is 5.11 Qt/hectare, while in India; it is 3.30 Qt/hectare (FAOSTAT 2012). Acreage, yield and production on a world basis have largely stayed at the same over the past five years. Despite the potential for increasing the production and productivity of sesame, there are a number of challenges inhibiting sesame production and productivity. Among the several production constraints, the most important include lack of improved cultivars and a poor seed supply system. In addition, there are severe biotic stresses, such as bacterial blight *Xanthomonas campestris* pv. sesami), phyllody (a Mycoplasma-like organism), Fusarium wilt (*Fusarium oxysporum*), powdery mildew (*Oidium erysiphoides*), Alternaria leaf spot (*Alternaria sesame*) and Cercospora leaf spot (*Cercospora sesame*). The abiotic stresses confronting sesame production include salinity, water logging, photoperiod insensitivity and frost.

The above stated constraints to the productivity pose the need for concerted efforts for sesame crop improvement. However, despite, being an ancient but an important oil crop, it is still at an early stage in its breeding history. More focused breeding efforts were undertaken only in recent decades, and even these only in very few research stations. The improvement programmes mostly relied on conventional methods through germplasm augmentation, characterization and selection. Characterization of available or existing genetic diversity of crops played a significant role in bringing out a variety with desirable market oriented physio-chemical traits. Information on genetic diversity is noteworthy when working to improve qualitative profile of the crop varieties. Available genetic diversity is either directly used for evaluation leading to selection or desired traits are combined into a single plant *via* hybridization and backcrossing. Sesame germplasm evaluation for a variety with high oil content and least/ zero anti-nutritional factors are based on genetic heritability estimates. Mutational techniques are routinely employed for broadening genetic diversity of sesame breeding material. 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. Recently, scientific researchers have investigated many physiological and pharmaceutical aspects of sesame seeds. Studies on antioxidants, anti-aging, the synergistic effect with tocopherols, serum lipid lowering, blood pressure lowering, and other functions have also been reported (Namiki, 2007). Despite such high value being placed on sesame seed, there have been very limited scientific studies validating these claims.

Genetic diversity studies in sesame

An elaborate estimation of genetic diversity present among the germplasms helps the breeder to attempt crosses between desirable diverse genotypes for generating sufficient genetic variability. Besides, diversity estimates in cultivated plants provide a rationale for conservation strategies and support the careful selection of starting material for breeding programs (Varshney *et al*., 2009). Diversity measures applied to crops usually have been limited to the assessment of genome polymorphism at the DNA level. Occasionally, selected morphological features are recorded and the content of key chemical constituents is determined, but unbiased and comprehensive chemical phenotypes have not been included systematically in diversity surveys. Most of the earlier studies on sesame diversity were confined to morphological characterization, evaluation of agronomic traits, reaction to biotic and abiotic stresses and biochemical parameters pertaining to seed oil fatty acid profiles. In cultivated sesame, seed oil content ranged from 40.4 to 59.8% fatty acids of this seed oil are mainly oleic acid (C18:1) (32.7 to 53.9%), linoleic acid (C18:2) (39.3 to 59%), palmitic acid (C16:0) (8.3 to 10.9%), stearic acid (C18:0) (3.4 to 6%), and arachidic acid (C20:0) (0.7 to 1%) (Yermanos *et al*., 1972; Weiss, 2000). However, fatty acid composition as well as oil content is influenced by various physiological, ecological and cultural factors. Mosjidis and Yermanos (1985) reported that seed samples from central and lateral capsules affected the fatty acid composition in sesame. A variation in agronomic practices, to some or more extent, influences the qualitative profile in sesame. Sowing date also influenced fatty acid composition of sesame by decreasing linoleic and increasing oleic and stearic acid content as sowing was delayed (Gupta *et al*., 1998). Eco-geographical impacts are also reflected in fatty acid profile of the crop similarly, Oil content is greatly affected by environmental factors (Gupta *et al*., 1998), the extraction procedure followed also have concern the oil content of the sesame genotypes. (Uzun and Cagirgan. 2006). Unsaturated fatty acid contents in sesame are higher in cultivars from temperate regions than in those from tropical regions (Lee and Kang, 1980). Moreover, the maturity of sesame seeds also causes changes in fatty acid profile (Crews *et al*., 2006). Not only these conditions affect fatty acid composition but also genotypic factors play an important role in the process, resulting in the fact that each genotype reveals slightly or entirely different fatty acid composition. The determinate growth habit, which is a very useful character enabling the possibility of mechanized harvesting by providing synchronous flowering in sesame, should also influence genotypic factors as well as environment with respect to fatty acid composition. However, there is no detailed study about the fatty acid composition of determinacy character even though it was induced first as early as the 1980s (Ashri,1989). The determinate genotypes generally had lower means for oil yield than in determinates. The direct effect of the number of fruiting branches on seed yield and oil content in determinate sesame was shown by Uzun and Cagirgan (2006). In conclusion, the fatty acids of determinate types were found to be of good composition, whereas their oil yields need to be improved by increasing their seed yield.

An overview of oil quality improvement in sesame

Plant seeds are sources of oils of nutritional, industrial and pharmaceutical importance. The suitability of oil for a particular purpose, however, is determined by its fatty acid composition. The high quality premium edible as well as industrially important oil of sesame has fetched world-wide interest in recent years. Presence of lignans *viz*; sesamin (0.4-1.1%), sesamolin (0.3-0.6%) and traces of sesamol and tocopherol in the oil are accountable for placing the sesame at uppermost place of global demand. On account of these components, natural products of sesame have been in practice since ancient times as health food additives for preventing

diseases and promoting well beings. However, despite the multilateral utilization and implications of sesame, the indigestible ingredient *viz*; Oxalic acid and Phytic acid present in seed coat of its seed make it unfit for direct consumption. These phytoconstituents, indeed have captured, in the current era also, the interest of consumers and scientists of the medical and pharmaceutical industries due to their antitumor, antimutagenic as well as anticarcinogenic properties (Shahidi *et al*., 2006). Generally sesame varieties with high oil content of around 50% in their seed along with higher lignans being there and less than 2.0% FFA in oil are considered of good quality to fetch awesome prices and demand in international market.

Characterization of sesame germplasm

Access to a wide range of genetic diversity is critical to the success of any crop breeding programs and the ability to identify genetic variation is indispensable for effective management and use of genetic resources (Varshney *et al*., 2009), and it majorly depends on characterization. Germplasm characterization involves, in the First instance, description of variation for morphological traits that are internationally accepted descriptors but are often associated with limitations due to G × E interactions. Besides, this approach has disadvantages such as they are often limited, highly heritable traits often show little variation over much of the material studied and trait expression, mainly of quantitative traits. Despite several limitations, this approach used to be in practice for a longer time, and is being used yet. A number of studies based on morphological markers have found a high genetic diversity in sesame populations (Bedigian & Harlan, 1986; Arriel *et al.*, 2007). Biochemical methods that include use of seed storage proteins, allozymes and isozymes, have been proved to be more successful than morphological characterization as the approach is effective in a better control of environmental influence. Among the biochemical techniques, sodium dodecyl sulphate polyacrylamide gel electrophoresis (SDS-PAGE) is widely used due to its easiness and effectiveness for telling the genetic construction of crop germplasm (Ghafoor & Ahmed, 2005; Jatoi *et al*., 2011; Nisar *et al*., 2011).

SDS-PAGE is considered to be a practical and dependable method because seed storage proteins are extremely sovereign of environmental fluctuations (Gepts, 1989; Javaid *et al*., 2004; Iqbal *et al*., 2005). Seed protein patterns obtained by electrophoresis have been effectively used to solve the taxonomic and evolutionary relationships amongst crops and their wild relatives, and study the various classes of storage proteins (Das & Mukarjee, 1995; Khan *et al*., 2010). In the 1980s and 1990s, using isozymes, various studies have confirmed wider diversity in sesame germplasm. However, studies on isozyme polymorphism were restricted to few enzymes and cultivars owing to the technical difficulties in handling protein based gels. Besides, isozymes and seed storage proteins can only screen a very small genome section of species; they are unable to detect low levels of variation. These shortcomings of morphological as well as biochemical markers are overcome by DNA-based techniques, which have potential to identify polymorphism represented by differences in DNA sequences, and moreover they can be used at any developmental stage of the plant and they cover the whole genome variability (Kumar and Sharma, 2011).

Molecular markers in the characterization of several agronomic traits of sesame

Mapping and sequencing of plant genomes would help to elucidate gene function, gene regulation and their expression. Development of high density integrated genetic linkage maps based on molecular markers is a prerequisite for use in marker assisted selection (MAS) and positional cloning of agronomically important genes in any crop species (Azhaguvel *et al.*, 2006). For a molecular marker to be useful to plant breeders, it must be assayed readily and reproducibly in a range of laboratories. Although the information on the conventional map is important to know the location of gene/s corresponding to pheonotypical traits; their usefulness is limited by the low number of morphological markers which are available to the plant breeder for crop improvement programs. Polymorphism in the nucleotide sequence is usually sufficient for it to function as molecular marker in mapping. These polymorphisms are revealed by molecular techniques such as restriction fragment length polymorphism (RFLP), amplified fragment length polymorphism (AFLP), simple sequence repeat or microsatellite (SSR), random amplified polymorphic DNA (RAPD) and cleavable amplified polymorphic sequences (CAPS). Genetic maps have been constructed in many crop plants using these markers on a single segregating population. An ideal molecular marker technique should be polymorphic and evenly distributed throughout the genome, and also provide adequate resolution of genetic differences. Besides, an ideal marker must have linkage to distinct phenotypes (Agarwal *et al*., 2008). Unfortunately no molecular marker technique is ideal for every situation. Techniques differ from each other with respect to important features such as genomic abundance, level of polymorphism detected, locus specificity, reproducibility, technical requirements, cost etc.

Despite the widespread use of molecular markers in other crops, their use in sesame remained dormant for until a decade. In the recent past, importance of molecular markers has been realized and have been used in germplasm assessment for understanding the geographic structure, molecular profiling of genotypes and in genetic mapping in sesame also. Molecular markers have been used primarily for evaluation of germplasm assessment of the local cultivars and land races or germplasm accessions and to partition genetic variation geographically (Johnson *et al*., 2007). Previous studies on sesame have mostly covered quantitative genetics (Wei *et al*., 2011), traditional genetic breeding (Were, 2006), and genetic relationships and diversity among sesame germplasm collections (Laurentin & Karlovsky, 2007). The most commonly employed markers in sesame are random amplified polymorphic DNA (RAPD), inter simple sequence repeat (ISSR) markers and amplified fragment length polymorphism (AFLP). These are the markers of choice for crops with inadequate genomic resources, do not require prior sequence information and scan the genome including the repetitive sequences. Assessment of genetic diversity in sesame was mainly focused on estimating genetic variation by combining molecular polymorphism and phenotypic variation (Johnson *et al*., 2007). AFLP markers were first used in sesame breeding and genetic studies in the early 2000 to construct genetic maps and to map genes controlling various agronomically important traits (Uzun *et al*., 2003).

Johnson *et al* (2007) characterized 96 accessions representing 29 countries from seven world regions using AFLP markers. There was lack of congruence between agro-morphological and molecular matrices indicating the need for both measures for complete characterization of sesame diversity (Johnson *et al*., 2007). ISSR primers were found to be more informative and disclosed more polymorphism than RAPD primers. Subsequently, studies of Johnson *et al*., (2007) indicated the robustness of AFLP marker system in terms of its high discriminating power, assay efficiency index, marker index, resolving power and genotype index and distinguished sesame diversity across broad geographic groups and in fingerprinting the genotypes. Perusal of diversity analysis studies indicate close clusters in germplasm and higher genetic variation was obtained only when the study included exotic germplasm, land races or wild species. This clearly reflects on the narrow genetic base on which the breeding programmes are formulated. All the studies unequivocally establish the existence of wide genetic diversity in sesame germplasm including wild species and indicate considerable potential for genetic improvement of the crop for agronomic and quality traits. An AFLP marker was identified linked to the *closed capsule* mutant trait in sesame using a bulked segregant analysis (BSA) approach to segregating progenies of a cross between the *closed capsule* mutant line '*cc3*', and the Turkish variety 'Muganli-57'.

Uzun *et al*., 2003 tested a total of 72 primer combinations to screen for linkage to the trait, but only one closely linked AFLP marker was identified. The linkage was confirmed by analyzing the AFLP profile from single plants. Later in the decade, other types of DNA markers *viz;* RAPD, ISSR have also been developed for the utilization in sesame breeding programs. Low genetic diversity (0.14–0.21) among groups was reported by Laurentin *et al*., 2008 in 32 sesame germplasm collections using amplified fragment length polymorphism (AFLP). Microsatellites are one of the most commonly used molecular markers to determine the genetic diversity in crop species. However, only a few studies used microsatellites to evaluate genetic diversity in sesame (e.g. Dixit *et al.*, 2005; Wei *et al.*, 2011). Molecular markers have been developed to identify morphological traits of sesame such as growth habit and closed capsule trait (Uzun *et al.*, 2003; Uzun and Cagirgan, 2009).

Recently, single nucleotide polymorphism (SNP) markers have become available, and because of their huge numbers and the ability to genotype without using electrophoretic gel systems, crop breeders and geneticists have moved quickly to use SNP markers in their work (Zhu *et al*., 2008). SNP markers are less informative than SSRs on a per locus basis, because SSRs can be multi-allelic. However, SNPs are much more abundant and genotyping hundreds of lines with thousands of SNP markers is now in routine. Although much effort has been devoted to cloning key genes and characterizing fatty acid elongation and unsaturated fatty acid biosynthesis in sesame (Kim *et al*., 2006), the molecular mechanisms behind fatty acid biosynthesis and metabolism still remain unclear. Publicly available datasets are of limited use for future sesame research, such as elucidating the molecular mechanisms of specific traits and understanding the complexity of the transcriptome, gene expression regulation, and gene networks. Progress in novel gene discovery and molecular breeding in sesame has been limited by the lack of genomic information. For example, only 3,328 expressed sequence tag (EST) sequences in sesame have been deposited in the dbEST GenBank database till January 2011(Suh *et al*., 2003). Transcriptome or EST sequencing has emerged to be an efficient way to generate functional genomic-level data for non-model organisms. The transcriptome is the complete set and quantity of transcripts in a cell at a specific developmental stage or under a physiological condition. The transcriptome provides information on gene expression, gene regulation, and amino acid content of proteins. Therefore, transcriptome analysis is essential to interpret the functional elements of the genome and reveal the molecular constituents of cells and tissues. Genomics mean can assist in identification of novel genes involved in the biosynthesis of sesame-specific flavor or lignans, and a better understanding of the metabolic pathways from photosynthates towards oil which can be stored and used. Expressed Sequence Tags (ESTs) generated by large-scale single-pass cDNA sequencing have proven valuable for the identification of novel genes in specific metabolic pathways.

In order to elucidate the metabolic pathways for lignans in developing sesame seeds and to identify genes involved in the accumulation of storage products and in the biosynthesis of antioxidant lignans, Suh *et al*. (2003) obtained 3,328 ESTs from a cDNA library of 5-25 days old immature sesame seeds. ESTs were clustered and analyzed by the BLASTX or FASTAX program against the GenBank NR and *Arabidopsis* proteome databases. They carried out a comparative analysis between developing sesame and *Arabidopsis* seed ESTs for gene expression profiles during development of green and non-green seeds. Analyses of these two seed EST sets helped to identify similar and different gene expression profiles during seed development, and to identify a large number of sesame seed-specific genes. Seed-specific expression of several candidate genes was confirmed by northern blot analysis. Suh *et al*. (2003) identified EST candidates for genes possibly involved in biosynthesis of sesame lignans, sesamin and sesamolin, and suggested a possible metabolic pathway for the generation of cofactors required for synthesis of storage lipid in non-green oilseeds. Laurentin *et al*. (2008) assessed metabolic diversity in sesame by non-targeted metabolic profiling and elucidated the relationship between metabolic and genome diversity.

They also observed different patterns of diversity at the genomic and a metabolic level, which indicates that selection plays a significant role in the evolution of metabolic diversity in sesame. Earlier Laurentin and Karlovsky (2007) and Ali *et al*. (2007) successfully used Amplified fragment length polymorphism (AFLP) to distinguish cultivars of sesame and to elucidate the genetic relationship among genotypes. Conclusion may be drawn that the use of MAS might be of potential help for crop improvement, its practical application in oilseed crops for the genetic improvement of resistance or tolerance to biotic and abiotic stress has been limited, being mainly hampered by lack of investment and the genetic complexity of most stress-related traits. The importance of molecular markers in marker assisted selection (MAS) is also being realized. Recently, sequence characterized amplicon region (SCARs) markers based on RAPD polymorphism were developed for the closely linked recessive monogenic genes *Li* (controlling very high linoleic acid content) and *Ms*

(controlling nuclear male sterility) (Hamdan *et al*., 2008). Bulked segregant analysis involving a population of 162 individuals from a cross between CLI (NMS) and CR 142 (high linoleic acid) led to construction of a linkage map with five RAPD-SCAR markers. The SCAR markers flanked both loci at 15.7 cM from the *Li* locus and 3.7 cM from the *Ms* locus. Recessive genetic male steriles are propagated through heterozygotes (*Msms*) which can be identified only by progeny testing. Mapping of nuclear male sterility gene allows early identification of lines carrying the malesterile allele precluding the need for progeny testing. Markers linked to high linoleic acid content will facilitate marker assisted selection programme aimed at introgression of *Li* alleles into desirable agronomic background. This study serves as a prelude for development of markers linked to agronomically desirable traits in sesame for accelerating the breeding programmes.

Biotechnological interventions for sesame crop improvement

Rapidly developing biotechnology applications aimed at improving major crops receive large investments and could, in theory, play a role in the promotion of minor or underutilized crop species in the tropics and subtropics. There are clear examples where biotechnology has been used practically to enhance the cultivation of underutilized plants at a field level. Tissue culture and micropropagation techniques are wider and have proven useful, but for other applications benefits are generally very confined at present, although ongoing work suggests genomic and genetic modification approaches may in future be significant for a subset of underutilized species like sesame. Successful outcomes, however, appear to be limited by a lack of integrated thinking during the use of biotechnology methods.

In vitro techniques

Plant tissue culture technology has been available to the plant breeders for nearly four decades and has been extensively employed for crop improvement in several oil seed crops, however very little information is available on *in vitro* culture of sesame. Sesame is found to be recalcitrant in nature. The first report on tissue culture in sesame was that of Lee *et al*. (1985) on shoot tip culture followed by George *et al*. (1987) using different explants of sesame. Effects of explants and hormone combinations on callus induction was studied by Kim *et al*. (1987) in order to obtain herbicide tolerant lines of sesame using *in vitro* selection. However, successful plant regeneration from herbicide tolerant callus was achieved by Chae *et al*. (1987). The effect of growth regulators on organ cultures (Kim and Byeon, 1991) and their combination with cold pretreatment in anther culture (Lee *et al*., 1988) of sesame revealed genotypic effects. In sesame, micropropagation is achieved from shoot tip (Rao and Vaidyanath, 1997), nodal explants (Gangopadhyay *et al*., 1998) and leaf (Sharma and Pareek, 1998) cultures. Somatic embryos have been obtained from zygotic embryos (Ram *et al*., 1990) and seedling-derived callus cultures (Mary and Jayabalan, 1997; Xu *et al*., 1997) with low plant conversion frequencies. Indirect adventitious shoot regeneration from hypocotyl and/or cotyledon explants has also been reported at low frequencies (Rao and Vaidyanath, 1997; Taskin and Turgut, 1997). van Zanten, 2001 also reported development of somatic embryos from hypocotyl derived calli and exploited embryo rescue to overcome disease problems through interspecific hybridization between the cultivated species and the disease resistant wild relatives *Sesamum alatum* and *S. radiatum.* Bhaskaran and Jayabalan (2006) reported standardization of a reproducible micropropagation protocol in cultivated varieties of sesame. Overproduction of secondary metabolites in sesame crop has been accounted as the major barrier in *in vitro* techniques of the crop (Baskaran and Jayabalan, 2006). Influence of macronutrients, plant growth hormones and genotype on adventitious shoot regeneration from cotyledon explants was reported in sesame by Were *et al*. (2006). High-frequency plant regeneration through direct adventitious shoot formation from de-embryonated cotyledon segments of sesame was achieved by Seo *et al*. (2007). Chattopadhyaya *et al*. (2010) established an efficient protocol for shoot regeneration from sesame internodes using the transverse thin cell layer (tTCL) culture method. Abdellatef *et al*. (2010) evaluated the *in vitro* regeneration capacity of sesame cultivars exposed to culture media containing ethylene inhibitors such as cobalt chloride and silver nitrate, and found growth promoting effects due to reduction in ethylene concentration followed by inhibition of ethylene action. Embryo culture procedures were developed for rescuing interspecific hybrids.

Genomics and Genetic Transformation

In recent years, an impressive number of advances in genetics and genomics have greatly enhanced the understanding of structural and functional aspects of plant genomes and have integrated basic knowledge in ways that can enhance our ability to improve crop plants to our benefit. Genomics is a new science that studies genome at a whole genome level by integrating the traditional disciplines of genetics with new technologies from informatics and automated systems (Varshney *et al*., 2009). Various sequencing projects to enhance the knowledge of major crops are present in the public domain and combining the new knowledge from genomic research with traditional breeding method is essential for enhancing crop improvement. Superior varieties can result from the discovery of novel genetic variation, improved selection techniques or the identification of genotypes with new or improved attributes caused by superior combinations of alleles at multiple loci (Varsheny *et al*., 2005). The improvement of some underutilized crops such as sesame, by modern biotechnology, has been lagging behind than cereals and other model plants. Important oilseed crops such as sesame being a crop of narrow genetic base which further hampered their analysis for a long time. Nevertheless, the advent of DNA marker technology has allowed progress in the genomics of these crops. Transfer of knowledge from model plants and advanced crops together with high throughput technologies will catalyze the analysis of entire transcriptomes and proteomes which will foster the development also in the neglected crops and substantially add to their agricultural value. Wang *et al*., 2014 reported a high-quality genome sequence of sesame assembled de novo with a contig N50 of 52.2 kb and a scaffold N50 of 2.1 Mb, containing an estimated 27,148 genes. The results revealed novel, independent whole genome duplication and the absence of the Toll/interleukin-1 receptor domain in resistance genes. Candidate genes and oil biosynthetic pathways contributing to high oil content were discovered by comparative genomic and transcriptomic

analyses. These revealed the expansion of type 1 lipid transfer genes by tandem duplication, the contraction of lipid degradation genes, and the differential expression of essential genes in the triacylglycerol biosynthesis pathway, particularly in the early stage of seed development. Resequencing data in 29 sesame accessions from 12 countries suggested that the high genetic diversity of lipid-related genes might be associated with the wide variation in oil content (Wang *et al*., 2014). Wild species of sesame possess genes for resistance to biotic and abiotic stresses (Joshi, 1961; Brar, 1982). However, introgression of useful genes from wild species into cultivars via conventional breeding has not been successful due to post-fertilization barriers (Tiwari *et al*., 2011). The only option left for improvement of sesame is to transfer genes from other sources through genetic transformation techniques. There seems considerable potential for sesame crop transformation for desired genes from other sources through genetic trans-formation techniques. Although, the recalcitrant nature of sesame to *in vitro* regeneration is the main obstacle to genetic transformation, sesame has been shown to be susceptible to *Agrobacterium tumefaciens*, which opens up the avenues for *Agrobacterium* mediated genenic transformation in the crop (Taskin *et al*., 1999). There are very few reports on shoot regeneration, with low frequencies in a few genotypes from cotyledon and/or hypocotyl explants followed by *Agrobacterium* mediated transformation (Rao and Vaidyanath, 1997; Taskin and Turgut, 1997; Were *et al*., 2006; Seo *et al*., 2007). For the first time, Yadav *et al*. (2010) reported conditions for establishing an *A. tumefaciens*-mediated transformation protocol for generation of fertile transgenic sesame plants. There are reports also (Ogasawara *et al*., 1993; Jin *et al*., 2005) showing successful establishment of hairy root cultures by *Agrobacterium rhizogenes* on sesame. Hairy root cultures using *Agrobacterium* rhizogenes have also been successfully established (Ogasawara *et al*., 1993; Jin *et al*., 2005). This was achieved through the development of an efficient method of plant regeneration through direct multiple shoot organogenesis from cotyledonary explants, and the establishment of an optimal selection system. Although there are several studies ongoing to have successful transgenic sesame crop, the technologies used for transformation have been relatively crude (Tiwari *et al*., 2011). There is a need to improve the efficiency of transformation, to limit the presence of unnecessary genes in the products, to direct insertion to specific sites, and to give more control over when, where, and how much expression of the transgene occurs.

Conclusion and future prospects

The sesame crop holds a significant potential in the global market with its important contribution of edible-cum-therapeutic oil as well as its valuable usage in industries. In recent years, owing to its lignin antioxidants, enriched level of poly unsaturated fatty acids, presence of essential amino acid rich proteins and vital minerals, sesame oil put forward best nutraceutical options. Industrial uses of sesame oil have been proved to be ecologically feasible as it addresses the environmental concerns raised by exclusive use of fossils fuels. From the application perspectives, technologies for reduction of anti-nutritional factors in the oil in one hand, while enhancing the level of PUFA and essential amino acids on the other need to be developed in the international research system both at genetics and genomics plateform. An integrated effort would only help the researchers to derive the maximal amount of desired output from sesame for the welfare of mankind.

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