Chapter 2 Breeding Major Oil Crops: Present Status and Future Research Needs

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Abstract Oils extracted from plants have been used predominantly as edible oil. Soybean, peanut, rapeseed mustard, sunflower, safflower, Sesamum, linseed, castor and cotton seed are predominant oil crops. Global status of nine major and minor oil crops has been discussed which includes their classification, contribution, major growing countries and objectives. Major objectives in oil crop improvement are enhancement of seed and oil yield, quality of oil according to its use, i.e. edible or industrial uses, breeding of varieties which fit in different cropping systems and breeding biotic and abiotic stress resistant/tolerant varieties. Achievements in varietal development programme of nine oil crops in India have also been discussed and future research needs to meet the increasing demand have also been highlighted. This review describes developments in use of biotechnological tools in seven edible oil crops, namely, Brassica, soybean, sunflower, groundnut, Sesamum, linseed and safflower and also highlights the prospects of using markers in genetic improvement of these crops. Molecular markers reported for genetic diversity assessment, mapping and tagging genes/OTLs for different qualitative and quantitative traits and their use in marker-assisted selection have been presented.

Keywords Oil crops • Breeding objectives • Research needs • Gene mapping • Genome maps • Molecular markers

1 Introduction

Oils extracted from plants have been used since ancient times and have been exploited in many ways. Predominantly, it is used as edible oil. It is also used in medicines and pharmaceuticals, industries, biodiesel, pet foods and component of

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many other products. Dietary fat, a concentrated source of energy, supplies about half of the calories and carries fat soluble vitamins. Its by-products are being used as feed, manures and find uses in many other industrial and domestic uses. There is large number of oil crops grown worldwide. Amongst them soybean, peanut, rape-seed mustard, sunflower, safflower, Sesamum, linseed, castor, cotton seed are predominant. Total world's oilseed production from major oil crops was 423.55 mt from 205.08 million hectares (mha) area during 2009–2010 (http://www.fas.usda.gov/psdonline). The leading countries in oilseed production are USA, Brazil, Argentina, China and India. The crop wise pretext is discussed here.

2 Soybean

Soybean (*Glycine max* L. (Merrill), 2n=40) a *Papilionaceae* family plant is the most important grain legume in terms of production and international trade. In addition to high protein content (40%), the soybean seeds contain 18–23% oil and thus add to the importance of the species as an edible oil yielding crop. Soybean accounted for 57% of the world's oilseed production. Soybean has the longest recorded history of cultivation among crop plants dating back to Chou dynasty in 664 BC and northern China is considered as the centre of its domestication. In India, this crop was grown in isolated areas since ancient times. The feasibility trial conducted during 1963–1964 with the introduced material from the USA marks its modern cultivation in this country. Systematic breeding programme was initiated at Pantnagar and Jabalpur and later at many other centres, which led to the development of a large number of improved varieties. Introduction of this temperate crop to sub-tropical climatic conditions made it more vulnerable to problems like seed longevity, poor growth rate due to changed photoperiod, various biotic and abiotic stresses, etc (Hegde 2009a).

2.1 Objectives

The most important breeding objective is yield enhancement. Since this crop is mainly grown under rainfed condition, genetic enhancement of yield under rainfed situation has been a major challenge. Tailoring of high yielding plant type includes the desirable features like determinate to semi-determinate growth habit, erect and non-lodging with 100–105 days maturity to escape moisture stress. On the other hand, some hybrids are reporting around 20% heterosis and the male sterile systems for seed production are available; however, the efficient pollen transfer mechanism is a major obstacle in exploitation of hybrid vigour in soybean. Genetic variability for oil quantity and quality is available. Indirect selection for seed density and specific gravity would lead to high oil yields. Beside quantity, varieties with high oleic acid and low linolenic acid need to be developed.

Other important objective is to enhance seed longevity. Soybean is known for its poor storability. Due to vulnerable position of its embryo, it is highly sensitive to injury. Deterioration in seed quality is very fast particularly under tropical climate during storage. Many small seeded varieties have better germination than bold seeded ones. This undesirable association needs to be broken and is possible through breeding. Although bold seeded genotypes with high seed longevity have also been reported. Varieties which are resistant to mechanical damage and maintain more than 70% germination after 8–9 months of ambient storage need to be developed. Accelerated aging, electrical conductivity and vigour tests are generally used for screening and identification of promising lines from the breeding material.

Stability of performance is of utmost importance in soybean. Early maturity and photoperiod insensitivity are prerequisites for better adaptability and its suitability to different cropping systems. Early maturity would further help in combating the terminal drought through escape mechanism. Host plant resistance against diseases like rust, root rot, stem canker, bacterial blight, yellow mosaic virus and insects like stem borers, gram pod borers and sting bug would further help in stabilizing the yields.

3 Brassicas

The brassicas commonly known as rapeseed mustard are important group of edible oils and vegetables crops belonging to Brassicaceae or Cruciferae family. This group comprises of six cultivated species, namely, Brassica campestris/rapa (2n=20, AA), Brassica nigra (2n=16, BB) and Brassica oleracea (2n=18, CC) are diploids; Brassica juncea (2n=36, AABB), Brassica napus (2n=38, AACC) and Brassica carinata (2n = 34, BBCC) are digenomic tetraploids, which evolved in nature following hybridization between the constituent diploid species. Rapeseed mustard is the third most important source of vegetable oil in the world and is grown in more than 50 countries across the globe. China, Canada, India, Germany, France, UK, Australia, Poland and USA are the major cultivators of different species. The estimated area, production and yield of rapeseed mustard in the world during 2009-2010 was 30.74 mha, 59.93 mt and 1.95 t/ha, respectively. Globally, India account for 21.7% area and 10.7% production (USDA 2010). During the last 7 years, there has been a considerable increase globally in productivity from 1.54 t/ha in 2003–2004 to 1.95 t/ ha in 2009-2010 and production from 39.42 mt in 2003-2004 to 59.93 mt in 2009-2010. Brassica rapa, B. napus and B. juncea are grown predominantly for oil and seed meal. India is the second largest country in rapeseed mustard production and more than 85% of its area under rapeseed mustard is occupied by Indian mustard B. juncea (L.) alone. At present, the maximum average productivity in our country is around 1.19 t/ha (2008–2009) which is much below than that of the other Brassica growing countries. In UK, France and Germany, the average productivity of rapeseed mustard is two to threefold higher than India and the world average is also more than

50% higher than that of India. A reason for this low productivity is mainly the poor stability of performance despite availability of improved varieties with high yield potential. Production and productivity statistics of past decade and their relationship with weather parameters and disease outbreak indicates that the main reasons of fluctuation are unpredicted rainfall (drought or untimely rains), high temperature at different growth stages and infestation of diseases and insect pests like white rust, *Alternaria* blight, *Sclerotinea* stem rot, powdery mildew, downy mildew and aphid.

3.1 Objectives

For breaking the yield barrier, population improvement programme was followed involving diverse parents. Through the intervention of biotechnological tools, yield OTLs are to be identified and can be introgressed in improved backgrounds using marker-assisted selection (MAS). Poor plant stand is one of the factor for non-realization of actual yield potential in timely sown crop, which is mainly because of high temperature at seedling stage. If late sowings are done, high temperature at reproductive stage leads to forced maturity resulting in reduced yield with low oil content. Hence, genotypes having inbuilt tolerance to high temperature at seedling stage as well as terminal heat tolerance are the need of hour. Mustard being a crop of marginal lands, genotypes with inbuilt mechanism to yield higher under scanty moisture conditions are required. Hence, genotypes with high water use efficiency can be exploited. Fertilizers applied are not used efficiently; hence development of high fertilizer use efficient lines is also required. Salinity is becoming one of the limiting factors in Brassica production which needs attention. Genotypes tolerant to heavy metals and enhanced CO₂ utilization also need attention in the times to come.

There is no resistant sources available for *Alternaria* blight, *Sclerotinea* stem rot, aphid and painted bug, and trans genes are the option for development of transgenic *Brassica* having inbuilt resistance for these biotic stresses. Pyramiding the genes/QTLs for various biotic and abiotic stresses using the plant biotechnology tools has to be explored.

It is realized that the improvement through the use of conventional breeding approaches is tending to level off, since these breeding approaches do not mobilize sufficient amount of genetic variation, whereas hybrids offer an opportunity for mobilizing greater amount of genetic variability and available high heterotic response in Indian mustard. In order to increase the yield potential of *Brassica*, hybrids are one of the most viable options for breaking the yield barriers. Presently, there is about 15% yield increase in case of hybrids. Diverse cytoplasmic sources may give high heterotic hybrids under three line hybrid development programme. For saving the time, the introgression of CMS/restorer system to the identified combiners should be taken up through marker-assisted backcross breeding. Genotypes with high harvest index, basal branching from ground level, long and higher primary and secondary branches with synchronous higher number of siliquae are desirable

for yield enhancement. Quality is an important concern in the times to come. Breeding of Canola types Indian mustard varieties is the need of the hour to make this crop globally competent. Oil content also needs to be enhanced from the average 38–39% to that of >45%.

4 Sunflower

Sunflower (*Helianthus annuus* L., 2n=34) an *Asteraceae* family plant is native to the temperate North America, which is the centre of diversity for this important edible oil-yielding species. Sunflower is grown in all continents. Europe and America account for nearly 70% of total area and 80% of total production (Damodaran and Hegde 2007). Its cultivation in Asian countries is comparatively recent. Asia accounts for nearly 20-22% of the global sunflower and contributes to about 18% of the production. The productivity of sunflower in Asia is about 1.0 t/ha which is lower than the world average. India is the largest grower of sunflower in the Asian continent. This is a short duration crop which is adaptable to a wide range of agroclimatic situations, having high yield potential, suitable for cultivation in all seasons due to its day neutral nature and can fit well in various inter and sequence cropping systems. However, the average yield of this crop in India is lowest; it is less than half the world average, and static hovering around 0.5-0.6 t/ha. Emergence of new diseases and large climatic variations, particularly recurrence of drought stress during critical growth stages, has affected stability and yield on a regular basis. Therefore, there is a need to reorient the breeding objectives considering the adverse agroecosystems or target population of environments where the crop is grown.

4.1 Objectives

Hybrids in sunflower have recorded two times higher seed yield than the open pollinated varieties. Narrow genetic base is the major bottleneck in further improving the yields. Release of large number of hybrids in the past has broadened the base of hybrids in the country. Still there is need to improve the diversity of the parental lines to achieve the higher level of heterosis in sunflower. Diversification of male sterility source may also help in improving stability of the hybrids. Beside seed yield, oil content, which is hovering between 35 and 40% in hybrids, is also equally important and needs to be improved up to 45% so that this crop may be made more profitable.

For stabilizing the yields, host plant resistance against major diseases like downy mildew, *Alternaria* leaf spot, rust and viral necrosis and insects like capitulum borer, tobacco caterpillar, Bihar hairy caterpillar, green semilooper, cabbage semilooper, cut worms, leaf hoppers and thrips is required in the parental stocks for their exploitation through hybrids. Introgression of resistance against major insects like *Heliothis*

and *Spodoptera*, *Bt* sunflower needs to be developed. Identification of resistance/ tolerance sources for drought related traits and their subsequent transfer in the improved genetic background would help in achieving the stability of production in diverse rainfed areas.

Being a crop of all seasons this crop is grown continuously after harvest of the earlier one which has led to micronutrient deficiency, toxicity and complex of diseases and insect pests leading to low yields. Breeding/management input is required to address this issue.

5 Groundnut

Groundnut (Arachis hypogaea L., 2n=40), a Papilionaceae family plant, is an allotetraploid having South American origin. Recent studies have indicated that it originated in northern Argentina or southern Bolivia from hybridization between the diploid wild species Arachis duranensis and Arachis ipaensis. It is the fourth most important oilseed crop in the world, grown mainly in tropical, subtropical and warm temperate climates. It is presently cultivated in 108 countries of the world. Asia with 63.4% area produces 71.7% of world groundnut production followed by Africa with 31.3% area and 18.6% production, and North-Central America with 3.7% area and 7.5% production. Important groundnut producing countries are China, India, Indonesia, Myanmar, Thailand and Vietnam in Asia; Nigeria, Senegal, Sudan, Zaire, Chad, Uganda, Republic of Ivory Coast, Mali, Burkina Faso, Guinea, Mozambique and Cameroon in Africa; Argentina and Brazil in South America and USA and Mexico in North America (Hegde 2009a). Its seeds are a rich source of edible oil (43–55%) and protein (25–28%). About two-thirds of world production is crushed for oil and the remaining one-third is consumed as food. Its cake is used as feed or for making other food products and haulms provide quality fodder. In India, it ranks third after soybean and Brassicas. Domesticated groundnut exhibits a considerable amount of genetic variation for morphological traits such as growth habit, seed colour and size, number of seeds per pod and patterns of flower production on the stems. Besides, variation exists for the nature of reaction against pathogens and insects.

5.1 Objectives

The major breeding objectives in this crop are development of high yielding cultivars of suitable duration to escape moisture stress with resistance to various biotic stresses (foliar diseases like rust and early and late leaf spots and aflatoxin contamination by *Aspergillus flavans*, pod and stem rot, etc.) and tolerance to different abiotic stresses (moisture stress). Continuous efforts have yielded genetic resistance for these diseases. Short and medium duration and confectionery type varieties with multiple tolerance/resistance have been developed by ICARISAT as well as NARS

in India. Significant progress has been seen in understanding and underlying the mechanism of drought tolerance in groundnut. As it has been established that yield under water limited conditions is a function of transpiration (T), transpiration use efficiency (TE) and harvest index (HI), large exploitable genetic variation has been observed in germplasm of groundnut for these traits (Rachaputi and Wright 2003). There is a need to develop a selection index integrating T, TE and HI with appropriate weights for use as selection criteria in a breeding programme (Chandra et al. 2003). In addition to resistance/tolerance to the prevailing biotic and abiotic stresses, a variety for becoming successful should be in harmony with the edaphic and climate factors of ecosystem. The duration of the variety, irrespective of its growth habit should match with the period of soil moisture availability particularly under rainfed situations. Novel techniques such as genetic transformation, molecular markers added selection and gene transfer from alien sources need to be exploited more for making an impact on groundnut research.

6 Sesamum

Sesamum (Sesamum indicum L. 2n=26) belongs to the family Pedaliaceae which has a wide distribution, covering tropical Africa, Madagascar, Arabia, India, Sri Lanka, tropical Australia and a few of the eastern islands of the Malayan Archipelago. It is an ancient oil yielding crop. Due to the presence of diverse wild species, Africa is considered the primary centre of origin, while India and Japan are considered as the two secondary centres of origin of this crop. India, China, Sudan, Mexico, Turkey, Burma and Pakistan are the important Sesamum producing countries. India ranks first, both in the area and production of this crop in the world. The annual area put under it in India is about 2.5 mha (45% of the world hectarage) and the total production is nearly 52,000 t. Its seeds contain 45-52% of edible oil (Hegde 2009b).

6.1 Objectives

Higher yields, improved plant architecture, adapted crop duration, resistance to diseases and pests and indehiscent capsules are the major objectives in this crop. The degree of dehiscence is a cultivar characteristic and is of great importance for mechanized harvesting. The leaf eating caterpillar (*Antigastra catalaulmlis* Dup.) and the gallfly (*Asphondylia sesalili* Felt) are the serious pests of *Sesamum*. Stem and root rot (*Macrophominia phaseoli* Maubl.), phyllody (virus, mycoplasina), bacterial leaf spot (*Pseudomonas sesami* Matkoff) and leaf curl are the important diseases of this crop which needs genetic interventions. Among the various options available for increasing the productivity, heterosis breeding is perhaps the most important way for the vertical yield increase in this crop. China has the distinction of successful exploitation of heterosis in this crop at commercial level with hybrid developed

through hand emasculation, GMS/CMS systems and exhibited the yield potential up to 3.0 t/ha. The programme on development of CMS lines through interspecific hybridization needs to be strengthened for exploiting some workable CMS system in this crop for hybrid development programme. This crop has been ignored for value addition to its oil. The development of varieties with low or zero anti-nutritional factors like oxalic and phytic acids needs attention for its value addition. In addition, the efforts should also be made to develop low free fatty acid (<2%) varieties of *Sesamum*. Increase in oil content is also one of the important components in varietal improvement of this crop.

7 Linseed

Linseed (*Linum usitatissimum* L., 2n=30) is a diploid, self-pollinated and homozygous species of *Linaceae* family. This genus comprises mostly herbs and shrubs in tropical and subtropical region. It is an important oilseed crop grown both for seed and fibre. It is an industrial oilseed crop and its each and every part has commercial and medicinal importance. India ranks second after Canada in terms of area and is at the fourth position in production after Canada, China and USA. The productivity of this crop is very low as it is grown under input starved and moisture stress conditions. The major diseases of this crop are wilt, rust, powdery mildew and *Alternaria* blight. Amongst the insects, bud fly is causing lot of losses to this crop.

7.1 Objectives

The average productivity of this crop at national (0.4 t/ha) as well as at global level (0.85 t/ha) is low in comparison to other oil crops like soybean, rapeseed mustard and groundnut. Hence, the breeding strategies for yield enhancement need immediate attention. Oil content is one of the important components in oil crops and it is around 28-30% in linseed varieties which has ample scopes for enhancement. Linseed oil has more than 50% linolenic acid which is fit for its industrial application but where linseed oil is being used as edible oil, the linolenic acid needs to be reduced. Efforts in this direction have already been successful with the development of low linolenic acid varieties LINOLA in Australia in 1984 and SOLIN in Canada in 1990. In India too national linseed programme in collaboration with BARC, Mumbai has developed some genotypes with less than 1% linolenic acid. Hence, the breeding efforts are needed further for development of low linolenic acid varieties, the oil of which can be widely used as cooking oil. As linseed is highly nutritious, efforts are needed to reduce its anti-nutrient components and also bio-convert its less acceptable omega-3 ALA into acceptable SDA. For achieving this objective, in addition to the conventional breeding, the biotechnological tools like marker-assisted breeding and genetic engineering may also be employed. Moisture stress being one

of the major constraints, the varieties with inbuilt water stress tolerance may be given more emphasis to enhance and stabilize the productivity for making this crop more remunerative. More concerted efforts for development of varieties resistant to different diseases like wilt, rust, powdery mildew and *Alternaria* blight are also required by using the different resistant donors already available in this crop.

8 Safflower

Safflower (*Carthamus tinctorius* L., 2n=24) is a member of the family *Compositae* or *Asteraceae*, cultivated mainly for its seed, which is used as edible oil and as birdseed. Traditionally, the crop was grown for its flowers, used for colouring and flavouring foods and making dyes, especially before cheaper aniline dyes became available, and in medicines. Oil has been produced commercially and for export for about 50 years, first as an oil source for the paint industry, now for its edible oil for cooking, margarine and salad oil. Over 60 countries grow safflower, but over half is produced in India (mainly for the domestic vegetable oil market). Production in the USA, Mexico, Ethiopia, Argentina and Australia comprises most of the remainder. China has also significant area under safflower (Li and Hans-Henning 1996). Varietal improvement programme on safflower was initiated during 1935 in India which resulted in release of some varieties specific for limited areas. The All India Coordinated Research Project on Safflower was established in 1972 which led to the development of 29 varieties and hybrids for different safflower growing areas of the country (Hegde 2009a).

8.1 Objectives

The average productivity of safflower is still low (0.65 t/ha) in comparison to 1.4–2.3 t/ha in other parts of the world. This necessitates in breeding varieties with enhanced yield potential. With the availability of GMS systems in this crop, hybrid development has become reality in 1997. Now the cytoplasmic genetic male sterility system is a new hope to develop the high yielding publicly acceptable hybrids surpassing the problems associated with GMS-based hybrids. Safflower hybrids can offer greater stability in less favoured environments subject to biotic and abiotic stresses. It is evident from high yield performance of safflower hybrid DSH 129, which yielded about 18% higher seed yield than varieties under wilt, moisture and P stress conditions under large-scale field demonstrations (Reddy et al. 2004). There is a possibility of development of hybrids with high oil content, disease/insect resistance and abiotic tolerance by choosing the appropriate parental lines.

Varieties tolerant to drought will also definitely help in enhancing the productivity of this crop as about 80% reduction in the yield of safflower has been reported due to prolonged moisture stress. For immediate future need, the exploration of germplasm for moisture stress tolerance is required by designing appropriate

screening techniques. Germination under saline soils followed by seedling survival and establishment is very important for appropriate plant stand leading to higher economic yields. For the precise selection of parental lines under abiotic stress resistance breeding programme, the physiological, biochemical and morphological traits responsible for resistance, their relation with economic yield and the genetic diversity in these traits need to be determined (Sinclair et al. 2004).

The oil content in the released varieties is ranging from 28 to 30% which needs an increase of 5–8% in this crop. In addition to different conventional breeding methods, mutation breeding and genetic engineering can also be the options for developing the high oil safflower lines. Fatty acid profile of this oil crop also needs alteration for its best commercial value. Due to high proportion of linoleic acid (78%) in its oil, it is considered as a healthy oil as it reduces blood cholesterol but makes shelf life of this oil very short and less suitable for frying purpose for its use in food industry. Appropriate reduction in linoleic acid and increase in oleic acid will eliminate this problem and will maintain the tag of healthy oil of this crop. Another aspect of safflower oil quality is increasing the gamma tocopherol content, which is antioxidant in nature. Concerted efforts should be made to assay the vast collection of germplasm for tocopherol diversity for initiating the breeding programme for this component.

9 Niger

Niger (*Guizotia abyssinica* (L.f.) Cass., 2n=30) is an *Asteraceae* family oil crop cultivated in Indian subcontinent and East African countries (Getinet and Sharma 1996). Its cultivation originated in the Ethiopian highlands and has spread to other parts of Ethiopia. Both Ethiopia and India are excellent sources of germplasm for varietal development. In 2002, the variety Early Bird Niger was developed and adapted to the United States by Glenn Page. Niger seeds contain about 40% edible oil with fatty acid composition of 75–80% linoleic acid, 7–8% palmitic and steric acids and 5–8% oleic acid (Dutta et al. 1994). The meal remaining after the oil extraction is free from any toxic substances but contains more crude fibre than most oilseed meal. Niger is a completely outcrossing species with self-incompatibility mechanism. Variability exists for morphological characters (Pradhan et al. 1995); however, these characters are not discrete and hence complicate the niger improvement programmes. Niger seed populations in Ethiopia and India are very heterogeneous, indicating the great potential for yield enhancement through breeding.

9.1 Objectives

Breeding objectives for niger seed are to increase seed yield and oil content and reduce shattering. With the development of single-headed plant types in sunflower and safflower, it has been postulated that single-headed dwarf types with uniform maturity must be developed for yield enhancement in this crop too. An increase in

oil content appears feasible because of existing genetic variability, which can be used in breeding research. As niger seed is self-incompatible, breeders in India and Ethiopia have adopted population improvement programmes such as mass selection and sibbing. Recently, a protocol for *Agrobacterium tumefaciens* mediated genetic modification was developed. This crop falls under minor oilseed crop in India and a lot of progress has been made after 1985. Fifteen improved varieties have been developed for general cultivation among the farmers. Well-known improved cultivars in India are Ootacamund, Deomali, Paiyur 1, IPG 76 and JNC 6.

10 Castor

Castor (*Ricinus communis* L., 2n=20) an *Euphorbiaceae* family plant is an important non-edible oil crop of the arid and semi-arid regions of the world. India, Brazil, China, Russia and Thailand are the major castor growing countries of the world. Castor is grown on about 1.26 mha area with about 1.14 mt production and world average productivity is about 0.90 t/ha. India's share in total castor area and production is 59.1 and 64%, respectively, with 1.5 t/ha average productivity which is much higher than the world average productivity. Castor seeds contain 40-55% oil, the highest among all cultivated oil crops. The kernels contain 64-71% oil. Its oil is world's most useful and economically important natural oil. Its oil contains 84–90% ricinoleic acid of total fatty acids which makes it as a unique vegetable oil. Castor oil is highly stable and variation in fatty acid is very minimal making it the best raw industrial oil. Castor cake is a very useful organic manure which contains 6.0% N, $2.5\% P_a O_c$ and $1.25\% K_a O$. It is a rich source of protein (25–40%), sugar (25%) and minerals (10%). But the presence of toxic constituents like ricin/Ricinus communis agglutin (RCA) makes it non-edible. There is a real breakthrough in the varietal improvement of this crop which is evident from the transformation of perennial types to annual types. A large number of high yielding hybrids and varieties have been developed. Although castor is a monoecious plant, the proportion of male and female flowers is greatly influenced by both genetic and non-genetic factors (temperature, humidity, plant age, nutritional factors, etc.). Identification of completely pistillate plants and presence of exploitable levels of heterosis paved the way for development of castor hybrids resulting in quantum jump in productivity of this crop (Shifriss 1961; Moshkin 1967; Zimmerman and Smith 1966). Some of the objectives which need interventions are as follows.

10.1 Objectives

Although good breakthrough has been made in the varietal development of this crop yet there is need to develop short duration varieties/hybrids suitable for specific situations like rainfed areas, semi-winter conditions, intercropping, mechanical harvesting, saline conditions and poor management conditions. Pistillate lines being used for hybrid development are highly sensitive to environment giving large number of ISF

under high temperature and water/nutritional stress and reversion in any order in S type. Therefore, breeding programme on development and diversification of stable and superior combining pistillate lines with disease resistance needs acceleration. Under these circumstances, there is an urgent need to develop CMS lines which is not yet achieved because castor is mono generic and no wild species exist. Due to long duration and monoculture this crop is exposed to many insect pests (semi looper, castor capsule borer, jassids, white fly and thrips) and diseases (Fusarium, Macrophomina root rot, reniform nematode and Botrytis grey rot) which causes 30-40% of yield losses. Drought under rainfed areas and salinity in major castor cultivation areas are the abiotic stresses which limit castor production. Concerted breeding efforts are required to incorporate the resistance/tolerance against these biotic and abiotic stresses. Hybrids and varieties with medium to bold light coloured seeds with high oil content (>50%) and high ricinoleic acid (>90%) are the millers' choice, hence efforts on breeding such genotypes should be concentrated. Ricin and RCA are two highly toxic endosperm proteins present in the deoiled castor cake which makes its cake unsuitable for animal and human consumption as a protein supplement. Utilizing the enormous variability available for protein content, breeding efforts are required to address these problems to make this crop more competitive and remunerative. Biotechnological approaches like efforts towards development of transgenics for insect resistance (Sujatha and Sailaja 2007) and silencing ricin and RCA genes are likely to deliver good returns in the times to come.

11 Varietal Improvement in India

Indian subcontinent is the natural repository of the oilseed crops, yet is importing about 40% of the total edible oil in the country. Its vegetable oil imports further raise by 14% and a sum of Rs. 32,000 crore was spent on this import during the oil year 2009-2010. This makes India the world's largest oil importer. Oilseed crops research in India got a boost in 1967, when the Indian Council of Agricultural Research sanctioned a multi-disciplinary and multi-location "All India Coordinated Research Project on Oilseeds" including five crops, namely, groundnut, rapeseed mustard, sesame, linseed and castor and subsequently niger, safflower and sunflower were also included under this project. To focus research on individual crops, Government of India started separate National Research Centres and AICRPs on groundnut, rapeseed mustard, soybean and linseed and elevated these centres later to directorates. This has led to the development of good number of improved varieties in these crops and their production and protection technologies. In the mean time, Government of India has launched the Technology Mission on Oilseeds and Pulses (TMOP) in 1986, which took a number of innovative and integrated measures to harness the best production, processing and marketing technologies. After the implementation of TMOP, area under oilseed crops increased from 19.0 to 26.1 mha, production from 10.83 to 24.94 mt and productivity from 0.57 to 0.955 t/ha between 1985–1986 and 2009–2010 (Table 2.1).

Table 2.1 Oilseed pr	d production (n	oduction (million tons) in India during 2001–2002 to 2009–2010	India during.	2001-2002 to	7009-2010					
Crops	1985–2086	2001-2002	2002-2003	2003-2004	2004-2005	2005-2006	2006-2007	2007-2008	2008-2009	2009-20
Groundnut	5.10	7.0	4.1	8.1	8.9	8.0	4.9	9.2	7.2	5.51
Rapeseed mustard	d 2.68	5.1	3.9	6.3	7.6	8.1	6.7	5.8	7.2	6.41
Soybean	1.02	5.6	4.6	7.8	6.9	8.3	8.7	9.4	9.1	10.05
Other six	2.03	3.0	2.2	3.0	3.1	3.5	2.9	5.4	4.2	2.97
Total	10.83	20.7	14.8	25.2	24.4	27.9	23.2	29.8	27.7	24.94

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	No. of varieties		
Name of the crop	Before TMOP	After TMOP	Total
Soybean	20	65	85
Groundnut	42	115	157
Rapeseed mustard	29	108	137
Sunflower	7	42	49
Sesame	28	48	76
Linseed	21	29	50
Safflower	9	20	29
Niger	1	15	16
Castor	16	19	35

 Table 2.2
 Crop wise varieties developed in eight oilseed crops in India

There is tremendous increase in productivity of these crops but it is still lower than the world's average. Furthermore, stability of production is always a cause of worry in India.

The impact of technology mission on oilseeds and pulses is visualized with the development of a large number of area specific high yielding varieties of all edible oilseed crops (Shanmugham and Gunasekaran 2003, 2008) (Table 2.2). As far as improved technology is concerned, we have the improved varieties with very high yield potential in all the crops. From the comparison of present yield levels, and area and production with that of pre-TMOP period, very clear picture comes out and shows that we have attained much success to reach to the self-sufficiency, but still a lot has to be achieved. The crop wise achievements in terms of varietal development are given later.

11.1 Soybean

Twenty varieties were released from 1969 to 1985, whereas 65 new high yielding varieties have been recommended for general cultivation by the farmers in a period of about 25 years, i.e. 1986–1987. The impact of these varieties can be observed by consistent increase in area, production and productivity of this crop. The most popular varieties of this crop are JS 335, JS 93 05 and MAUS 71 covering more than 85% area and are contributed significantly in the better production of this crop. Some new varieties are also covering the area gradually which will also help in increasing the production of this crop in the times to come.

11.2 Rapeseed Mustard

This group of crop is a very complex one with four species, namely, *B. juncea*, *B. napus*, *B. rapa* (cvs toria, yellow sarson, brown sarson) and *B. carinata* grown for edible oils in India. The major area is under *B. juncea* and it contributes more than

85% of the total rapeseed mustard production. There are more than 137 varieties released for all the four oliferous species of *Brassica*. Presently, there are varieties with 2.5 t/ha of yield potential. In addition to varieties, hybrid development programme in *B. juncea* is also very strong and three hybrids have already been released for general cultivation. The dominating varieties of Indian mustard are Pusa Bold, Pusa Jai Kisan, Varuna, RH 30, Laxmi, Maya, Kanti, Rohini and Benoy (B 9) of *B. rapa* cv. Yellow sarson.

11.3 Groundnut

Groundnut is also one of the three most important oilseed crops in India. A total of 157 varieties have been developed since 1969 of which 42 varieties were developed up to 1985 and 86 improved varieties have been released for general cultivation since 1986–2007 in this crop. The highest production has gone up to 8.1 mt during 2003–2004 but again due to weather vulnerability, the production has drastically come down to 4.9 mt during 2006–2007. There are very high yielding varieties in this crop and the major contributor in the production of this crop is varieties like M 335, TAG 24, ICGS 76, TG 7A, AK 12 24, HNG 10, etc.

11.4 Sunflower

Sunflower is also one of the important oilseed crops contributing towards the national oil pool. Although this crop is covering about 10% of the country's total area but it fits well in all cropping systems due to its photo and thermo-insensitivity. This crop is of late introduction in the country and the first variety was developed during 1978. Since then 49 varieties and hybrids have been developed and released for general cultivation by the various public and private sector organizations. This is the only crop which has more than 80% sunflower growing area under the hybrids. From a negligible area during 1980–1981, now this crop has shown its presence in the Indian oil economy. The widely grown high yielding hybrids in sunflower are KBSH 44, KBSH 1, Poineer 6460, Poineer 3322. The most popular stable variety Morden which was released in 1982 is still having about 20% area of sunflower under cultivation.

11.5 Sesame

Although sesame is grown in almost all the states of the country but the major states where sesame cultivation is being done are Rajasthan, Gujarat, Madhya Pradesh, Orissa and Maharashtra. As breeding for high yielding varieties is concerned a lot

of efforts have been made for genetic enhancement of yield in this crop and as a result about 76 varieties have been developed of which 48 were developed after the implementation of TMOP. The varieties with about 1.0 t/ha yield potential have been developed for rainfed conditions too.

11.6 Linseed

Linseed is one of the minor oilseed crop grown in India. In this crop also a lot of breeding work has been done and 50 varieties have been developed. The seed yield potential of the improved varieties under irrigated conditions is 1.2–1.5 t/ha.

11.7 Safflower

It is another minor oilseed crop. A lot of efforts have been made in genetic enhancement of seed yield and 29 improved varieties have been developed in safflower.

11.8 *Niger*

This crop also falls under minor oilseed crop in India and a lot of progress has been made after 1985. Fifteen improved varieties have been developed for general cultivation.

11.9 Castor

India has made a big breakthrough in castor breeding programme. The first castor hybrid GCH 3 based on an exotic pistillate line was released for general cultivation in 1968. It is non-edible oil crop where 35 varieties and hybrids have been developed and are contributing in making India a global leader in castor production.

12 Research Needs for Yield Improvement and Its Stabilization

Development of varieties resistant to biotic stresses: In all the nine oilseed field crops grown in the country, the biotic stresses like insect pests and diseases effect the crops adversely in one or the other years due to which the production and

productivity fluctuates to unexpected levels. In almost all the crops, barring few area specific examples, the insect pests and diseases cause havoc to these crops in the lack of resistant/tolerant varieties. Hence efforts are needed to develop such varieties for yield enhancement as well as stabilizing the production of these crops. Use of modern biotechnological tools will definitely help in development of varieties for biotic and abiotic stresses.

Drought tolerant varieties with enhanced water use efficiency: Water stress at various stages of crop growth in all the edible oilseed crops is another major limiting factor for realizing the potential yield of present day varieties. Specific efforts are required to breed the varieties having high degree of tolerance to moisture stress along with high water use efficiency to utilize the available moisture in under field conditions to minimize the losses to the crop.

Development of varieties resistant to other abiotic stresses: Other than water stress other abiotic stresses are frost in mustard, salinity in almost all oilseed crops, high temperatures at the time of sowing and maturity in the rabi oilseeds like rapeseed mustard and linseed. Efforts are needed to overcome these stresses by tailoring genotypes tolerant to these stresses in respective crops.

Development of hybrids: For breaking the yield ceiling, exploration of various possibilities which can help in increasing the yield potential of the different oilseed crops is required. It is realized that the improvement through the use of conventional breeding approaches is tending to level off, since these breeding approaches do not mobilize sufficient amount of genetic variation, whereas hybrids offer an opportunity for mobilizing greater amount of genetic variability and available high heterotic response in different crops. In order to increase the yield potential of soybean, *Brassica*, safflower, sesame, linseed and niger hybrid development programme needs to be intensified. With the encouraging results of hybrids in sunflower, a special network programme may be launched for development of hybrids in oilseed crops like rapeseed mustard, soybean, niger, safflower, sesame and linseed.

Improvement of quality of oil and seed meal: Specifically in rapeseed mustard, the emphasis should be made to develop double zero varieties (erucic acid <2% and glucosinolate <30 µmoles/g of defatted seed meal cake). For improving the keeping quality of soybean oil, efforts should be made to reduce the linoleic acid content. In the crops like *Sesamum* and linseed, also improvement in quality may be taken at priority for value addition to their oil. Ricin and RCA are the two toxic proteins present in castor deoiled cake which also need genetic interventions.

Development of varieties with improved water use efficiency: Water is the most precious natural resource in the times to come. Oilseeds are already grown on marginal lands with limited irrigation facility. Therefore, efforts are needed to develop oil crop varieties with high water use efficiency.

Development of varieties with improved nutrient use efficiency: The agronomical experiments show that the nitrogen requirement of almost all the oilseed crops is 60–80 kg/ha. The analysis of soils and plant samples shows a gap between nitrogen

utilized by the plant and its availability in the soil. The higher dozes, i.e. more than 80 kg/ha of nitrogen does not yield good results. Hence, there is an urgent need to develop varieties which have high nutrient use efficiency.

13 Use of Molecular Tools for Oil Crop Improvement

For improvement of some of the biotic and abiotic stresses, there is problem either due to complex genetic control of that trait or non-availability of resistant source or non-availability of screening techniques or environmental effect on the traits under improvement. In such conditions, the possibility of using molecular tools like MAS helps in improvement of a trait. These techniques will not only help in the transfer of desirable trait but it will reduce the time taken for introgression of a particular trait. Where no source of resistance is available in the germplasm of particular crop, the transgenic approach may be explored for introgression of the resistance from other species.

Conventional methods of improving crops use the genetic variation available within the crossable limits. The germplasm provides the required parental lines for recombination breeding and making heterotic hybrids. Selection of right kind of parental genotypes, therefore, is the key to the success of a breeding programme. Those involved in genetic enhancement of crops heavily depend on the available passport data or results of limited evaluation of a sub-set of germplasm. A majority of the germplasm, although constitute the primary gene pool remain unutilized. Once the parental lines are chosen, they are inter-mated to generate segregating populations from which the desirable recombinants carrying the required gene combinations are selected. This process of selection is mainly based on phenotype in conventional schemes. Skilful eyes of the conventional breeder therefore play a vital role in selecting the desirable types from the pool of mostly undesirable segregants. Phenotype, however, is the product of interaction of genotype and environment. Particularly in respect to complex quantitative traits such as seed and oil yield, disease resistance, drought tolerance, etc., phenotype may not always reflect the actual genetic worth of the genotype. Even in case of Mendelian traits, selection of desirable segregants requires creation of selection environments, which may not be possible for routine screening of large populations. In contrast, selection based directly on genotype itself is more precise and efficient. Use of molecular markers to identify desirable recombinants, which is commonly known as MAS, makes gains from selection more predictive. The resources available in different oilseed crops with emphasis on the recent developments for carrying out marker-assisted breeding highlight the successful use of markers in selection and provide the prospect of MAS in oilseed improvement is summarized (Table 2.3).

A good progress has been made in soybean, *Brassica* and groundnut in development of molecular markers and genome maps, mapping and tagging QTLs and their application in MAS. The other oil crops need further biotechnological interventions for improvement of some of the specific traits which has been summarized as strength, weakness, opportunity and thrust for these crops (Table 2.4).

Table 2.3 Molecular tools for oil crop improvement

Crop	Marker/ trait	References
Development of	f molecular markers and ge	rnome maps in oilseed crops
Soybean	RFLP	Lark et al. (1993); Skorupska et al. (1993); Shoemaker and Specht (1995); Lorenzen et al. (1995); Xia et al. (2007)
	AFLP	Kiem et al. (1997); Xia et al. (2007)
	SSR	Cregan et al. (1999); Song et al. (2004); Xia et al. (2007)
	SNP	Yoon et al. (2007); Hyten et al. (2008)
Brassica spp.	RFLP	Figdore et al. (1988)
	Isozyme markers	Arus and Orton (1983); Chen et al. (1989)
	EST Mining	Bhati et al. (2010)
B. oleracea	RFLP and RAPD	Slocum et al. (1990); Kianian and Quiros (1992); Landry et al. (1992); Kearsay et al. (1996); Ramsay et al. (1996); Voorrips et al. (1997); Li and Quiros (2001); Saal et al. (2001); Gao et al. (2007)
B. rapa	RFLP and RAPD	Song et al. (1991) Chyi et al. (1992);
		Kole et al. (1997)
	SSR, IP	Li et al. (2010a)
B. nigra	RFLP and RAPD	Truco and Quiros (1994); Lagercrantz and Lydiate (1995)
B. napus	RFLP and RAPD	Hoenecke and Chyi (1991); Landry et al. (1991); Ferreira et al. (1994); Uzunova et al. (1995); Foisset et al. (1996)
	SSR	Lydiate and Sharpe (2003)
	SRAP	Sun et al. (2007)
B. juncea	RFLP, AFLP, RAPD	Sharma et al. (1994); Cheung et al. (1997); Axelson et al. (2000); Mohapatra et al. (2002); Sharma et al. (2002); Pradhan et al. (2003); Mahmood et al. (2005), Kalita et al. (2007)
	SSR	Koundal et al. (2008); Parida et al. (2010); Yadava et al. (2009); Pradhan et al. (2011)
	IP	Panjabi et al. (2008)
Groundnut	RAPD	Halward et al. (1992); Garcia et al. (1995)
	RFLP	Halward et al. (1991); Kochert et al. (1991); Paik-Ro et al. (1992); Halward et al. (1993)
	SSR	Cuc et al. (2008); Jayashree et al. (2005); Moretzsohn et al. (2005); Wang et al. (2007); Varshney et al. (2009)
	EST	Luo et al. (2005)
Sunflower	RFLP	Gentzbittel et al. (1994); Berry et al. (1995); Jan et al. (1998)
	AFLP	Gentzbittel et al. (1995); Langer et al. (2003); Tamborindeguy et al. (2004)
	SSR	Paniego et al. (2002); Yu et al. (2003); Tang et al. (2002); Heesacker et al. (2008)
	SNP	Kolkman et al. (2007); Fusari et al. (2008)

(continued)

Table 2.3 (continued)

Crop	Marker/ trait	References
Sesamum	RAPD	Bhat et al. (1999); Davila et al. (2003)
	SSR	Dixit et al. (2005)
	AFLP	Laurentin and Karlovasky (2006); Laurentin and Karlovsky (2007)
	RAPD and ISSR	Sharma et al. (2009)
Linseed	Isozymes, RAPD, AFLP, RFLP	Spielmeyer et al. (1998); Oh et al. (2000); Fu et al. (2002), 2003; Krulickova et al. (2002); Adugna et al. (2006); Diederichsen and Fu (2006); Roose et al. (2006); Diederichsen (2007)
Safflower	RAPD	Amiri et al. (2001)
	AFLP	Johnson et al. (2007)
	RAPD, ISSR, AFLP	Sehgal and Raina (2005)
	ISSR	Yang et al. (2007)
Mapping and t	agging QTLs	
Soybean	Phytophthora infestans	Diers et al. (1991); Polzin et al. (1994)
·	Corn earworm (<i>Helicoverpa zea</i> Boddie)	Rector et al. (1998); Li et al. (1998)
	Soybean aphid (Aphis glycines)	Rouf-Mian et al. (2008)
	Super-nodulation	Landau Ellis et al. (1991)
	Cyst nematode resistance	Concibido et al. (1994) Mudge et al. (1997); Schuster et al. (2001); Guo et al. (2005)
	Hard seededness	Kiem et al. (1990a)
	Seed shape traits	Salas et al. (2006)
	Sprout-related traits	Lee et al. (2001)
	Seed longevity	Singh et al. (2008)
	Height and maturity	Mansur et al. (1993a)
	Seed oil and protein content	Diers et al. (1992); Lark et al. (1994)
	Reproductive and morphological traits	Kiem et al. (1990b); Mansur et al. (1993b)
	Salt tolerance	Lee et al. (2004)
	Oil quality	Bachlava et al. (2008); Li et al. (2008)
B. oleracea	Plasmodiophora brassicae	Figdore et al. (1993); Voorrips et al. (1997)
	Xanthomonas campestris	Camarago et al. (1995)
B. rapa	Club root	Saito et al. (2006); Werner et al. (2008)
	Xanthomonas campestris	Soengas et al. (2007)
	Albugo candida	Kole et al. (1996)
	Fatty acids	Teutonico and Osborn (1994); Tanhuanpaa et al. (1996, 1998)
	Seed coat colour	Teutonico and Osborn (1994); Chen et al. (1997); Rahman et al. (2007)
B. nigra	Flowering time	Lagercrantz et al. (1996)
B. napus	Leptosphaeria maculans	Dion et al. (1995); Ferreira et al. (1995a); Leflon et al. (2007)
	Turnip mosaic virus	Walsh et al. (1999)

(continued)

Table 2.3 (continued)

Crop	Marker/ trait	References
	Sclerotinia sclerotiorum	Zhao and Meng (2003)
	Verticillium wilt	Happstadius et al. (2003)
	Albugo candida	Ferreira et al. (1995c)
	Vernalization requirement	Ferreira et al. (1995b); Teutonico and Osborn (1995); Camarago and Osborn (1996)
	Oil content, protein, fatty acid	Arondel et al. (1992); Ecke et al. (1995); Hu et al. (1995); Tanhuanpaa et al. (1995); Jourden et al. (1996a, b); Jourden et al. (1996c); Thormann et al. (1996); Barret et al. (1998b); Fourmann et al. (1998); Hu et al. (1999); Schierholt et al. (2000); Zhao et al. (2006); Delourme et al. (2006); Qiu et al. (2006); Rahman et al. (2008); Nath and Goswami (2009)
	Glucosinolates	Uzunova et al. (1995); Toroser et al. (1995); De Quiroz and Mithen (1996); Hasan et al. (2008)
	Seed coat colour	Van Deynze et al. (1995)
	Male sterility/fertility restorer genes	Delourme et al. (1994); Jean et al. (1997); Delourme et al. (1998); Yi et al. (2006); Huang et al. (2007); He et al. (2008)
	Yield	Shi et al. (2009)
В. јипсеа	Albugo candida	Cheung et al. (1998); Prabhu et al. (1998); Mukherjee et al. (2001); Varshney et al. (2004); Panjabi et al. (2010)
	Seed coat colour	Upadhyay et al. (1996); Negi et al. (2000); Li et al. (2010b)
	Oil content	Sharma et al. (1999); Sharma et al. (2002)
	Erucic acid	Gupta et al. (2004)
	Glucosinolates	Stringam and Thiagarajah (1995); Good et al., (2003); Mahmood et al. (2003); Ripley and Roslinsky (2005); Ramchiary et al. (2007); Bisht et al. (2009)
	Moricandia arvensis	Ashutosh et al. (2007)
Groundnut	Nematode resistance	Garcia et al. (1995)
	Aphid resistance	Herselman et al. (2004)
	Rust resistance	Varma et al. (2005); Mondal et al. (2007)
	Drought tolerance	Varshney et al. (2009)
Sunflower	Fertility restoration and nuclear male sterility	Gentzbittel et al. (1995); Kusterer et al. (2002); Perez et al. (2005); Chen et al. (2006); Feng and Jan (2008)
	Branching	Gentzbittel et al. (1995); Rojas-Barros et al. (2008)
	Downy mildew	Mouzeyar et al. (1995); Slabaugh et al. (2003); Brahm et al. (2000)
	Orobanche	Tang et al. (2002)
	Rust (Puccinia helianthi)	Lawson et al. (1998)
	Chlorotic mottle virus	Lenardon et al. (2005)
	Oil quantity and quality	Perez et al. (2004)

(continued)

Table 2.3 (continued)

Crop	Marker/ trait	References
	High stearic acid content	Perez et al. (2006)
	Tph1 gene controlling beta - tocopherol accumulation	Vera-Ruiz et al. (2006)
	Pollen sterility and morphological traits	Kim and Rieseberg (1999)
	Restoring pollen fertility	Horn et al. (2002)
	Seed morphological traits	Yue et al. (2008b)
	Flowering	Leon et al. (2000)
	Lemon ray flower colour	Yue et al. (2008a)
	In vitro regeneration efficiency	Berrios et al. (2000)
	Drought tolerance	Jamaux et al. (1997); Herve et al. (2001); Kiani et al. (2007)
	Chlorophyll deficiency	Yue et al. (2009)
	Nutrient uptake	Lexer et al. (2003)
Sesamum	Closed capsule	Uzun et al. (2003)
Linseed	Flax rust (<i>Melampsora lini</i>)	Chen et al. (2001)
	Fibre quality	Roach and Deyholos (2007, 2008)
Marker assiste	ed selection (MAS)	
Soybean	Corn earworm resistance in soybean	Walker et al. (2002)
	Pyramiding of soybean mosaic virus resistance genes	Saghai-maroof et al. (2008)
Sunflower	Identification of maintainer	Yue et al. (2007)

 Table 2.4
 SWOT analysis of some oil crops

Crop	Strength	Weakness	Opportunity	Thrust
Sunflower	Saturated maps, international, characterized gene pool	Still MAS not much adopted for QTLs	MAS could be adopted for several traits	Alternaria, yield plateau
Safflower	Skeletal map, markers (recently) germplasm	Very small group working on markers	Saturated maps, use of MAS, germplasm	Alternaria wilt
Sesame	Germplasm genomic resources	No map, very small group working on markers	Saturated maps, use of MAS, germplasm	Capsule shattering
Linseed	Germplasm genomic resources	No map, small group	MAPS and MAS	Bud fly

14 Future Prospects of Marker-Assisted Selection in Improvement of Oilseed Crops

Since last 25 years after the publication of the first paper in 1986 on the development and use of RFLP markers for construction of linkage maps in tomato and maize, considerable progress has been made in the application of molecular techniques in oil crops. Now the focus has shifted to the use of sequence-based STS and SSR markers to generate very high density genome maps and tag gene/QTLs in *Brassica*, soybean, sunflower and groundnut. In some of the oilseed crops, SNPs are also being discovered and used to understand genetic diversity pattern. The first requirement for successful use of markers in breeding has been fulfilled at least for some of the traits with the availability of tightly linked markers. Besides, MAS with the use of other molecular markers has been demonstrated for both qualitative and quantitative traits.

Use of the markers was limited by the factors like recombination between the marker and the target gene, low level of polymorphism between parents with contrasting traits and lower resolution of QTLs due to interaction with the environment. With the recent developments in the design of genome-wide sequence based SSR and SNP markers, it would not be difficult to find solutions to these problems particularly in crops like soybean, sunflower, *Brassica* and in the near future in ground-nut. Availability of high-density genetic and physical maps will enable finding markers physically closer to the target gene that would not allow failure of MAS due to genetic recombination in these crops. Development of allele-specific markers, markers based on the sequences of the genes, polymorphic SNP markers would eliminate the possibilities of breakdown of the marker-trait linkage, low level of polymorphism in narrow crosses, etc. Construction of high density genome maps using SSR markers is the desirable, which would allow map-based characterization of genomes and rapid tagging of useful genes.

With the available tightly linked markers as in case of nematode and virus resistance in soybean, MAS for qualitative traits seems immediately feasible. Pyramiding of a number of genes against different races of a particular pathogen and also against different pathogens, nematodes and insects should now be aimed at, which would allow sustaining the gains in productivity of the oilseed crops. Enhancing productivity further and stabilizing production particularly under abiotic stresses would require strategic use of markers in these crops. Many QTLs for seed and oil yield as well as for salt and drought tolerance in crops like soybean, sunflower and *Brassica* have been mapped. There is a need to validate and fine map these QTLs to identify tightly linked markers. Detection of QTL and its validation has to be carried out using a large population (>200 individuals) across several locations. Their expression needs to be confirmed in the target/new genetic backgrounds. More than one population may be used in parallel to understand the effect of different genetic backgrounds. It would be essential to understand the kind and the extent of epistatic interactions to identify desirable QTL combinations to be used in different situations. All these

demand greater amount of research efforts, liberal funding, creation of additional infrastructure for precise phenotyping and high throughput genotyping, and newer experimental strategies.

The potential application of MAS in genetic improvement of the oilseed crops is quite high. More efforts are required in the coming years for realization of potential of MAS under field conditions in the form of commercial release of new varieties. Optimization of the cost of genotyping is required for routinely handling large samples as demanded by plant breeding experiments. Fortunately, due to significant reduction in cost, the genotyping technology is developing very fast, however, the investment in designing robust sequence based validated markers for important traits in oilseed crops should be viewed in the context of advantages in terms of saving time, effort and cost in the long run. While pursuing MAS particularly for difficult-to-phenotype traits, it should be kept in mind that use of markers is no substitute for conventional breeding. Conscious and strategic integration of MAS with traditional breeding of oilseed crops is desirable to harvest the benefits it offers.

References

- Adugna W, Labuschagne MT, Viljoen CD (2006) The use of morphological and AFLP markers in diversity analysis of linseed. Biodivers Conserv 15:3193–3205
- Amiri RM, Yazdi Samadi B, Ghanadha MR, Abd MC (2001) Detection of DNA polymorphism in landrace populations of safflower in Iran using RAPD-PCR technique. Iran J Agric Sci 32(4):737–745
- Arondel V, Lemieux B, Hwang T, Gibson S, Goodman HM, Somerville CR (1992) Map-based cloning of a gene controlling omega-3 fatty acid desaturation in *Arabidopsis*. Science 258:1352–1355
- Arus P, Orton TJ (1983) Inheritance and linkage relationships of isozyme loci in *Brassica oleracea*. J Hered 74:405–412
- Ashutosh, Sharma PC, Prakash S, Bhat SR (2007) Identification of AFLP markers linked to the male fertility restorer gene of CMS (*Moricandia arvensis*) *Brassica juncea* and conversion to SCAR marker. Theor Appl Genet 114(2):385–392
- Axelson T, Bowman CM, Sharpe AG, Lydiate DJ, Lagercrantz U (2000) Amphidiploid *Brassica juncea* contains conserved progenitor genomes. Genome 43:679–688
- Bachlava E, Dewey RE, Auclair J, Wang S, Burton JW, Cardinal AJ (2008) Mapping genes encoding microsomal ω-6 desaturase enzymes and their cosegregation with QTL affecting oleate content in sovbean. Crop Sci 48:640–650
- Barret P, Delourme R, Renard M, Domergue F, Lessire L, Delseny M, Roscoe TJ (1998) A rapeseed *FAE1* gene is linked to the E1 locus associated with variation in the content of erucic acid. Theor Appl Genet 96:177–186
- Berrios EF, Gentzbittel L, Kayyal H, Alibert G, Sarrafi A (2000) AFLP mapping of QTLs for in vitro organogenesis traits using recombinant inbred lines in sunflower (*Helianthus annuus* L.). Theor Appl Genet 101:1299–1306
- Berry ST, Leon AJ, Hanfrey CC, Challis P, Burkholz A, Barnes SR, Rufener GK, Lee M, Caligari PDS (1995) Molecular markers analysis of *Helianthus annuus* L. 2. Construction of an RFLP map for cultivated sunflower. Theor Appl Genet 91:195–199
- Bhat KV, Prashant PB, Lakhanpaul S (1999) Study of genetic diversity in Indian and exotic sesame (*Sesamum indicum* L.) germplasm using random amplified polymorphic DNA (RAPD) markers. Euphytica 110:21–33

- Bhati J, Sonah H, Jhang T, Singh NK, Sharma TR (2010) Comparative analysis and EST mining reveals high degree of conservation among five *Brassicaceae* species. Comparative and functional genomics, Article ID 520238, 13p. doi: 10.1155/2010/520238
- Bisht NC, Gupta V, Ramchiary N, Sodhi YS, Mukhopadhyay A, Arumugam N, Pental D, Pradhan AK (2009) Fine mapping of loci involved with glucosinolate biosynthesis in oilseed mustard (*Brassica juncea*) using genomic information from allied species. Theor Appl Genet 118:413–421
- Brahm L, Rocher T, Friedt W (2000) PCR-based markers facilitating marker assisted selection in sunflower for resistance to downy mildew. Crop Sci 40:676–682
- Camarago LEA, Osborn TC (1996) Mapping loci controlling flowering time in *Brassica oleracea*. Theor Appl Genet 92:610–616
- Camarago LEA, Williams PH, Osborn TC (1995) Mapping of quantitative trait loci controlling resistance of *Brassica oleracea* to *Xanthomonas campestris* pv. *campestris* in the field and green house. Phytopathology 85:1296–1300
- Chandra S, Nigam SN, Cruickshank AW, Bandopadhyaya A, Harikrishna S (2003) Selection index for identifying high yielding genotypes in irrigated and rainfed environments. Ann Appl Biol 143:303–310
- Chen BY, Heneen WK, Simonsen V (1989) Comparative and genetic studies of isozymes in resynthesized and cultivated *Brassica napus* L., *B. campestris* and *B. alboglabra* Bailey. Theor Appl Genet 77:673–679
- Chen BY, Jorgensen RB, Cheng BF, Heneen WK (1997) Identification and chromosomal assignment of RAPD marker linked with a gene for seed coat colour in a *Brassica campestris-albog-labra* addition line. Hereditas 126:133–138
- Chen Y, Kenaschuk E, Dribnenki B (2001) Inheritance of rust resistance genes and molecular markers in microspore derived populations of flax. Plant Breed 120:82–84
- Chen J, Hu J, Vick BA, Jan CC (2006) Molecular mapping of a nuclear male-sterility gene in sunflower (*Helianthus annuus* L.) using TRAP and SSR markers. Theor Appl Genet 113:122–127
- Cheung WY, Friesen L, Rakow GFW, Seguin Swartz G, Landry BS (1997) An RFLP based linkage map of mustard [*Brassica juncea* (L) Czern and Coss]. Theor Appl Genet 94:841–851
- Cheung WY, Gugel RK, Landry BS (1998) Identification of RFLP markers linked to the white rust resistance gene (*Acr*) in mustard [*Brassica juncea* (L.) Czern and Coss.]. Genome 41:626–628
- Chyi YS, Hoeneke ME, Sernyk JL (1992) A genetic linkage map of restriction fragment length polymorphism loci for *Brassica rapa* (syn *campestris*). Genome 35:746–757
- Concibido VC, Denny RL, Boutin SR, Hautea R, Orf JH, Young ND (1994) DNA marker analysis of loci underlying resistance to soybean cyst nematode (*Heterodera glycines* Ichinohe). Crop Sci 34:240–246
- Cregan PB, Jarvik T, Bush AL, Shoemaker RC, Lark KG, Kahler AL, Kaya N, VanToai TT, Lohnes DG, Chung J, Specht JE (1999) An integrated genetic linkage map of soybean genome. Crop Sci 39:1464–1490
- Cuc M, Mace Emma S, Crouch Jonathan H, Quang Vu D, Long Tran D, Varshney Rajeev K (2008) Isolation and characterization of novel microsatellite markers and their application for diversity assessment in cultivated groundnut (*Arachis hypogaea*). BMC Plant Biol 8:55
- Damodaran T, Hegde DM (2007) Oilseeds situation: a statistical compendium. Directorate of Oilseed Research, Hyderabad
- Davila M, Laurentin H, Castillo MA (2003) Usefulness of RAPD markers for identification of sesame germplasm. Agro Trop Maracay 53(3):259–273
- De Quiroz HC, Mithen R (1996) Molecular markers for low glucosinolate alleles in oilseed rape (*Brassica napus* L.). Mol Breed 2:277–281
- Delourme R, Bouchereau A, Hubert N, Renard M, Landry BS (1994) Identification of RAPD markers linked to a fertility restorer gene for the Ogura radish cytoplasmic male sterility of rapeseed (*Brassica napus* L). Theor Appl Genet 88:741–748

- Delourme R, Foisset N, Horvais R, Barret P, Champagne G, Cheung WY, Landry BS, Renard M (1998) Characterisation of the radish introgression carrying the *Rfo* restorer gene for the *Ogu*-INRA cytoplasmic male sterility in rapeseed (*Brassica napus* L). Theor Appl Genet 97:129–134
- Delourme R, Falentin C, Huteau V, Clouet V, Horvais R, Gandon B, Specel S, Hanneton L, Dheu JE, Deschamps M, Margale E, Vincourt P, Renard M (2006) Genetic control of oil content in oilseed rape *Brassica napus* L. Theor Appl Genet 113(7):1331–1345
- Diederichsen A (2007) Ex situ collections of cultivated flax (Linum usitatissimum L.) and other species of the genus Linum L. Genet Resourc Crop Evol 54:661–678
- Diederichsen A, Fu YB (2006) Phenotypic and molecular (RAPD) differentiation of four infraspecific groups of cultivated flax (*Linum usitatissimum* L. subsp. *usitatissimum*). Genet Resourc Crop Evol 53:77–90
- Diers BW, Mansur L, Imsande J, Shoemaker R (1991) Mapping *Phytophthora* resistance loci in soybean with restriction fragment length polymorphism markers. Crop Sci 32:377–383
- Diers BW, Fehr W, Keim P, Shoemaker RC (1992) RFLP analysis of soybean seed protein and oil content. Theor Appl Genet 83:608–612
- Dion Y, Gugel RK, Rakow GFW, Seguin Swartz G, Landry BS (1995) RFLP mapping of resistance to the blackleg disease [casual agent, *Leptosphaeria maculans* (Desm) Ces et de Not.] in canola (*Brassica napus* L). Theor Appl Genet 91:1190–1194
- Dixit A, Jin MH, Chung JW, Yu JW, Chung HK, Ma KH, Park YJ, Cho EG (2005) Development of polymorphic microsatellite markers in sesame (*Sesamum indicum* L.). Mol Ecol Notes 5(4):736–738
- Dutta PC, Helmersson S, Kebedu E, Alema G, Appelqvist L-A (1994) Variation in lipid composition of niger seed (*Guizotia abyssinica* Cass) samples collected from different regions in Ethiopia. J Am Oil Chem Soc 71(8):839–843
- Ecke W, Uzunova M, Weissleder K (1995) Mapping the genome of rapeseed (Brassica napus L) II. Localization of genes controlling erucic acid synthesis and oil content. Localization of genes controlling erucic acid synthesis and oil content. Theor Appl Genet 91:972–977
- Feng J, Jan CC (2008) Introgression and molecular tagging of Rf_4 , a new male fertility restoration gene from wild sunflower $Helianthus\ maximiliani\ L$. Theor Appl Genet 117:241–249
- Ferreira ME, Williams PH, Osborn TC (1994) RFLP mapping of *Brassica napus* using doubled haploid lines. Theor Appl Genet 89:615–621
- Ferreira ME, Rimmer SR, Williams PH, Osborn TC (1995a) Mapping loci controlling *Brassica napus* resistance to *Leptosphaeria maculans* under different screening conditions. Genetics 85:213–217
- Ferreira ME, Satagopan J, Yandell BS, Williams PH, Osborn TC (1995b) Mapping loci controlling vernalization requirement and flowering time in *Brassica napus*. Theor Appl Genet 90:727–732
- Ferreira ME, Williams PH, Osborn TC (1995c) Mapping loci controlling resistance to *Albugo candida* in *Brassica napus* using molecular markers. Phytopathology 85:218–220
- Figdore SS, Kennard WC, Song KM, Slocum MK, Osborn TC (1988) Assessment of the degree of restriction fragment length polymorphism in *Brassica*. Theor Appl Genet 75:833–840
- Figdore SS, Ferreira ME, Slocum MK, Williams PH (1993) Association of RFLP markers with trait loci affecting clubroot resistance and morphological characters in *Brassica oleracea* L. Euphytica 69:33–44
- Foisset N, Delourme R, Barret P, Hubert N, Landry BS, Renard M (1996) Molecular mapping analysis of *Brassica napus* using isozyme, RAPD and RFLP markers on doubled haploid progeny. Theor Appl Genet 93:1017–1025
- Fourmann M, Barret P, Renard M, Pelletier G, Delourme R, Brunel D (1998) The two genes homologous to *Arabidopsis FAE1* co-segregate with the two loci governing erucic acid content in *Brassica napus*. Theor Appl Genet 96:852–858
- Fu YB, Diederichsen A, Richards KW, Peterson G (2002) Genetic diversity within a range of cultivars and landraces of flax (*Linum usitatissimum* L.) as revealed by RAPDs. Genet Resour Crop Evol 49:167–174

- Fu YB, Rowland GG, Duguid SD, Richards KW (2003) RAPD analysis of 54 North American flax cultivars. Crop Sci 43:1510–1515
- Fusari CM, Verónica VL, Hopp HE, Heinz RA, Paniego Norma B (2008) Identification of single nucleotide polymorphisms and analysis of linkage disequilibrium in sunflower elite inbred lines using the candidate gene approach. BMC Plant Biol 8:1–14
- Gao M, Li G, Yang B, Qiu D, Farnham M, Quiros C (2007) High-density *Brassica oleracea* linkage map: identification of useful new linkages. Theor Appl Genet 115(2):277–287
- Garcia GM, Stalker HT, Kochert G (1995) Introgression analysis of an interspecific hybrid population in peanut (*Arachis hypogaea* L.) using RFLP and RAPD markers. Genome 38:166–176
- Gentzbittel L, Zhang YX, Vear F, Griveau B, Nicolas P (1994) RFLP studies of genetic relationship among inbred lines of the cultivated sunflower. *Helianthus annuus* L.: evidence for distinct restorer and maintainer germplasm pools. Theor Appl Genet 89:419–425
- Gentzbittel L, Vear F, Zhang YX, Berville A, Nicolas P (1995) Development of a consensus linkage RFLP map of cultivated sunflower (*Helianthus annuus* L). Theor Appl Genet 89:419–425
- Getinet A, Sharma SM (1996) Niger [*Guizotia abyssinica* (L.f.) Cass.]. Promoting the conservation and use of underutilized and neglected crops.5. International Plant Genetic Resources Institute, Rome, 59p. ISBN 92-9043-292-6
- Good AG, Stringam GR, Mahmood T, Ekuere U, Yeh F (2003) Molecular mapping of seed aliphatic glucosinolates in *Brassica juncea*. Genome 46(5):753–760
- Guo B, Sleper DA, Arelli PR, Shannon JG, Nguyen HT (2005) Identification of QTLs associated with resistance to soybean cyst nematode races 2, 3 and 5 in soybean PI 90763. Theor Appl Genet 111:965–971
- Gupta V, Mukhopadhaya A, Arumugam N, Sodhi YS, Pental D, Pradhan AK (2004) Molecular tagging of erucic acid trait in oilseed mustard (*Brassica juncea*) by QTL mapping and single nucleotide polymorphism in *FAE1* gene. Theor Appl Genet 108:743–749
- Halward TM, Stalker HT, Larue EA, Kochert G (1991) Genetic variation detected with molecular markers among un-adapted germplasm resources of cultivated peanut and related wild species. Genome 34:1013–1020
- Halward TM, Stalker HT, Larue EA, Kochert G (1992) Use of single primer DNA amplifications in genetic studies of peanut (*Arachis hypogaea*). Plant Mol Biol 18:315–325
- Halward TM, Stalker HT, Kochert G (1993) Development of an RFLP linkage map in diploid peanut species. Theor Appl Genet 87:379–384
- Happstadius I, Ljungberg A, Kristiansson B, Dixelius C (2003) Identification of *Brassica oleracea* germplasm with improved resistance to *Verticillium* wilt. Plant Breed 122:30–34
- Hasan M, Friedt W, Kühnemann Pons J, Freitag NM, Link K, Snowdon RJ (2008) Association of gene-linked SSR markers to seed glucosinolate content in oilseed rape (*Brassica napus* ssp. napus). Theor Appl Genet 116(8):1035–1049
- He J, Ke L, Hong D, Xie Y, Wang G, Liu P, Yang G (2008) Fine mapping of a recessive genic male sterility gene (Bnms3) in rapeseed (*Brassica napus*) with AFLP and *Arabidopsis* derived PCR markers. Theor Appl Genet 117(1):11–18
- Heesacker A, Kishore VK, Gao W, Tang S, Kolkman JM, Gingle A, Matvienko M, Kozik A, Michelmore RM, Lai Z, Rieseberg LH, Knapp SJ (2008) SSRs and INDELs mined from the sunflower EST database: abundance, polymorphisms, and cross-taxa utility. Theor Appl Genet 117:1021–1029
- Hegde DM (2009a) Vegetable oils scenario:approaches to meet the growing demands. Indian Society of Oilseeds Research, Directorate of Oilseed Research, Hyderabad
- Hegde DM (2009b) Can India achieve self reliance in vegetable oils? Souvenir published during national symposium on vegetable oils scenario: approaches to meet the growing demands organized by Indian Society of Oilseeds Research? Directorate of Oilseed Research, Hyderabad
- Herselman L, Thwaites R, Kimmins FM, Courtois B, Merwe PJA, Van-der-Seal SE (2004) Identification and mapping of AFLP markers linked to peanut (*Arachis hypogaea* L.) resistance to the aphid vector of groundnut rosette disease. Theor Appl Genet 109:1426–1433
- Herve D, Fabre F, Berrios EF, Leroux N, Chaarani GA, Planchon C, Sarrafi A, Gentzbittel L (2001) QTL analysis of photosynthesis and water status traits in sunflower (*Helianthus annuus* L.) under greenhouse conditions. J Exp Bot 52(362):1857–1864

Hoenecke M, Chyi YS (1991) Comparison of *Brassica napus* and *B. rapa* genomes based on restriction fragment length polymorphism mapping. In: Proceedings of the 8th International Rapeseed Congress, vol 7, Saskatchewan, pp 1102–1107

- Horn R, Kusterer B, Lazarescu E, Prufe M, Ozdemir N, Friedt W (2002) Molecular diversity of CMS sources and fertility restoration in the genus *Helianthus*. HELIA 25:29–40
- Hu J, Quiros C, Arus P, Struss D, Robbelen G (1995) Mapping of a gene determining linolenic acid concentration in rapeseed with DNA-based markers. Theor Appl Genet 90:258–262
- Hu J, Li G, Struss D, Quiros CF (1999) SCAR and RAPD markers associated with 18-carbon fatty acids in rapeseed, *Brassica napus*. Plant Breed 118:145–150
- Huang Z, Chen Y, Yi B, Xiao L, Ma C, Tu J, Fu T (2007) Fine mapping of the recessive genic male sterility gene (*Bnms3*) in *Brassica napus* L. Theor Appl Genet 115(1):113–118
- Hyten DL, Song Q, Choi IY, Yoon MS, Specht JE, Matukumalli LK, Nelson RL, Shoemaker RC, Young ND, Cregan PB (2008) High-throughput genotyping with the GoldenGate assay in the complex genome of soybean. Theor Appl Genet 116(7):945–952
- Jamaux I, Steinmetz A, Belhassen E, Farrar J (1997) Looking for molecular and physiological markers of osmotic adjustment in sunflower. Putting plant physiology on the map: genetic analysis of development and adaptive traits. In: Proceedings of the 2nd new phytologist symposium, Bangor, pp 117–127
- Jan CC, Vick BA, Miller JF, Kahler AL, Butler ET (1998) Construction of an RFLP linkage map for cultivated sunflower. Theor Appl Genet 96:15–22
- Jayashree B, Morag F, Dan I, Doyle J, Crouch JH (2005) Analysis of genomic sequences from peanut (Arachis hypogaea). J Biotechnol 8(3):226–237
- Jean M, Brown GG, Landry BS (1997) Genetic mapping of nuclear fertility restorer genes for the Polima cytoplasmic male sterility in canola (*Brassica napus* L) using DNA markers. Theor Appl Genet 95:321–328
- Johnson RC, Kisha TJ, Evans MA (2007) Characterizing safflower germplasm with AFLP molecular markers. Crop Sci 47(4):1728–1736
- Jourden C, Barret P, Brunel D, Delourme R, Renard M (1996a) Specific molecular marker of genes controlling linolenic acid content in rapeseed. Theor Appl Genet 93:512–518
- Jourden C, Barret P, Horvais R, Delourme R, Renard M (1996b) Identification of RAPD marker linked to linolenic acid genes in rapeseed. Euphytica 90:351–357
- Jourden C, Barret P, Horvais R, Foisset N, Delourme R, Renard M (1996c) Identification of RAPD markers linked to loci controlling erucic acid level in rapeseed. Mol Breed 2:61–71
- Kalita MC, Mohapatra T, Dhandapani A, Yadava DK, Srinivasan K, Mukherjee AK, Sharma RP (2007) Comparative evaluation of RAPD, ISSR and Anchored-SSR markers in assessment of genetic diversity and fingerprinting of oilseed *Brassica* genotypes. J Plant Biochem Biotechnol 15(1):41–48
- Kearsay MJ, Ramsay LD, Jennings DE, Lydiate DJ, Bohoun EJR, Marshall DF (1996) Higher recombination frequency in female compared to male meiosis in *Brassica oleracea*. Theor Appl Genet 92:363–367
- Kiani SP, Grieu P, Maury P, Hewezi T, Gentzbittel L, Sarrafi A (2007) Genetic variability for physiological traits under drought conditions and differential expression of water stress-associated genes in sunflower (*Helianthus annuus* L.). Theor Appl Genet 114(2):193–207
- Kianian SF, Quiros CF (1992) Generation of *Brassica oleracea* composite RFLP map: linkage arrangements across various populations and evolutionary implications. Theor Appl Genet 84:544–554
- Kiem P, Diers BW, Olson TC, Shoemaker RC (1990a) RFLP mapping in soybean: association between marker loci and variation in quantitative traits. Genetics 126:735–742
- Kiem P, Diers BW, Shoemaker RC (1990b) Genetic analysis of soybean hard seededness with molecular markers. Theor Appl Genet 79:465–469
- Kiem P, Schupp JM, Travis SE, Clayton K, Zhu T, Liang S, Ferriera A, Webb DM (1997) A high density soybean genetic map based on AFLP markers. Crop Science 37:537–543
- Kim SC, Rieseberg LH (1999) Genetic architecture of species differences in annual sunflowers: implications for adaptive trait introgression. Genetics 153:965–977

- Kochert G, Halward T, Branch WD, Simpson CE (1991) RFLP variability in peanut (*Arachis hypogaea* L.) cultivars and wild species. Theor Appl Genet 81:565–570
- Kole C, Teutonico R, Williams PH, Osborn TC (1996) Molecular mapping of a locus controlling resistance to *Albugo candida* in *Brassica rapa*. Phytopathology 86:367–369
- Kole C, Kole P, Vogelzang R, Osborn TC (1997) Genetic linkage map of a *Brassica rapa* recombinant inbred population. J Hered 88:553–557
- Kolkman JM, Berry ST, Leon AJ, Slabaugh MB, Tang S, Gao W, Shintani DK, Burke JM, Knapp SJ (2007) Single nucleotide polymorphisms and linkage disequilibrium in sunflower. Genetics 177:457–468
- Koundal V, Parida SK, Yadava DK, Ali A, Koundal KR, Mohapatra T (2008) Evaluation of microsattelite markers for genome mapping in Indian mustard (*Brassica juncea* L.). J Plant Biochem Biotechnol 17(1):69–72
- Krulickova K, Posvec Z, Griga M (2002) Identification of flax and linseed cultivars by isozyme markers. Biol Plant 45:327–336
- Kusterer B, Prufe M, Lazarescu E, Ozdemir N, Friedt W, Horn R (2002) Mapping of the restorer gene *rf1* in sunflower (*Helianthus annuus* L.). HELIA 25:41–46
- Lagercrantz U, Lydiate DJ (1995) RFLP mapping in *Brassica nigra* indicates differing recombination rates in male and female meioses. Genome 38:255–264
- Lagercrantz U, Putterill J, Coupland G, Lydiate D (1996) Comparative mapping of *Arabidpsis* and *Brassica*, fine scale genome colinearity and congruence of genes controlling flowering time. Plant J 9:13–20
- Landau Ellis D, Angermuller S, Shoemaker R, Gresshoff PM (1991) The genetic locus controlling supernodulation in soybean (*Glycine max* L.) co-segregates tightly with a cloned molecular marker. Mol Gen Genet 228:221–226
- Landry BS, Hubert N, Etoh T, Harada JJ, Lincoln SE (1991) A genetic map for *Brassica napus* based on restriction fragment length polymorphisms detected with expressed DNA sequences. Genome 34:543–552
- Landry BS, Hubert N, Crete R, Chiang MS, Lincoln SE, Etoh T (1992) A genetic map for *Brassica oleracea* based on RFLP markers detected with expressed DNA sequences and mapping of resistance genes to race 2 of *Plasmodiophora brassicae* (Woronin). Genome 35:409–420
- Langer K, Lorieux M, Desmarais E, Griveau Y, Gentzbittel L, Berville A (2003) Combined mapping of DALP and AFLP markers in cultivated sunflower using F₉ recombinant inbred lines. Theor Appl Genet 106:1068–1074
- Lark KG, Weisemann JM, Matthews BF, Palmer R, Chase K, Macalma T (1993) A genetic map of soybean (*Glycine max* L.) using an intraspecific cross of two cultivars: 'Minosy' and 'Noir 1'. Theor Appl Genet 86(8):901–906
- Lark KG, Orf J, Mansur LM (1994) Epistatic expression of quantitative trait loci (QTL) in soybean [Glycine max (L.) Merr.] determines by QTL association with RFLP alleles. Theor Appl Genet 88:486–489
- Laurentin HE, Karlovasky P (2006) Genetic relationship and diversity in a sesame (*Sesamum indicum* L.) germplasm collection using amplified fragment length polymorphism. BMC Genet 7:10
- Laurentin HE, Karlovsky P (2007) AFLP fingerprinting of sesame (*Sesamum indicum* L.) cultivars: identification, genetic relationship and comparison of AFLP informativeness parameters. Genet Resour Crop Evol 54(7):1437–1446
- Lawson WR, Goulter KC, Henry RJ, Kong GA, Kochman JK (1998) Marker assisted selection for two rust resistance genes in sunflower. Mol Breed 4:227–234
- Lee SH, Park KY, Lee HS, Park EH, Boerma HR (2001) Genetic mapping of QTLs conditioning soybean sprout yield and quality. Theor Appl Genet 103(5):702–709
- Lee GJ, Boerma HR, Villagarcia MR, Zhou X, Carter TE Jr, Li Z, Gibbs MO (2004) A major QTL conditioning salt tolerance in S-100 soybean and descendent cultivars. Theor Appl Genet 109(8):1610–1619
- Leflon M, Brun H, Eber F, Delourme R, Lucas MO, Vallee P, Ermel M, Balesdent MH, Chèvre AM (2007) Detection, introgression and localization of genes conferring specific resistance to Leptosphaeria maculans from Brassica rapa into B. napus. Theor Appl Genet 115(7):897–906

Lenardon SL, Bazzalo M, Abratti G, Cimino C, Galella M, Grondona M, Giolitti F, Leon AJ (2005) Screening sunflower for resistance to sunflower chlorotic mottle virus and mapping the Rmco-1 resistance gene. Crop Sci 45:735–739

- Leon AJ, Andrade FH, Lee M (2000) Genetic mapping of factors affecting quantitative variation for flowering in sunflower. Crop Sci 40:404–407
- Lexer C, Welch ME, Durphy JL, Rieseberg LH (2003) Natural selection for salt tolerance quantitative trait loci (QTLs) in wild sunflower hybrids: implications for the origin of *Helianthus paradoxus*, a diploid hybrid species. Mol Ecol 12:1225–1235
- Li D, Hans-Henning M (1996) Safflower. *Carthamus tinctorius* L. Promoting the conservation and use of underutilized and neglected crops. 7. Institute of Plant Genetics and Crop Plant Research, Gatersleben/International Plant Genetic Resources Institute, Rome
- Li G, Quiros CF (2001) Sequence-related amplified polymorphism (SRAP), a new marker system based on a simple PCR reaction: its application to mapping and gene tagging in *Brassica*. Theor Appl Genet 103(2–3):455–461
- Li Y, Guan R, Liu Z, Ma Y, Wang L, Li L, Lin F, Luan W, Chen P, Yan Z, Guan Y, Zhu L, Ning X, Smulders MJM, Li W, Piao R, Cui Y, Yu Z, Guan M, Rector BG, All JN, Parrott WA, Boerma HR (1998) Identification of molecular markers linked to quantitative trait loci for soybean resistance to corn earworm. Theor Appl Genet 96:786–790
- Li Y, Guan R, Liu Z, Ma Y, Wang L, Li L, Lin F, Luan W, Chen P, Yan Z, Guan Y, Zhu L, Ning X, Smulders MJ, Li W, Piao R, Cui Y, Yu Z, Guan M, Chang R, Hou A, Shi A, Zhang B, Zhu S, Qiu L (2008) Genetic structure and diversity of cultivated soybean *Glycine max* (L.) Merr landraces in China. Theor Appl Genet 117(6):857–871
- Li X, Ramchiary N, Choi SR, Nguyen DV, Hossain MJ, Yang HK, Lim YP (2010a) Development of a high density integrated reference genetic linkage map for the multinational *Brassica rapa* genome sequencing project. Genome 53(11):939–947
- Li YM, Jun LX, Yun GC, Li LL (2010b) Cloning and SNP analysis of *TT1* gene in *Brassica juncea*. Acta Agron Sin 36(10):1634–1641
- Lorenzen LL, Boutin S, Yang N, Specht JE, Shoemaker RC (1995) Soybean pedigree analysis using map based molecular markers. I. Tracking RFLP markers in cultivars. Crop Sci 35:1326–1336
- Luo M, Dang P, Guo BZ, He G, Holbrook CC, Bausher MG, Lee RD (2005) Generation of expressed sequence tags (ESTs) for gene discovery and marker development in cultivated peanut. Crop Sci 45:346–353
- Lydiate D, Sharpe A (2003) Aligning genetic maps of *Brassica napus* using microsatellite markers. Plant and Animal Genome XI, San Diego, USA
- Mahmood T, Ekuere U, Yeh F, Good AG, Stringam GR (2003) Molecular mapping of seed aliphatic glucosinolates in *Brassica juncea*. Genome 46:753–760
- Mahmood T, Rahman MH, Stringam GR, Yeh F, Allen G (2005) Molecular markers for yield components in *Brassica juncea* do these assist in breeding for high seed yield? Euphytica 144:157–167
- Mansur LM, Orf J, Lark KG (1993a) Determining the linkage of quantitative trait loci to RFLP markers using extreme phenotypes of recombinant inbred of soybean (*Glycine max* L. Merr.). Theor Appl Genet 86:914–918
- Mansur LM, Lark KG, Kross H, Oliveira A (1993b) Interval mapping of quantitative trait loci for reproductive, morphological and seed traits of soybean (*Glycine max* L.). Theor Appl Genet 86:907–913
- Mohapatra T, Upadhyay A, Sharma A, Sharma RP (2002) Detection and mapping of duplicate loci in *Brassica juncea*. J Plant Biochem Biotechnol 11:37–42
- Mondal S, Badigannavar AM, Murty GSS (2007) RAPD markers linked to a rust resistance gene in cultivated groundnut (*Arachis hypogaea* L.). Euphytica 159:233–239
- Moretzsohn MC, Leoi L, Proite K, Guimarães PM, Leal-Bertioli SCM, Gimenes MA, Martins WS, Valls JFM, Grattapaglia D, Bertioli DJ (2005) A microsatellite-based, gene-rich linkage map for the AA genome of *Arachis* (Fabaceae). Theor Appl Genet 111(6):1060–1071
- Moshkin VA (1967) Castor. Oxonian, Ltd. New Delhi. p, 315

- Mouzeyar S, Roeckel Drevet P, Gentzbittel L, Philippon J, Labrouhe D, De T, Vear F, Nicolas P (1995) RFLP and RAPD mapping of the sunflower *P11* locus for resistance to *Plasmopara halstedii* race 1. Theor Appl Genet 91:733–737
- Mudge J, Cregan PB, Kenworthy JP, Kenworthy WJ, Orf IH, Young ND (1997) Two microstaellite markers that flank the major soybean cyst nematode resistance locus. Crop Sci 37:1611–1615
- Mukherjee AK, Mohapatra T, Varshney A, Sharma R, Sharma RP (2001) Molecular mapping of a locus controlling resistance to Albugo candida in Brassica juncea. Plant Breed 120(6):483–487
- Nath UK, Goswami G (2009) Inheritance and variation of erucic acid content in a transgenic rapeseed (*Brassica napus* L.) doubled haploid population. Mol Breed 23:125–138
- Negi MS, Devic M, Delseny M, Lakshmikumaran M (2000) Identification of AFLP fragments linked to seed coat colour in *Brassica juncea* and conversion to SCAR marker for rapid selection. Theor Appl Genet 101:146–152
- Oh T, Gorman M, Cullis C (2000) RFLP and RAPD mapping in flax (*Linum usitatissimum*). Theor Appl Genet 101:590–593
- Paik-Ro OG, Smith RL, Knauft DA (1992) Restriction fragment length polymorphism evaluation of six peanut species with the *Arachis* section. Theor Appl Genet 84:201–208
- Paniego N, Echaide M, Muñoz M, Fernandez L, Torales S, Faccio P, Fuxan ICM, Zandomeni R, Suárez EY, Hopp HE (2002) Microsatellite isolation and characterization in sunflower (*Helianthus annuus* L.). Genome 45:34–43
- Panjabi P, Yadava SK, Sharma P, Kaur A, Kumar A, Arumugam N, Sodhi YS, Mukhopadhyay A, Gupta V, Pradhan AK, Pental D (2010) Molecular mapping reveals two independent loci conferring resistance to *Albugo candida* in the east European germplasm of oilseed mustard *Brassica juncea*. Theor Appl Genet 121:137–145
- Panjabi P, Jagannath A, Bisht NC, Padmaja LK, Sharma S, Gupta V, Pradhan AK, Pental D (2008) Comparative mapping of *Brassica juncea* and *Arabidopsis thaliana* using Intron Polymorphism (IP) markers: homoeologous relationships, diversification and evolution of the A, B and C, Brassica genomes. BMC Genom 9:113
- Parida S, Yadava DK, Mohapatra T (2010) Microsatellites in *Brassica* unigenes: relative abundance, marker design and use in comparative physical mapping and genome analysis. Genome 53:55–67
- Perez VB, Knapp SJ, Leon AJ, Fernandez MJM, Berry ST (2004) Mapping minor QTL for increased stearic acid content in sunflower seed oil. Mol Breed 13:313–322
- Perez VB, Berry ST, Velasco L, Fernandez MJM, Gandhi S, Freeman C, Heesacker A, Knapp SJ, Leon AJ (2005) Molecular mapping of nuclear male sterility genes in sunflower. Crop Sci 45:1851–1857
- Perez VB, Velasco L, Munoz-Ruz JM, Fernandez Martinez JM (2006) Inheritance of high stearic acid content in the sunflower mutant CAS-14. Crop Sci 46:22–29
- Polzin KM, Lohnes DG, Nickell CD, Shoemaker RC (1994) Integration of *Rps2*, *Rmd* and *Rj2* into linkage group J of the soybean molecular map. J Hered 85:300–303
- Prabhu KV, Somers DJ, Rakow G, Gugel RK (1998) Molecular markers linked to white rust resistance in mustard *Brassica juncea*. Theor Appl Genet 97:865–870
- Pradhan NK, Mishra RC, Paikary RK (1995) Genetic variability and character association in niger. Ind J Genet Plant Breed 55:457–459
- Pradhan A, Gupta V, Mukhopadhyay A, Arumugam N, Sodhi Y, Pental D (2003) A high-density linkage map in *Brassica juncea* (Indian mustard) using AFLP and RFLP markers. Theor Appl Genet 106(4):607–614
- Pradhan A, Nelson MN, Plummer JA, Cowling WA, Yan G (2011) Characterization of *Brassica nigra* collections using simple sequence repeat markers reveals distinct groups associated with geographical location, and frequent mislabelling of species identity. Genome 54(1):5–63
- Qiu D, Morgan C, Shi J, Long Y, Liu J, Li R, Zhuang X, Wang Y, Tan X, Dietrich E, Weihmann T, Everett C, Vanstraelen S, Beckett P, Fraser F, Trick M, Barnes S, Wilmer J, Schmidt R, Li J, Li D, Meng J, Bancroft I (2006) A comparative linkage map of oilseed rape and its use for QTL analysis of seed oil and erucic acid content. Theor Appl Genet 114(1):67–80

- Rachaputi NC, Wright GC (2003) Physiological basis for selection of peanut in breeding for improved drought resistance. In: Cruickshank AW, Rachaputi NC, Wright GC, Nigam SN (eds) Breeding of drought resistant peanut. Australian Centre for International Agricultural Research, Canberra; ACIAR Proceedings No. 112, pp 10–14
- Rahman M, McVetty PBE, Li G (2007) Development of SRAP, SNP and Multiplexed SCAR molecular markers for the major seed coat color gene in *Brassica rapa* L. Theor Appl Genet 115(8):1101–1107
- Rahman M, Sun Z, McVetty PBE, Li G (2008) High throughput genome-specific and gene-specific molecular markers for erucic acid genes in *Brassica napus* (L.) for marker-assisted selection in plant breeding. Theor Appl Genet 117(6):895–904
- Ramchiary N, Bisth NC, Gupta V, Mukhopadhaya A, Arunmugam N, Sodhi YS, Pental D, Pradhan AK (2007) QTL analysis reveals context-dependent loci for seed glucosinolate trait in the oil-seed *Brassica juncea*: importance of recurrent selection backcross scheme for identification of QTL. Theor Appl Genet 116:77–85
- Ramsay LD, Jennings DE, Bohuon EJR, Arthur AE, Lydiate DJ, Kearsey MJ, Marshall DF (1996)

 The construction of a substitution library of recombinant backcross lines in *Brassica oleracea* for the precision mapping of quantitative loci. Genome 39:558–567
- Rector BG, All JN, Parrott WA, Boerma HR (1998) Identification of molecular markers linked to quantitative trait loci for soybean resistance to corn earworm. Theor Appl Genet 96(6–7):786–790
- Reddy BN, Devi D, Gawand PB, Ramesh A, Pratibha G (2004) Oil cultivation for moisture and nutrient stress. NATP Project Report (ROPS12). Directorate of Oilseeds Research, Hyderabad
- Ripley VL, Roslinsky V (2005) Identification of an ISSR marker for 2-propenyl glucosinolate content in *Brassica juncea* and conversion to SCAR marker. Mol Breed 16:57–66
- Roach M, Deyholos M (2007) Microarray analysis of flax (*Linum usitatissimum* L.) stems identifies transcripts enriched in fibre-bearing phloem tissues. Mol Genet Genom 278:149–165
- Roach M, Deyholos M (2008) Microarray analysis of developing flax hypocotyls identifies novel transcripts correlated with specific stages of phloem fibre differentiation. Ann Bot 102(3):317–330
- Rojas-Barros P, Hu J, Jan CC (2008) Molecular mapping of an apical branching gene of cultivated sunflower (*Helianthus annuus* L.). Theor Appl Genet 117:9–28
- Roose AC, Cariou PE, Vautrin D, Tavernier R, Solignac M (2006) Polymorphic microsatellite loci in *Linum usitatissimum*. Mol Ecol Notes 6:796–799
- Rouf-Mian MA, Kang ST, Beil SE, Hammond RB (2008) Genetic linkage mapping of the soybean aphid resistance gene in PI 243540. Theor Appl Genet 117(6):955–962
- Saal B, Plieske J, Hu J, Quiros CF, Struss D (2001) Microsatellite markers for genome analysis in Brassica. II. Assignment of rapeseed microsatellites to the A and C genomes and genetic mapping in Brassica oleracea L. Theor Appl Genet 102:695–699
- Saghai-Maroof MA, Jeong SC, Gunduz I, Tucker DM, Buss GR, Tolin SA (2008) Pyramiding of soybean mosaic virus resistance genes by marker assisted selection. Crop Sci 48:517–526
- Saito M, Kubo N, Matsumoto S, Suwabe K, Tsukada M, Hirai M (2006) Fine mapping of the clubroot resistance gene, *Crr3*, in *Brassica rapa*. Theor Appl Genet 114(1):81–91
- Salas P, Oyarzo-Llaipen JC, Wang D, Chase K, Mansur L (2006) Genetic mapping of seed shape in three populations of recombinant inbred lines of soybean (*Glycine max L. Merr.*). Theor Appl Genet 113(8):1459–1466
- Schierholt A, Becker HC, Ecke W (2000) Mapping a high oleic acid mutation in winter oilseed rape (*Brassica napus* L.). Theor Appl Genet 101:897–901
- Schuster I, Abdelnoor RV, Marin SRR, Carvalho VP, Kiihl RAS, Silva JFV, Sediyama CS, Barros EG, Moreira MA (2001) Identification of a new major QTL associated with resistance to soybean cyst nematode (*Heterodera glycines*). Theor Appl Genet 102(1):91–96
- Sehgal D, Raina SN (2005) Genotyping safflower (*Carthamus tinctorius*) cultivars by DNA finger-prints. Euphytica 146(1/2):67–76
- Shanmugham C, Gunasekaran M (2003) National catalogue for notified and denotified varieties under section, of seed act 1966 (1966–2002). Central Seed Committee, DAC, Ministry of Agriculture, GOI, New Delhi

- Shanmugham C, Gunasekaran M (2008) National catalogue for notified varieties (2003–2007). Central Seed Committee, DAC, Ministry of Agriculture, GOI, New Delhi
- Sharma A, Mohopatra T, Sharma RP (1994) Molecular mapping and character tagging in *Brassica juncea*. I Degree, nature and linkage relationship of RFLPs and their association with quantitative traits. J Plant Biochem Biotechnol 3:85–89
- Sharma R, Mohapatra T, Mukherjee AK, Singh KP, Sharma RP (1999) Molecular markers for seed oil content in Indian mustard. J Plant Biochem Biotechnol 8:61–64
- Sharma R, Aggarwal RAK, Kumar R, Mohapatra T, Sharma RP (2002) Construction of RAPD linkage map and localization of QTLs for oleic acid level using recombinant inbreds in mustard. Genome 45(3):467–472
- Sharma SN, Kumar V, Mathur S (2009) Comparative analysis of RAPD and ISSR markers for characterization of sesame (*Sesamum indicum* L.) genotypes. J Plant Biochem Biotechnol 18(1):37–43
- Shi J, Li R, Qui D, Jiang C, Long Y, Morgan C, Bancroft I, Zhao J, Meng J (2009) Unraveling the complex trait of crop yield with quantitative trait loci mapping in *B. napus*. Genetics 182:851–861
- Shifriss O (1961) Conventional and non-conventional systems controlling sex variations in *Ricinus*. J Genet 57:361–388
- Shoemaker RC, Specht JE (1995) Integration of the soybean molecular and classical genetic linkage groups. Crop Sci 35:436–446
- Sinclair TS, Larry CP, Sneller CH (2004) Crop transformation and challenge to increase yield potential. Trends Plant Sci 9:70–75
- Singh RK, Raipuria RK, Bhatia VS, Rani A, Husain SM, Chauhan D, Chauhan GS, Mohapatra T (2008) SSR markers associated with seed longevity in soybean. Seed Sci Technol 36(1):162–167
- Skorupska HT, Shoemaker RC, Warner A, Shipe ER, Bridges WC (1993) Restriction fragment length polymorphism in soybean germplasm of the southern USA. Crop Sci 33:1169–1176
- Slabaugh MB, Yu JK, Tang S, Heesacker A, Hu X et al (2003) Haplotyping and mapping a large cluster of downy mildew resistance gene candidates in sunflower using multilocus intron fragment length polymorphisms. Plant Biotechnol J 1:167–185
- Slocum MK, Figdore SS, Kenard WC, Suzuki JY, Osborn TC (1990) Linkage arrangement of restriction fragment length polymorphic loci in *Brassica oleracea*. Theor Appl Genet 80:57–64
- Soengas P, Hand P, Vicente JG, Pole JM, Pink DAC (2007) Identification of quantitative trait loci for resistance to *Xanthomonas campestris* pv. *campestris* in *Brassica rapa*. Theor Appl Genet 114(4):637–645
- Song KM, Suzuki JY, Slocum MK, Williams PH, Osborn TC (1991) A linkage map of *Brassica rapa* (syn *campestris*) based on restriction fragment length polymorphism loci. Theor Appl Genet 82:296–304
- Song QJ, Marek LF, Shoemaker RC, Lark KG, Concibido VC, Delannay X, Specht JE, Cregan PB (2004) A new integrated genetic linkage map of the soybean. Theor Appl Genet 109(1):122–128
- Spielmeyer W, Green A, Bittisnich D, Mendham N, Lagudah E (1998) Identification of quantitative trait loci contribution to *Fusarium* wilt resistance on an AFLP linkage map of flax (*Linum usitatissimum*). Theor Appl Genet 97:633–641
- Stringam GR, Thiagarajah MR (1995) Inheritance of alkenyl glucosinolate in traditional and microspore-derived doubled haploid populations of *Brassica juncea* L. Czern and Coss. In: Proceedings of the 9th international rapeseed congress rapeseed today and tomorrow, Cambridge, pp 804–806
- Sujatha M, Sailaja M (2007) Development of transgenic castor for insect resistance. In: Extended summaries, National Seminar on Changing Global Vegetable Oils, Directorate of Oilseeds Research, Hyderabad. pp 7–8
- Sun Z, Wang Z, Tu J, Zhang J, Yu F, McVetty PBE, Li G (2007) An ultradense genetic recombination map for *Brassica napus*, consisting of 13551 SRAP markers. Theor Appl Genet 114(8):1305–1317
- Tamborindeguy C, Ben C, Jardinaud F, Gentzbittel L, Liboz T (2004) Mass cloning of differential and non-differential transcript-derived fragments from cDNA-AFLP experiments in sunflower. Plant Mol Biol Rep 22:165–171

50

Tang S, Yu JK, Slabaugh MB, Shintani DK, Knapp SJ (2002) Simple sequence repeat map of the sunflower genome. Theor Appl Genet 105:1124–1136

- Tanhuanpaa PK, Vilkki JP, Vilkki HJ (1995) Association of a RAPD marker with linolenic acid concentration in the seed oil of rapeseed (*Brassica napus* L). Genome 38:414–416
- Tanhuanpaa PK, Vikki JP, Vikki HJ (1996) Mapping of a QTL for oleic acid concentration in spring turnip rape (*Brassica rapa* ssp *oleifera*). Theor Appl Genet 92:952–956
- Tanhuanpaa P, Vilkki J, Vihinen M (1998) Mapping and cloning of *FAD2* gene to develop allelespecific PCR for oleic acid in spring turnip rape (*Brassica rapa* ssp. *oleifera*). Mol Breed 4:543–550
- Teutonico RA, Osborn TC (1994) Mapping of RFLP and quantitative trait loci in *Brassica rapa* and comparison to the linkage maps of *B. napus*, *B. oleracea* and *Arabidopsis thaliana*. Theor Appl Genet 89:885–894
- Teutonico RA, Osborn TC (1995) Mapping loci controlling vernalization requirement in *Brassica rapa*. Theor Appl Genet 91:1279–1283
- Thormann CE, Romero J, Mantet J, Osborn TC (1996) Mapping loci controlling the concentration of erucic and linolenic acids in seed oil of *Brassica napus* L. Theor Appl Genet 93:282–286
- Toroser D, Thormann CE, Osborn TC, Mithen R (1995) RFLP mapping of quantitative trait loci controlling seed aliphatic glucosinolate content in oilseed rape (*Brassica napus* L). Theor Appl Genet 91:802–808
- Truco MJ, Quiros CF (1994) Structure and organization of the B genome based on a linkage map in *Brassica nigra*. Theor Appl Genet 89:590–598
- Upadhyay A, Mohapatra T, Pai RA, Sharma RP (1996) Molecular mapping and character tagging in Indian mustard (*Brassica juncea*) II. RFLP marker association with seed coat colour and quantitative traits. J Plant Biochem Biotechnol 5:17–22
- Uzun B, Lee D, Donini P, Gagirgan ML (2003) Identification of a molecular marker linked to the closed capsule mutant trait in sesame using AFLP. Plant Breed 122:95–97
- Uzunova M, Ecke W, Weissleder K, Robbelen G (1995) Mapping the genome of rapeseed (*Brassica napus* L) I. Construction of an RFLP linkage map and localization of QTLs for seed glucosinolate content. Theor Appl Genet 90:194–204
- Van Deynze AE, Landry BS, Pauls KP (1995) The identification of restriction fragment length polymorphisms linked to seed colour genes in *Brassica napus*. Genome 38:534–542
- Varma TSN, Dwivedi SL, Pande S, Gowda MVC (2005) SSR markers associated with resistance to rust (*Puccinia arachidis* Speg.) in groundnut (*Arachis hypogaea* L.). SABRAO J Breed Genet 37(2):107–119
- Varshney A, Mohapatra T, Sharma RP (2004) Development and validation of CAPS and AFLP markers for white rust resistance gene in *Brassica juncea*. Theor Appl Genet 109:153–159
- Varshney RK, Bertioli DJ, Moretzsohn MC, Vadez V, Krishnamurthy L, Aruna R, Nigam SN, Moss BJ, Seetha K, Ravi K, He G, Knapp SJ, Hoisington DA (2009) The first SSR-based genetic linkage map for cultivated groundnut (*Arachis hypogaea* L.). Theor Appl Genet 118:729–739
- Vera-Ruiz EM, Leonardo V, Leon AJ, Fernandez Martinez JM, Perez VB (2006) Genetic mapping of the Tph1 gene controlling beta tocopherol accumulation in sunflower seeds. Mol Breed 17:291-296
- Voorrips RE, Jongerius MC, Kanne HJ (1997) Mapping of two genes for resistance to clubroot (*Plasmodiophora brassicae*) in a population of doubled haploid lines of *Brassica oleracea* by means of RFLP and AFLP markers. Theor Appl Genet 94:75–82
- Walker D, Boerma HR, All J, Parrott W (2002) Combining *cry1Ac* with QTL alleles from PI 229358 to improve soybean resistance to lepidopteran pests. Mol Breed 9:43–51
- Walsh JA, Sharpe AG, Jenner CE, Lydiate DJ (1999) Characterisation of resistance to turnip mosaic virus in oilseed rape (*Brassica napus*) and genetic mapping of TuRB01. Theor Appl Genet 99:1149–1154
- Wang CT, Yang XD, Chen DX, Yu SL, Liu GZ, Yue YT, Jian ZX (2007) Isolation of simple sequence repeats from groundnut. J Biotechnol 10(3):473–480

- Werner S, Diederichsen E, Frauen M, Schondelmaier J, Jung C (2008) Genetic mapping of clubroot resistance genes in oilseed rape. Theor Appl Genet 116(3):363–372
- Xia Z, Tsubokura Y, Hoshi M, Hanawa M, Yano C, Okamura K, Ahmed TA, Anai T, Watanabe S, Hayashi M, Kawai T, Hossain KG, Masaki H, Asai K, Yamanaka N, Kubo N, Kadowaki K, Nagamura Y, Yano M, Sasaki T, Harada K (2007) An integrated high-density linkage map of soybean with RFLP, SSR, STS, and AFLP markers using a single F₂ population. DNA Res 14:1–13
- Yadava DK, Parida SK, Dwivedi VK, Varshney A, Ghazi IA, Sujata V, Mohapatra T (2009) Cross-transferability and polymorphic potential of genomic STMS markers of *Brassica* species. J Plant Biochem Biotechnol 18(1):29–36
- Yang Y, Xia WW, Zheng YL, Chen L, Liu RJ, Huang CY (2007) Genetic diversity and relationships among safflower (*Carthamus tinctorius* L.) analyzed by inter-simple sequence repeats (ISSRs). Genet Resourc Crop Evol 54(5):1043–1051
- Yi B, Chen Y, Lei S, Tu J, Fu T (2006) Fine mapping of the recessive genic male-sterile gene (Bnms1) in *Brassica napus* L. Theor Appl Genet 113(4):643–650
- Yoon MS, Song QJ, Choi IY, Specht JE, Hyten DL, Cregan PB (2007) BARCSoySNP23: a panel of 23 selected SNPs for soybean cultivar identification. Theor Appl Genet 114(5):885–899
- Yu JK, Tang S, Slabaugh MB, Heesacker A, Cole G, Herring M, Soper J, Han F, Chu WC, Webb DM, Thompson L, Edwards KJ, Berry S, Leon AJ, Grondona M, Olungu C, Maes N, Knapp SJ (2003) Towards a saturated molecular genetic linkage map for cultivated sunflower. Crop Science 43:367–387
- Yue B, Miller JF, Hu J (2007) Experimenting with marker-assisted selection in confection sunflower germplasm enhancement. www.sunflowernsa.com/research/research-workshop/documents/Yue
- Yue B, Vick BA, Yuan W, Hu J (2008a) Mapping one of the two genes controlling lemon ray flower color in sunflower (*Helianthus annuus* L.). J Hered 99:564–567
- Yue B, Xiwen C, Wenge Y, Brady AV, Hu J (2008) Mapping the quantitative trait loci (QTL) controlling seed morphology in sunflower (*Helianthus annuus* L.). www.sunflowernsa.com/research/research-workshop/documents/Yue
- Yue B, Cai X, Vick BA, Huc J (2009) Genetic diversity and relationships among 177 public sunflower inbred lines assessed by TRAP markers. Crop Science 49:1242–1249
- Zhao J, Meng J (2003) Genetic analysis of loci associated with partial resistance to *Sclerotinia* sclerotiorum in rapeseed (*Brassica napus* L.). Theor Appl Genet 106:759–764
- Zhao J, Becker HC, Zhang D, Zhang Y, Ecke W (2006) Conditional QTL mapping of oil content in rapeseed with respect to protein content and traits related to plant development and grain yield. Theor Appl Genet 113(1):33–38
- Zimmerman LH, Smith JD (1966) Production of F1 seed in castor beans by use of sex genes sensitive to environment. Crop Sci 6:406–409