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Broadening the genetic base of sesame (*Sesamum indicum* L.) through germplasm enhancement

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Abstract

Sesame (*Sesamum indicum* L.) is one of the world's oldest oil crops and has been cultivated in Asia from ancient times. India has a rich diversity of this crop and a landrace collection is maintained at the National Genebank at the National Bureau of Plant Genetic Resources (NBPGR). The breeding potential of this germplasm has been hardly exploited to date. The major hindrance for the utilization of these resources is the transfer of diversity into a form that can be easily used by breeders and farmers. As part of a core collection strategy, a selection was made of 24 of the most diverse and unadapted parental lines, including one accession of the wild species *S. mulayanum*, and these were intercrossed in various combinations to maximize genetic diversity and to develop locally adapted pools of genetic resources. A weak and decentralized selection regime was maintained at four selected target sites on the progeny of 103 crosses. The range of variation in the selected F_4 progenies was assessed, and promising types with desired plant characteristics and high seed yield were selected. Realized genetic gains, especially for yield-related traits, were also assessed. Only a limited fraction of the existing diversity held in the genebank was used in the present study and there is much more diversity available for large-scale genetic enhancement of sesame in the future.

Keywords: core collection; germplasm enhancement; *Sesamum indicum* L.

Introduction

Sesame (*Sesamum indicum* L.) is one of the world's oldest oilseed crops and has been cultivated in Asia since ancient times. It is the sixth most important oilseed crop, grown over 7.27 million ha (>50% in Asia, and 30% in Africa), with a total world production of 2.82 million tonnes and an average yield of 388 kg/ha (FAO, 2002). Although its cultivation range stretches between 40°N and 40°S, it is grown mainly in the tropics in smallholdings, often under marginal or stressed conditions. It is an important source of high-quality edible oil and protein food for poor farmers in the major sesame-growing countries. India accounts for 40% of the world's sesame area and 27% of its production (FAO, 2002). As many as 36 species have been described, mostly endemic to Africa, but with a few confined to India (Kobayashi, 1981). Nevertheless, India has a rich diversity of cultivated sesame (Joshi, 1961; Nayar and Mehra, 1970; Simmonds, 1976; Bisht *et al.*, 1998, 1999; Bhat *et al.*, 1999), and it has been suggested that domestication occurred on the Indian subcontinent (Bedigian *et al.*, 1985, 1986).

Sesame productivity is relatively low compared to that of other oilseed crops. The major yield constraints relate to instability in yield, narrow adaptability, drought

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susceptibility, non-synchronous maturity, poor stand establishment, lack of fertilizer response, profuse branching, lack of seed retention, low harvest index and susceptibility to insect pests and pathogens (Thangavelu, 1994). However, cultivation is often confined to marginal and sub-marginal lands, and as a component of mixed cropping systems. Varieties selected from local landraces are generally adapted only to the environments from which they were derived; introduction and introgression of diverse germplasm have not been undertaken on any systematic basis. To maintain and even expand sesame productivity, several key breeding objectives need to be attained. Primary among these are improved yield potential and harvest index, seed retention, uniform maturation through determinate habit, and resistance to insect pests/diseases (Ashri, 1994; Sharma, 1994).

The National Bureau of Plant Genetic Resources (NBPGR), New Delhi, maintains over 6000 accessions of sesame, including the world sesame collection. Wide diversity is available in the existing germplasm for various morphological and yield-related traits (Chopra and Thomas, 1982; Umesh Chandra *et al.*, 1983; Loknathan *et al.*, 1993; Bisht *et al.*, 1998, 1999). By utilizing this genetic diversity, it should be possible to improve the productivity of existing sesame cultivars. The present investigation describes strategies for the use of a core collection to achieve genetic base broadening of sesame. The core was formed from a small set of representative accessions, and these were used to test general combining ability with local germplasm with a particular view to yield enhancement (Frankel and Brown, 1984; Abel and Pollal, 1991; Spagnoletti-Zeuli and Qualset, 1995; Hodgkin *et al.*, 1995; van Hintum, 1999; Bisht *et al.*, 2004).

Materials and methods

The NBPGR sesame core collection consists of 343 accessions (Bisht *et al.*, 1998, 1999), which have been systematically characterized during the last 5–6 years at four NBPGR locations, Delhi, Akola (Maharashtra), Thrissur (Kerala) and Jodhpur (Rajasthan), with data recorded for 32 distinct morphological characters. Locally adapted (but largely unadapted to other locations) genotypes were identified based on ecogeography and morphological characterization/evaluation data and used to select 19 landrace lines for a random intercrossing study. In addition, four exotic accessions and one wild species (*S. mulayanum*) were included to introduce variation for resistance to phyllody and drought tolerance. These 24 accessions (listed in Table 1), selected as parents for intercrossing, showed a high degree of variability with respect to morphological and yield-related traits. Most had only moderate yield potential. In all, 103 crosses in various combinations were made by standard hybridization procedures.

The materials were grown at four target environments: the University of Agricultural Sciences (UAS), Dharwad, and at three NBPGR centres at Cuttack, Amravati and Delhi. Such diverse environments allow the detection and exploitation of genotype × environment interaction. At Delhi, the F_2 progenies were grown in replicated trials (two replications) using a randomized block design. Desired types were selected for further advancement in F_3. Further selections were made within replicated F_3 progeny trials. The identity of each selected F_2 plant progeny was maintained in the later generations. At the F_3 generation only part of the capsules were picked from the selected plants for further progeny advancement. The remaining pods of the selected plants were bulk harvested together with the leftover plants. The F_3 bulk progeny harvest and selected F_3 progenies from the Delhi centre were made available to the breeders at Dharwad, Cuttack and Amravati for assessment of adaptability. Selected F_2-derived F_4 progeny lines were grown in a replicated (three replications) randomized block design adopting recommended agronomic practices at all locations and further selection of superior progeny lines was made at F_4 for desirable plant type and yield potential.

Variation among F_4 progeny lines, and correlations between various yield-related quantitative traits were compared with the parental lines and F_2 bulk progenies to provide a clearer understanding of the attributes of specific pre-breeding lines. Randomized block design data were analysed using the MSTATC Statistical Package (Michigan State University, USA). Realized genetic gain (Falconer, 1989) of selected F_4 progenies over the F_2 bulks (as base populations) was computed for seed yield and other related traits.

Weak and decentralized selection was applied at Dharwad, Cuttack and Amravati in order to initiate the development of location-specific adapted germplasm, which can be expected to take 8–10 years before true potential can be recognized. An important feature of local genetic adaptation is horizontal resistance to diseases by growing the populations in 'hot spots' and allowing natural selection to operate. Data on selections made at the Delhi location and trials of F_4 progenies evaluated at Delhi and Dharwad are presented in this paper in order to demonstrate the potential of landrace germplasm over a relatively short time-scale.

Results

More than 300 single F_2 plant selections were made for various desirable traits from a number of cross

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Table 1. Germplasm accessions used for genetic enhancement of sesame

Accession	Origin	Salient features
IC-204078	Andhra Pradesh	Moderate branching, very early maturing, low plant height, small capsules, low yield potential
IC-204099	Andhra Pradesh	Less branched, early maturing, moderate yield potential
IC-204337	Rajasthan	Less branched, early maturity, medium tall, bold seeds, moderate yield potential, susceptible to phyllody
IC-204524	Gujarat	Moderate branching, medium maturity, relatively longer capsules, low yield potential, susceptible to phyllody
IC-204628	Karnataka	Highly branched, medium tall, medium to late maturity, moderate yield potential
IC-204653	Kerala	Highly branched, medium to late maturity, tall and moderate to high yield potential
IC-204653	Kerala	Moderate branching, late maturity, moderate to high yield potential
IC-204681	West Bengal	Highly branched, multilocular (six to eight), early maturity, moderate yield potential
IC-204773	Nagaland	Highly branched bushy type, late maturity, photosensitive, resistance to phyllody and leaf roller, medium plant height, moderate yield potential
IC-204814	Mizoram	Highly branched, medium to late maturity, medium tall, low yield potential, resistance to phyllody and insect pests
IC-204843	Bihar	Medium branching, multilocular capsules, early to medium maturity, medium tall, bold seeded, moderate to high yield potential
IC-205000	Assam	Highly branched bushy type, late maturity, photosensitive, resistance to phyllody and leaf roller, tall, moderate to high yield potential
IC-205209	Andhra Pradesh	Moderate branching, late maturity, medium tall, low yield potential
IC-205314	Uttar Pradesh	Moderate branching, relatively long capsules, bold seeds, high yield potential, susceptibility to phyllody
IC-205479	Himachal Pradesh	Less branched, early maturity, bold seeds, low yield potential
IC-205509	Orissa	Moderate branching, medium maturity, medium plant height, high yield potential
IC-205595	Orissa	Moderate branching, late maturity, tall, low yield potential
IC-205730	Rajasthan	Unbranched, medium maturity, relatively long capsules, medium tall, bold seeds, low yield potential, susceptible to phyllody
IC-205817	Tamil Nadu	Moderately branched, relatively long capsules, medium to late maturity, tall, moderate yield potential
EC-346125-1	Greece	Moderately branched, tall, medium-sized capsules, early maturity, moderate yield potential
EC-346489	Afghanistan	Late maturity, small capsules, white seeds
EC-346987	Unknown	Moderately branched, medium-sized capsules, moderate yield potential
EC-377025	Somalia	Unbranched, glabrous stem, long capsules, low yield potential, low susceptibility to phyllody
DLH-2 (*S. mulayanum*)	Delhi	Branched, thin glabrous stem, tall, purple flower, black seeds, low susceptibility to phyllody

IC- and EC- prefixes denote accessions of indigenous and exotic origin, respectively.

combinations. Transgressive segregation was revealed for various characters, particularly in crosses involving the most genetically diverse parents. In the F_3 generation, further single plant selections were made and 103 progenies were advanced to F_4. At Delhi, individuals showing early maturity and resistance to biotic stresses and improved yield have been advanced to the F_4 generation. The major emphasis was on achieving wide adaptability together with moderate to high grain yield. F_2 populations of crosses between day neutral and short-day parents demonstrated continuous variation. Additionally, transgressive segregants were observed for both early and late flowering types. Resistance to phyllody and insect pests could be transferred from the photoperiod-sensitive and highly bushy parental lines from the north-eastern region of India and a wild species germplasm, *S. mulayanum* (DLH-2), collected from the Delhi ridge.

The range of variation for various quantitative yield-related traits (Table 2) indicated that there has been substantial genetic improvement in the enhanced progenies for characters such as early flowering/maturity, plant height, number of capsules per plant, capsule length, seeds per capsule and seed yield. The correlations between various pairs of characters of selected F_4 progenies are presented in Table 3. As compared to the F_2 bulk progenies, through selection, a good deal of positive and significant desirable correlations could be established between seed yield and other related traits such as number of capsules per plant, capsule length and 1000-seed weight. Contrary to this, significant negative correlations of seed yield with capsule length and 1000-seed weight were recorded in parental lines and F_2 base populations (Table 3).

Interesting segregating populations were generated from the crosses EC-346125-1 × DLH-2, EC-346489 × DLH-2, EC-377025 × IC-204773, IC-204996 × IC-204653 and IC-205000 × IC-205509. Selections from the crosses involving exotic germplasm and a wild species accession (EC-346125-1 × DLH-2 and EC-346489 × DLH-2) were highly resistant to phyllody, drought tolerant and displayed moderate to high seed yield potential. Substantial genetic gain for seed yield was recorded in these selected progeny lines (Table 4) as compared to F_2 bulk progenies of the respective crosses (as base populations). The selected progenies of crosses involving four indigenous accessions (IC-204996 × IC-204653 and IC-205000 × IC-205509) were exceptionally high yielding with high genetic gain and other desired morphological traits.

Discussion

Locally adapted material from diverse agro-ecological conditions was selected from the core collection, as

Table 2. Range of variation for some yield-related traits of parents, F_2 progeny bulks and F_4 progeny lines

Character	Parents				F_2 progeny bulks				Enhanced F_4 progenies			
	Min.	Max.	Mean	CV (%)	Min.	Max.	Mean	CV (%)	Min.	Max.	Mean	CV (%)
Days to flowering	31.00	70.00	41.94	11.83	29.00	59.00	39.64	19.66	27.0	47.0	36.5	18.9
Days to maturity	69.00	130.00	98.62	8.38	63.00	99.00	78.3	9.53	61.0	97.0	72.1	10.1
First capsule-bearing node	3.00	13.00	7.3	39.29	3.00	16.00	8.20	41.39	3.00	11.00	6.23	27.77
Capsules per node	1.00	3.00	1.01	50.54	1.00	3.00	1.13	48.30	1.00	3.00	1.19	44.54
Plant height (cm)	22.30	120.30	82.47	19.66	26.00	138.00	83.00	27.60	29.0	179.0	87.8	42.0
Branches per plant	0.00	8.00	3.20	45.57	0.00	9.00	4.36	41.30	2.00	6.0	3.5	31.4
Capsules per plant	8.00	84.00	28.81	50.08	10.00	152.00	53.21	53.21	34.60	179.0	88.5	37.5
Locules per capsule	1.00	2.00	1.07	22.30	1.00	2.00	1.02	20.23	1.00	2.00	1.04	20.19
Capsule length (cm)	1.40	3.20	2.22	12.47	1.52	3.60	2.30	13.21	1.80	3.60	2.70	11.80
Seeds per capsule	20.00	78.00	57.57	20.67	27.00	82.00	60.20	13.21	46.00	84.00	63.32	15.29
1000-seed weight (g)	1.50	3.70	2.60	15.62	1.63	3.60	2.70	16.23	2.00	3.40	2.80	8.10
Yield per m^2	23.00	160.00	89.57	68.18	27.00	172.30	93.21	52.39	25.20	182.00	101.20	40.02

Min., minimum; Max., maximum; CV, coefficient of variation.

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Table 3. Correlations between quantitative characters of F_4 progeny lines with F_2 bulks (in parentheses)

Days to flowering	1.00										
Days to maturity	0.81** (0.78*)	1.00									
First capsule-bearing node	0.69** (0.07)	0.51** (0.15)	1.00								
Capsules per node	−0.01 (0.40**)	−0.02 (0.56**)	−0.24* (0.05)	1.00							
Plant height	0.32** (−0.05)	0.35** (0.01)	0.62** (0.16)	−0.07 (−0.05)	1.00						
Branches per plant	−0.27* (−0.25)	−0.29** (−0.24)	0.39** (0.47**)	−0.53** (−0.22)	0.27* (0.26)	1.00					
Capsules per plant	−0.03 (0.18)	−0.01 (0.11)	0.45** (−0.25)	−0.17 (−0.18)	0.71** (−0.07)	0.16 (−0.40**)	1.00				
Capsule length	−0.33** (0.08)	−0.31** (0.11)	−0.19 (−0.12)	−0.01 (0.50**)	−0.03 (−0.03)	−0.09 (0.13)	0.08 (−0.44**)	1.00			
Seeds per capsule	−0.07 (−0.25)	−0.12 (0.23)	−0.10 (−0.62**)	0.05 (−0.44**)	−0.10 (−0.10)	−0.35** (−0.10)	−0.22* (0.32*)	0.31** (0.15)	1.00		
1000-seed weight	0.23* (−0.19)	0.38** (−0.06)	0.20 (0.36*)	−0.09 (0.26)	0.33** (0.11)	0.09 (0.20)	0.23* (0.20)	0.06 (0.22)	−0.28** (−0.15)	1.00	
Yield per m^2	0.07 (−0.22)	0.05 (−0.10)	0.34** (0.07)	−0.28** (−0.49)	0.18 (0.13)	0.07 (0.02)	0.38** (−0.10)	0.23* (−0.62**)	−0.08 (−0.23)	0.24* (−0.47**)	1.00

Values in parentheses are the correlation coefficients of F_2 bulks.
*$P < 0.05$, **$P < 0.01$.

Table 4. Realized genetic gain (%) in yield-related traits of selected F_2-derived F_4 progeny means over F_2 bulk progeny means

Selection	Cross	Plant height	Days to flowering	Days to maturity	Branches per plant	Capsules per plant	Yield per plant
34-1	EC-346125-1 × DLH-2	33.0 (117.0)	25.0 (36.0)	13.4 (71.0)	100.0 (4.0)	337.9 (61.3)	43.6 (5.2)
35-1	EC-346125-1 × DLH-2	46.7 (142.0)	25.0 (36.0)	13.4 (71.0)	50.0 (3.0)	416.7 (124.0)	212.2 (9.5)
55-2	EC-346125-1 × DLH-2	2.0 (121.0)	25.0 (36.0)	7.3 (76.0)	−50.0 (3.0)	62.3 100.6)	98.2 (6.1)
61-2	EC-377025 × IC-204099	0.0 (120.0)	18.6 (35.0)	1.4 (71.0)	200.0 (6.0)	99.2 (109.3)	36.5 (6.1)
40-2	EC-377025 × IC-204773	−1.0 (97.0)	26.5 (36.0)	22.0 (64.0)	−33.3 (4.0)	96.5 (167.0)	62.5 (6.0)
66-1	EC-377025 × IC-204773	65.8 (126.0)	22.4 (38.0)	22.0 (64.0)	66.7 (5.0)	3.1 (67.0)	362.9 (6.6)
21-2	EC-377025 × IC-204996	8.8 (123.0)	9.5 (38.0)	1.3 (74.0)	100.0 (2.0)	62.2 (73.0)	214.5 (5.2)
9-1	IC-204099 × IC-205000	23.1 (96.0)	9.8 (37.0)	13.4 (71.0)	33.3 (4.0)	16.2 (79.0)	222.7 (6.8)
1-1	IC-204681 × IC-204773	29.4 (110.0)	14.5 (47.0)	5.6 (85.0)	0.0 (5.0)	85.7 (113.3)	110.2 (5.8)
27-1	IC-204681 × IC-204773	61.2 (137.0)	25.5 (41.0)	4.4 (94.0)	−40.0 (3.0)	127.9 (139.0)	85.0 (5.1)
11-1	IC-204814-1 × EC-346489	−21.9 (82.0)	26.2 (31.0)	15.6 (65.0)	−40.0 (3.0)	17.1 (44.5)	131.4 (5.7)
26-1	IC-204996 × IC-204653	10.2 (130.0)	8.5 (43.0)	5.1 (74.0)	20.0 (6.0)	−9.1 (83.6)	152.8 (6.6)
63-1	IC-204996 × IC-204653	25.0 (110.0)	29.8 (33.0)	12.8 (68.0)	−33.3 (2.0)	24.4 (36.3)	634.0 (8.3)
37-3	IC-205000 × IC-205509	68.9 (125.0)	32.1 (36.0)	9.1 (70.0)	−25.0 (3.0)	43.2 (71.6)	108.3 (6.3)
38-1	IC-205000 × IC-205509	98.5 (133.0)	32.1 (36.0)	9.1 (70.0)	33.3 (4.0)	10.9 (71.0)	145.6 (6.0)
45-3	IC-205000 × IC-205509	71.6 (127.0)	28.3 (38.0)	5.2 (73.0)	0.0 (4.0)	16.1 (76.6)	226.2 (8.1)
	RT-54 (check)	(87.0)	(37.0)	(73.0)	(5.0)	(56.0)	(5.1)
	RT-127 (check)	(141.0)	(56.0)	(92.0)	(2.0)	(52.0)	(5.3)

Mean values for selected F_4 progenies given in parentheses; realized gains for days to flowering and maturity is for earliness.

parents, for intercrossing. Major emphasis has been given to selecting segregants showing low susceptibility to the major insect pests and pathogens. The parental lines were from the north-eastern region of India (e.g. IC-204773, IC-204814 and IC-205000). These genotypes were photosensitive, highly branched, bushy and later maturing types. When crossed with single stem type accessions with long capsules and early maturity, interesting segregating material with desired traits such as moderate branching (two to three), medium maturity and long capsules with high seed density was generated. F_2 populations from crosses between day-neutral and short-day cultivars demonstrated continuous variation for flowering time. On the basis of high levels of heritability values (data not shown) most of the variability seen in these F_2 populations was of genetic origin. Additionally, transgressive segregants were observed for both early and late flowering types. Resistance to phyllody and insect pests was transferred from the photoperiod-sensitive and highly bushy parental lines from the north-eastern region of India and a wild species germplasm, *S. mulayanum* (DLH-2), collected from the Delhi ridge.

The range of variation for various quantitative yield-related traits (Table 2) indicated substantial genetic improvement in the enhanced progenies for characters such as early flowering/maturity, plant height, number of capsules per plant, capsule length, seeds per capsule and seed yield. Developing ideotypes showing wide adaptability, and high and stable yield, for a wide range of environments appears to be possible. There remains sufficient variation among F_4 progenies to allow selection for resistance to biotic/abiotic stresses, desirable plant types for different cropping systems and seed yield. The correlations between various pairs of characters (Table 3) can help to provide indirect selection tools

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for high-yielding types. However, to realize significant genetic improvement in sesame, the number of capsules per node, the number of capsules per plant, the capsule length and the 1000-seed weight need to be considered together during the selection process.

Some of the uni-culmed (unbranched) type selections made from the cross EC-346125-1 × DLH-2 were relatively low yielders on per plant basis but may be suitable under medium to high inputs and high plant density. Moderately branched types at lower nodes are probably more suited to low input conditions. Sharma (1985) and Thangavelu *et al.* (1985) recommended plant types with two to three branches and uniform synchronized capsule maturity as the ideal plant types under Indian conditions. The uni-culmed types mostly carried three capsules per node, rather than the single capsule carried by branched types. Transgressive segregants from the cross EC-341125-1 × DLH-2, however, included branched type progenies with multiple capsules. Capsule length and the number of capsules per node have been reported to be neutral traits in determining seed yield (Ashri, 1988) but this study established a positive significant association between capsule length and seed yield in some progenies. Similarly, high-yielding selections could be made for branched type progenies with multiple capsules per node.

In this study, a number of diverse parental lines were crossed in various combinations, and a weak decentralized selection was maintained at four target environments. The programme was kept distinct from conventional breeding programmes. Our results demonstrate the potential of germplasm accessions held

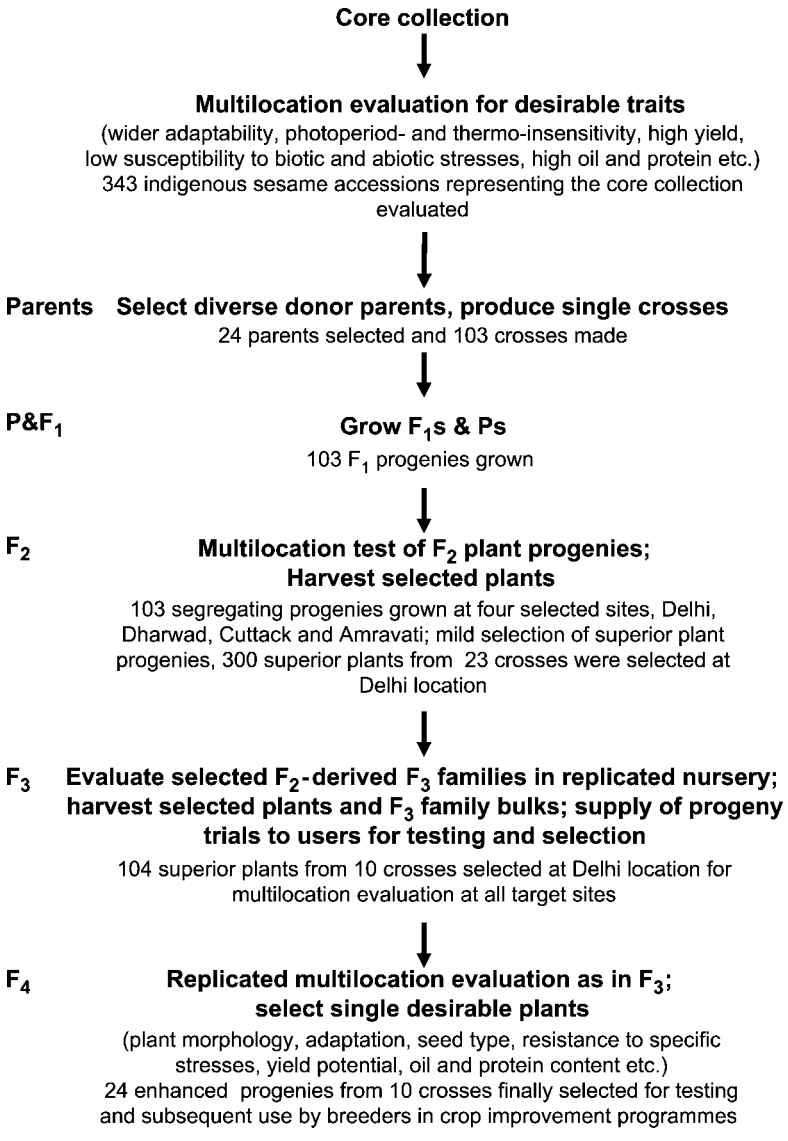

Fig. 1. Strategy for the use of a core collection in germplasm enhancement.

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in genebanks for use in crop improvement through pre-breeding over a relatively short time-scale. We have shown that the core sesame collection is a useful resource for starting material for germplasm enhancement, and we suggest that the enhanced materials (listed in Table 4) (Fig. 1) derived will be attractive to plant breeders. These lines are currently under multilocation evaluation at five breeding centres under the All India Coordinated Sesame Improvement Programme. Of course, only a limited fraction of total diversity present in the core collection was utilized in the present study, allowing plenty of scope for any future large-scale sesame genetic base-broadening programme. Such programmes require an appraisal of the state of diversity of the crop and of the state of use of diversity of the crop that would help to provide a more objective basis for future needs and priorities (Cooper *et al*., 2001; Spillane and Gepts, 2001; Spoor and Simmonds, 2001).

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