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INDUCED ALLOTETRAPLOIDY IN SESAME

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ABSTRACT

Allotetraploidy was induced by means of colchicine treatment in *Sesamum indicum* L. × S. *mulayanum* Nair, hybrids. The allotetraploid resembled diploid hybrid having pansy violet colouration of corolla (intermediate between two parents), blackish seed coat with reticulation and resistance to insect, *Antigastra catalaunalis* (like wild parents), but it differed from the parents as well as the diploid hybrid showing luxurious growth in respect of height, branching, flower, fruit and seed characters. Gametic complement revealed n = 26 chromosomes appearing in different combinations of bivalents (15.6), quadrivalents (5.1), trivalents (0.04) and univalents (0.16) per cell. Allosyndesis leading to multivalent association of chromosomes might be responsible for reduction in pollen fertility and seed formation in the allotetraploid. But total yield in the 4n hybrid was higher than that in the diploid. Genetic relationship between the two species has also been indicated.

Key words: *Sesamum*, hybrid, allotetraploidy.

Allopolyploidy is often used as an important tool in plant breeding. Facilitating transfer of desirable traits through interspecific hybridization, it offers scope of understanding genome relationship [1, 2] and enables to solve breeding problems [3]. Allopolyploidy was successfully exploited in transfer of disease resistance [4, 5] and in creation of the novel crop, Triticale (6n), incorporated with desirable potentialities [6]. Reports of removal of interspecific sterility through amphidiploidy in *S. indicum* × *S. prostratum*, *S. orientale* × *S. prostatum* and *S. indicum* × *S. laciniatum* are available [7- 12]. Successful hybridization of *S. indicum* × *S. mulayanum* indicated genetic closeness of the two species facilitating transfer of resistance to *Antigastra catalaunalis* from the wild parent *S. mulayanum*, which is desired to avert loss of yield in sesame [13]. For better understanding of the interrelationship between the two genomes, the interspecific hybrid of *S. indicum* × *S. mulayanum* was cytogenetically evaluated in the present investigation through allopolyploidization.

MATERIALS AND METHODS

The shoot apices of F_1 hybrids of *Sesamum indicum* L. × *S. mulayanum* Nair cross were treated at the first pair of leaf stage with 0.25% freshly prepared aqueous solution of clochicine for 6 hours for two consecutive days by cotton plug method. Requisite precautions were taken to prevent drying up of the colchicine solution and to maintain its concentration constantly. Each day after the treatment the shoot apices were washed carefully.

Phenotypic manifestations of the F_1 hybrids and the allotetraploid (C_0 generation) were studied under identical field conditions.

Meiotic studies were carried out using flower buds of appropriate size fixed at 8.30 A.M. to 9.30 A.M. in propiono-ethanol (1:3) for one hour and anthers were smeared in 1% propiono-carmine solution. Pollen sterility was determined by propino-carmine method.

RESULTS AND DISCUSSION

One of the treated hybrids was morphologically distinct from the diploid hybrids. Its allotetraploid (n = 26) nature was later on confirmed by chromosome count and pollen size as well as fertility. It was reported earlier that the diploid hybrid could be identified by pansy violet colouration (intermediate between two parents) of corolla, and violet colour along dehiscence line on anther, blackish reticulate seed coat and resistance to insect, *Antigastra catalaunalis* like wild parent [13]. The allotetraploid resembled the diploid hybrid in these parameters but the former was distinguished from the latter by exuberence of growth (Fig. 1) increased root length and plant height, high fruit set, increased number of branches, bigger size of flower (Fig. 2) and seed, and heavier weight and higher germination percentage of seeds (Table 1). These gigas phenotypic variations in the allotetraploid might be the possible consequence of enhanced biochemical effect due to favourable genetic interactions in the duplicated genome of the hybrid.

Meiotic analysis of metaphase I and diakinesis stages in 87 PMCs has revealed the following types of average chromosome association per cell –15.6 II (12-18) + 5.1 IV (3-6) + 0.04 III (0-2) + 0.16 I (0-4) (Fig. 3). Anaphasic separation of chromosomes was affected but equal separation of 26-26 chromosomes was noted (Fig. 4) in 67.66% cases. Pollen sterility (18%) has marginally increased compared to F_1 hybrid (12%) with subsequent reduction in seed formation, although fruit setting enhanced considerably. Irregular pairing and other anaphasic disturbances might be ascribed for reduced pollen fertility and seed formation.

In the diploid hybrid frequent occurrence of four univalents has been marked but bivalent association was predominant (66%) apparently due to homology between

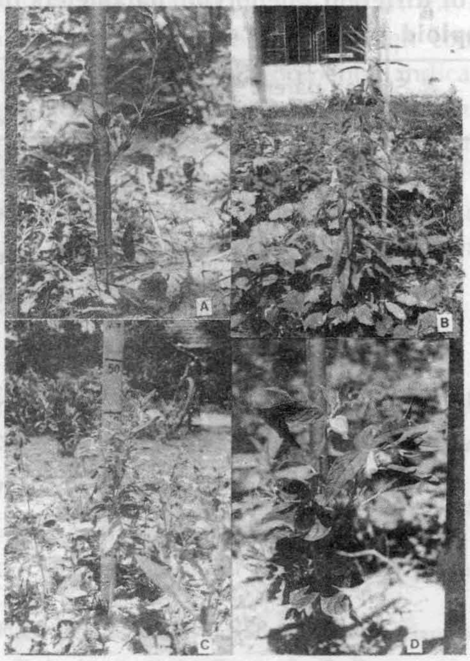

Fig. 1. Entire plant of *Sesamum indicum* (A), *Sesamum mulayanum* (B), F_1 hybrid (C) and allotetraploid (D)

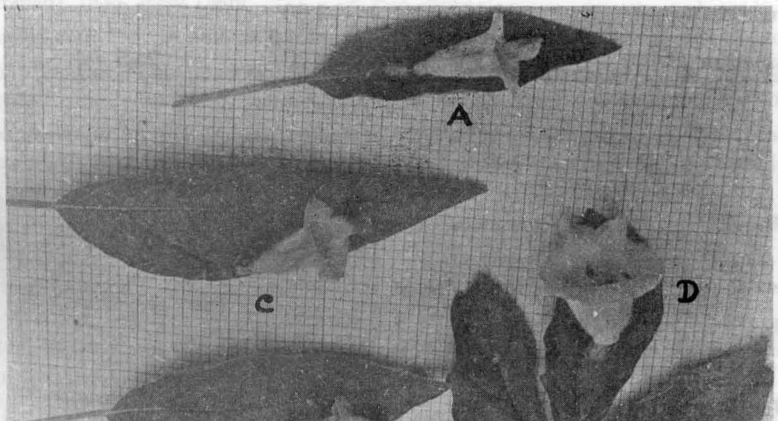

Fig. 2. Colour and size of flower of *Sesamum indicum* (A), *S. mulayanum* (B), F_1 hybrid (C) and allotetraploid (D)

Table 1. Comparison of different phenotypic parameters in the parents, F_1 hybrids and allotetraploid plant

Plant material character	Stigma parent (*S.indicum*)	Pollen parent (*S.mulayanum*)	F_1 hybrid plant (2n)	Allotetraploid plant (4n)
Root length (cm.)	15.12 (±5.04)	14.50 (±7.98)	13.01 (±2.20)	18.0
Stem height (cm.)	95.32 (±4.96)	89.42 (±8.23)	124.00 (±5.56)	155.0
Total branch (no.)	6.48 (±5.90)	3.80 (±2.57)	6.51 (±5.72)	13.0
Primary branch (no.)	3.27 (±1.34)	2.31 (±1.49)	5.25 (±3.20)	6.0
Flower				
Corolla tube length (cm.)	3.33 (±0.21)	2.90 (±0.20)	3.50 (±0.30)	4.02 (±0.25)
Corolla tube breadth (cm.)	2.00 (±0.15)	1.92 (±0.16)	2.31 (±0.16)	2.85 (±0.17)
Pollen size (polar axis) in µm)	67.81 (±4.90)	63.92 (±1.97)	19.42 (±1.93)	40.21 (±11.16)
Pollen sterility (%)	26.25	28.75	12.00	18.00
Total capsule/plant (no.)	58.25 (±1.82)	41.36 (±0.08)	50.09 (±2.62)	95.00
Seed/capsule (no.)	55.40 (±7.21)	56.50 (±1.00)	52.31 (±4.04)	26.12 (±4.81)
Seed length (cm.)	0.31	0.30	0.30	0.35
1000-seed weight (gm.)	2.10	1.80	2.00	2.75
Seed germination (%)	68.1	19.00	24.5	32.00

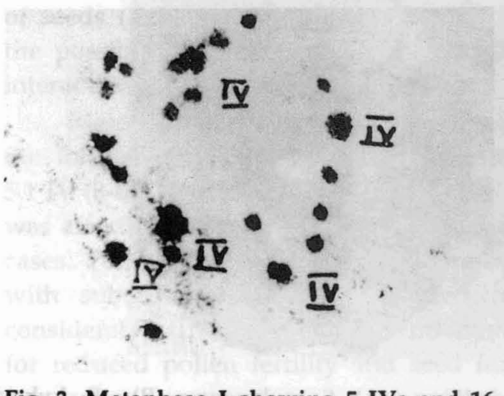

Fig. 3. Metaphase I showing 5 IVs and 16 IIs in the allotetraploid

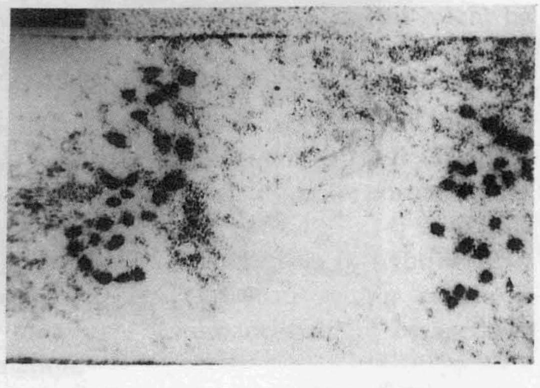

Fig. 4. Anaphase I showing 26-26 regular distribution in the allotetraploid

the parental genomes [13]. Multivalent association in the allotetraploid occurred in low frequency indicating preferential pairing between complete homologous mates from the same parental genome. This phenomenon indicates that the two parental genomes have differentiated structurally, though the residual homology is sufficient to result in predominant bivalent pairing in F_1 hybrids. It can be inferred that the chromosomes of the two species belong to the same genomic group. Present investigation has also brightened the possibility of improvement in the yield potentiality of sesame by transferring insect resistance from *S. mulayanum* and utilizing interspecific hybrid vigour through allopolyploidy.

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