



CODEN [USA]: IAJPBB

ISSN: 2349-7750

**INDO AMERICAN JOURNAL OF  
PHARMACEUTICAL SCIENCES**<http://doi.org/10.5281/zenodo.1020114>Available online at: <http://www.iajps.com>

Research Article

**CYTOGENETICAL STUDIES OF MACROMUTANTS  
INDUCED BY NANOPARTICLES (Cu, CdS, CuO and  
ZnO-NPs) IN *SESAMUM INDICUM* L.**Debadrito Das<sup>1</sup>, Animesh Kumar Datta <sup>1\*</sup>, Divya Vishambhar Kumbhakar <sup>1</sup>, Bapi Ghosh<sup>1</sup> and Ankita Pramanik <sup>1</sup>, Sandip Halder <sup>2</sup><sup>1</sup> Department of Botany, Cytogenetics, Genetics and Plant Breeding Section, University of Kalyani, Kalyani 741235.<sup>2</sup> Department of Botany, Berhampore Girl's college, Berhampore 742101.**Abstract**

A total of 23 phenotypic mutants were screened in  $M_2$  plant population (7112) of *Sesamum indicum* L. (Family: Pedaliaceae) affecting seedling colour, leaf traits, stem characteristics, branching nature, floral colour, fruit characteristics and maturity following dry seed (moisture content – 7.40%) treatments with nanoparticles (copper, cadmium sulphide, copper oxide and zinc oxide – 1.00, 2.00 and 4.00  $\mu\text{g/ml}$ , 3 and 6h durations), ethyl methanesulphonate (EMS – 0.25, 0.50 and 1.00%, 3 and 6h) and gamma irradiations (50, 100, 200, 400 and 600 Gy). Viable mutation frequency is found higher in gamma irradiation followed by ZnO-NPs, CuO-NPs, Cu-NPs, CdS-NPs and EMS. A total of 9 different macromutants types are found in Cu-, CuO- and ZnO-NPs, 11 in EMS and 13 in CdS-NPs and gamma irradiations. Excepting viridis (non-viable), all macromutants bred true at  $M_3$ . Reciprocal crossings performed between mutant and normal plant types suggest that the mutant traits are controlled by nuclear genes (monogenic recessive and digenic) and they segregated in accordance to Mendelian pattern of segregations. Meiotic analyses reveal that normal and mutant plants were cytologically alike ( $2n=26$ ) suggesting that mutation is not the consequence of chromosomal disturbances. Results highlight mutagenic potentiality of NPs alike to that of the conventional mutagens used as positive controls.

**Key words:** *Sesamum indicum*, macromutation, nanoparticles, EMS, gamma irradiations, cytogenetical studies**Corresponding author:****Animesh Kumar Datta,**Department of Botany,  
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Please cite this article in press as Animesh Kumar Datta *et al*, *Cytogenetical Studies of Macromutants Induced by Nanoparticles (Cu, CdS, CuO and ZnO-NPs) in Sesamum indicum* L., *Indo Am. J. P. Sci*, 2017; 4(10).

**INTRODUCTION:**

Nanoparticles (NPs, at least one dimension <100 nm) are reported to interact with DNA of plant species [1] causing DNA lesions (Ag-NPs) and mispairing during replication and bringing about mutagenic changes [2] or fixed into mutation [3]. Nel et al. [4] also highlighted that carbon nanotubes (CNTs) can induce DNA damage and mutagenesis. Kumbhakar et al. [5,6] opined that Cu- and CdS-NPs inducing chromosomal alterations in meiotic cells can bring about heritable consequences in subsequent generations. Halder et al. [7,8] pioneerly reported stable, heritable phenotypic changes in *Macrotyloma uniflorum* as the consequences of Cu- and CdS-NPs treatments. Therefore, NPs interaction with plant DNA is significant for genome alteration which may lead to gene mutation. If so, it will be opening up new dimension in agriculture science and crop improvement. The present endeavour highlights the potentiality of engineered nanoparticles (copper – Cu, cadmium sulphide – CdS, copper oxide – CuO and zinc oxide – ZnO) in inducing stable, heritable phenotypic mutation in *Sesamum indicum* L. var. B67 (Family: Pedaliaceae, common name – sesame, plant species yielding oil of commerce along with immense pharmaceutical importance – [9,10]) in comparison to conventional mutagens ethyl methanesulphonate (EMS) and gamma irradiations. Cytogenetical aspects of the induced mutants are described.

**MATERIALS AND METHODS:****Germplasm**

*Sesamum indicum* L. var B67 (moisture content: 7.40%) seeds were collected from Pulse and Oil Seed Research Station, Govt of West Bengal, Berhampore, India as breeder stocks.

**Nanoparticles**

Copper, cadmium sulphide, copper oxide and zinc oxide nanoparticles were synthesised using wet chemical co-precipitation techniques and opto-physically characterised (data published elsewhere)

**Treatments**

Seeds of variety B-67 were exposed to synthesized nanoparticles (1.0, 2.0 and 4.0 µg/ml, 3 and 6 h duration) and to conventional mutagens (EMS: 0.25, 0.50 and 1.00%, 3 and 6 h, diluted in 0.2 M KH<sub>2</sub>PO<sub>4</sub>:0.2 M K<sub>2</sub>HPO<sub>4</sub> :: 50.3:49.7, pH 6.8; Gamma irradiations: 50, 100, 200, 400 and 600 Gy, source: Co<sup>60</sup>, source to distance 10 cm, dose rate 35.5 Gy/ min). Treated seeds (NPs and EMS) were washed in ddH<sub>2</sub>O for 2 h. Untreated seeds and seeds treated with bulk materials (4.0 µg/ml, 6h) were kept as controls. Two hundred seeds were exposed in each lot.

**Raising of plant population**

Treated (NPs, EMS and gamma irradiations) and control (dry and bulk CdS) seeds (100 seeds from

each treatment) were sown in experimental field plot of the Department of Botany, Kalyani University (West Bengal plain) in 4th week of February 2013 to raise M<sub>1</sub> population (February to July as irrigated crop). Selfed seeds (first formed floral buds were bagged) of each surviving M<sub>1</sub> plants were collected in separate zipped polythene packets and stored in a desiccator. M<sub>2</sub> population was grown from selfed M<sub>1</sub> seeds in plant to row progenies in the year 2014. Distance between plants and rows were maintained uniformly as 15 cm and 30 cm respectively.

**Detection of macromutants and its inheritance**

Phenotypic variants [distinctive phenotypic trait(s) variation from normal trait(s)] were screened from seedling to maturity of M<sub>2</sub> plants. The phenotypic variants were confirmed as macromutants at M<sub>3</sub> from selfed segregation and from reciprocal crossings. Macromutant frequency was estimated as per 100 M<sub>2</sub> plants [11]. No fertilizer application was made during plant growth period.

M<sub>2</sub> mutants (used as female parent) were crossed with pollen grains (90% to 98% pollen grain fertility) from control plants (possessing normal phenotypic traits) and F<sub>1</sub> plants were raised. All F<sub>1</sub> were phenotypically normal. F<sub>1</sub> plants were selfed and F<sub>2</sub> progenies were grown. Segregation pattern obtained were computed following  $\chi^2$ -test analysis for study of inheritance of trait(s).

**Meiotic chromosome behaviour**

Meiotic chromosome behaviour of mutants and as well as of control plants were assessed at M<sub>3</sub>. Floral buds of suitable sizes of each plant type were fixed (5 am–6 am; pilot trials reveal best time for detection of divisional plates) in Carnoy's fixative (ethanol: acetic acid: chloroform::6:3:1) for a period of 72 h. Three changes were given in the fixative at an interval of 24 h. Floral buds were subsequently preserved in 70% alcohol under refrigeration (16°C±1°C). Pollen mother cells (PMCs) and pollen grain obtained from anther squash preparations were stained in 2% aceto-carmin solution. Uniformly stained pollen grains were considered as fertile [12]. Metaphase I (MI) and anaphase I (AI) cells were observed. Suitable cytological preparations were photomicrographed.

**RESULT AND DISCUSSION:****Macromutant types and frequency**

A total of 23 distinct phenotypic variants are screened from 7112 plant population at M<sub>2</sub> following NPs and conventional mutagen treatments and the variants are confirmed as mutants at M<sub>3</sub>. Out of the 23 types, only one (*viridis*) mutant type is found non-viable as it dried up at the seedling stage. The mutant types recorded are 9 in Cu-, CuO- and ZnO-NPs, 13 in CdS-NPs, 11 in EMS and 13 in gamma irradiations. Calculated viable mutation frequency across doses

(Figure 1) is 1.06% (total-1.06%) in Cu-NPs, 0.96% (total-0.96%) in CdS-NPs, 1.17% (total-1.17%) in CuO-NPs, 1.30% (total-1.30%) in ZnO-NPs, 0.61% (total-0.70%) in EMS and 1.51% (total-1.51%) in gamma irradiations. Mutation frequency is not dose dependent. Compared to normal trait(s) (Figure 2a), the macromutants noted are found to affect seedling colour (*viridis*), leaf trait (*broad leaf I and II, coarse leaf, narrow leaf, ovate leaf, crumpled leaf, elongated pinnae I and II*

and *quadri-petiolar leaf*), stem characteristics (*thick stem* – Figure 2f), branching pattern (*lax branching, branching from base, bushy and unbranched* – Figure 2e), floral characteristics (*multichambered fruit* – Figure 2d, *tri- and quadri-axillary fruit* – Figure 2b,c and *globular fruit*) and maturity (*early flowering*). All the treating agents show predominance of mutation affecting leaf traits.

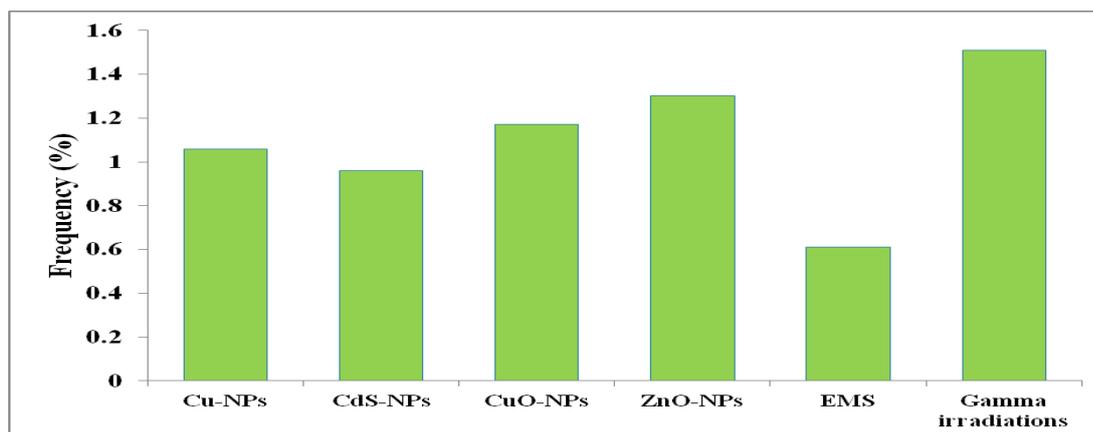


Fig 1: Viable mutation frequency in different treating agents.



Fig 2: Normal (a) and mutant (b–f) plant types of *Sesamum indicum*. (a) Normal; (b) *quadra-fruits per node*; (c) *tri-fruits per node*; (d) *multilocular fruits*; (e) *unbranched*; (f) *thick stem with long petiole*.

**Table 1: Overview of the occurrence of macromutants in different treated materials across doses**

Plant type	EMS	Gamma irradiation	Cu-NPs	CdS-NPs	CuO-NPs	ZnO
<i>Viridis</i>	0.15	-	-	-	-	-
<i>Broad leaf I</i>	0.08	-	0.15	0.09	0.16	0.24
<i>Broad leaf II</i>	-	-	0.15	-	0.16	-
<i>Elongated petiole I</i>	-	0.43	-	0.13	-	0.18
<i>Elongated petiole II</i>	-	-	-	0.11	0.30	0.24
<i>Quadripetiolar node</i>	-	-	-	-	-	0.03
<i>Coarse leaf</i>	0.08	0.12	0.15	0.09	0.14	0.09
<i>Thick stem</i>	-	0.27	0.15	0.02	0.19	0.21
<i>Crumpled leaf</i>	-	0.04	-	-	-	-
<i>Ovate leaf</i>	-	0.04	-	-	-	-
<i>Small leaf</i>	0.04	-	-	-	-	-
<i>Narrow leaf</i>	-	-	-	0.09	-	-
<i>Branching from base</i>	0.04	-	-	0.09	0.04	0.03
<i>Unbranched</i>	0.04	0.04	-	-	-	-
<i>Bushy</i>	0.04	0.12	-	-	0.07	-
<i>Dwarf</i>	0.08	0.12	-	-	-	-
<i>Pigmented flower</i>	0.08	-	0.06	0.02	-	-
<i>White flower</i>	0.04	0.08	0.03	0.02	-	0.12
<i>Early flowering</i>	-	-	-	0.07	-	-
<i>Triaxillary fruits</i>	-	0.04	-	0.02	-	-
<i>Quadriaxillary fruit</i>	-	0.19	0.15	0.02	-	-
<i>Globular fruit</i>	-	-	0.03	-	0.04	-
<i>Multichambered fruit</i>	0.11	0.04	0.06	0.09	0.07	0.18
<b>Total</b>	11	12	09	13	09	09

**Table 2: Male meiotic configurations and pollen grain fertility in normal and mutant plant types at M<sub>3</sub>**

Plant types	No. of PMCs scored at MI	Mean/cell		No. of cells scored at AI	PMCs with 13/13 segregation (%)	No. of pollen grains scored	Pollen grain fertility (%)
		II	I				
Normal	77	12.93	0.14	28	100.0	773	87.58
<i>Broad leaf I</i>	70	12.90	0.20	37	100.0	360	77.78
<i>Broad leaf II</i>	83	12.89	0.22	52	100.0	396	75.42
<i>Coarse leaf</i>	66	12.79	0.42	21	90.5	563	67.50
<i>Ovate leaf</i>	93	12.91	0.18	17	100.0	910	65.71
<i>Narrow leaf</i>	82	12.88	0.24	34	100.0	838	74.34
<i>Elongated petiole</i>	85	12.90	0.20	29	100.0	202	78.70
<i>Thick stem</i>	87	12.93	0.14	19	100.0	565	31.86
<i>White flower</i>	62	12.90	0.20	33	96.9	382	78.70
<i>Pigmented flower</i>	61	12.89	0.22	16	100.0	272	64.10
<i>Bushy</i>	96	12.80	0.40	43	90.7	502	81.48
<i>Unbranched</i>	71	12.87	0.26	28	100.0	267	62.27
<i>Branching from base</i>	51	12.92	0.16	31	100.0	462	90.46
<i>Triaxillary fruit</i>	67	12.87	0.26	29	100.0	218	72.17
<i>Quadriaxillary fruit</i>	81	12.95	0.10	27	100.0	466	76.40
<i>Tripetiolar node</i>	89	12.92	0.16	21	100.0	577	79.40
<i>Multichambered fruit</i>	69	12.88	0.24	37	100.0	455	84.36
<i>Globular fruit</i>	58	12.93	0.14	16	100.0	182	59.86
<i>Dwarf</i>	61	12.71	0.58	36	83.3	269	4.12
<i>Early flowering</i>	74	12.91	0.18	22	100.0	773	87.58

Broad leaf II, narrow leaf, elongated petiole II, quadri-petiolar node, early flowering and globular fruit mutants are scored specifically in NPs treated population. No mutants are spotted specific to Cu- and CuO-NPs whereas narrow leaf and early flowering plant types are identified only in CdS-NPs treated population. Quadri-petiolar node mutant plant type is specific to ZnO-NPs. Few mutants are also found to occur only in conventional mutagen treatments (EMS- *small leaf* and *dwarf*; gamma irradiation-*crumpled leaf*, *ovate leaf* and *unbranched*). Tri- and quadri-axillary fruit per node, unbranched (provide enhance plantation per unit area), bushy and branching from base are most significant mutants in the plant species which closely correspond to the plant ideotype being looked for in the species. Furthermore enhance yield in the mutants will be significant for pharmacological practices. No macromutants are scored in dry control and bulk controls.

Across doses of treatments, macromutants appeared in the following order; Cu- *thick stem* > *broad leaf I* = *broad leaf II* = *coarse leaf* = *multichambered fruit* > *pigmented flower* = *white flower* = *globular fruit* > *quadra-axillary fruit*, CdS- *thick stem* > *elongated petiole I* = *triaxillary fruit* > *elongated petiole II* > *broad leaf I* = *narrow leaf* = *coarse leaf* = *multichambered fruit* > *early flowering* > *white flower* > *pigmented flower* = *branching from base* = *quadra-axillary fruit*, CuO- *elongated petiole I* > *thick stem* > *broad leaf I* = *broad leaf II* > *coarse leaf* > *multichambered fruit* = *globular fruit* >

*bushy* > *branching from base*, ZnO-NPs - *broad leaf I* = *elongated petiole I* > *thick stem* > *elongated petiole I* = *multichambered fruit* > *white flower* > *coarse leaf* > *quadri-petiolar node* = *branching from base*, EMS- *viridis* > *multichambered fruit* > *broad leaf* = *coarse leaf* = *dwarf* > *small leaf* = *branching from base* = *unbranched* = *bushy* = *white flower* and gamma irradiations - . In the present study, most of the identified mutant plant types are distributed uniformly irrespective of nature of the treating agents thereby suggesting the existence of possible genomic hotspot prone to treating agents. Thus, the NPs possesses mutagenic potentiality and can bring about similar phenotypic alterations as that of the conventional mutagens.

#### Meiotic analysis of the macromutants

Male meiotic analysis reveals  $2n=26$  always in control and mutant plant types (Figure 3a-d). Meiotic study from  $M_3$  plant types suggests that mean chromosomal association per cell is  $12.93II+0.07I$  in untreated control plant and it ranges from  $12.71II+0.29I$  to  $12.95II+0.05I$  in mutants. Most of the mutants show balanced anaphase I (Figure 3d) segregation (13/13) excepting coarse leaf (90.5%), white flower (96.9%), bushy (90.7%) and dwarf (83.3%) plant types. Pollen grain fertility is 87.6% in control and it reduces in mutants (87.6%-early flowering to 4.1%-dwarf) excepting branching from base (90.5%). Meiotic studies reveal that the mutants are the consequence of gene mutation rather than chromosomal anomalies.

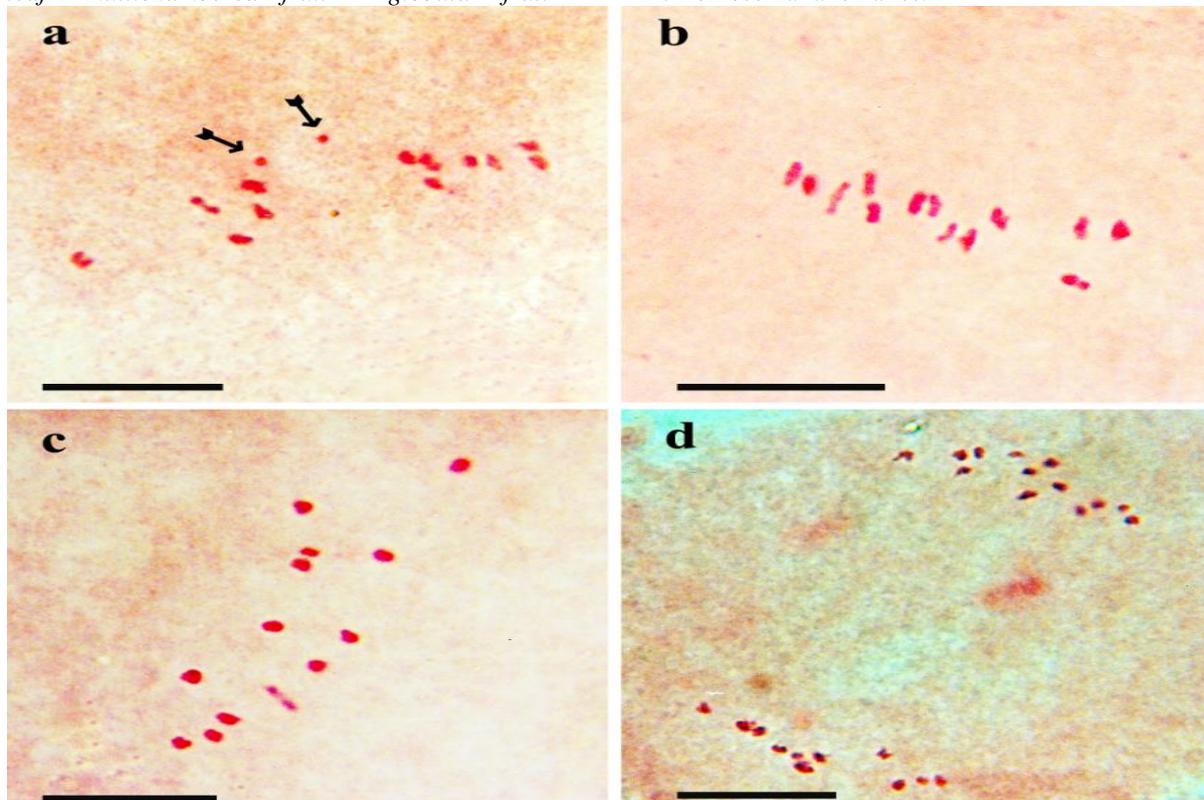


Fig 3: Meiotic configurations of *S. indicum* showing  $2n=26$  chromosomes at metaphase I (a-b) and anaphase I (c) (a)  $12II+2I$  (↔); (b-c)  $13II$ ; (d)  $13:13$  separation.

***Inheritance patterns of the mutant traits***

Reciprocal crossing performed between control and mutant plant types yield all F<sub>1</sub> plants with normal phenotype(s). F<sub>1</sub> plant types are selfed which segregated at F<sub>2</sub> into normal and mutant phenotypes. Segregation analysis using  $\chi^2$  test suggests mutant trait(s) inheritance are in accordance with Mendelian pattern. Mutant traits are either monogenic (3:1–*coarse leaf, ovate leaf, elongated petiole I, thick stem, white flower, pigmented flower, bushy, unbranched, globular fruit, dwarf, early flowering and narrow leaf*) or digenic (9:7–*broad leaf I and II, triaxillary fruit, quadraxillary fruit, tripetiolar node, multilocular fruit*; 15:1–*branching from base*) recessive in nature. Significantly, the mutant namely *broad leaf I* and *elongated petiole I* (Figure 2f) are associated with *thick stem* trait always. On selfing the mutants with associated traits bred true at M<sub>3</sub>. No segregants between the associated mutant traits is noted neither at F<sub>1</sub> reciprocal crossing (between normal and mutant plant type) nor selfed progenies at F<sub>2</sub> suggesting possible pleiotropic gene action controlling the mutants with associated traits. Furthermore, reciprocal crossings yielding similar results in all cases indicate that the mutant traits are controlled by nuclear genes.

**CONCLUSION:**

The present investigation highlights that NPs (Cu, CdS, CuO and ZnO) can induce stable, heritable (in accordance with Mendelian segregation pattern) phenotypic mutations like that of conventional mutagens. However, experimental novelty using next generation sequencer (NGS) can through more light on nano-bio interaction specifically in understanding the role of NPs interacting with DNA for genomic alteration.

**ACKNOWLEDGEMENTS**

Financial assistance from DST, GOI, INDIA is gratefully acknowledged.

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