

# MUTATIONAL ANALYSIS OF PLOIDY LEVEL IN *ORYZA SATIVA*

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SINCE the determination of chromosome number in *Oryza sativa* by Kuwada<sup>7</sup> divergent views as to whether it is a diploid or a secondary auto- or allopolyploid, have been expressed by various workers. Based on the occurrence of secondary association Lawrence<sup>8</sup> considered rice as a secondary polyploid derived from an ancestor having seven pairs of chromosomes. Sakai,<sup>12</sup> Nandi<sup>10</sup> and Okuno,<sup>11</sup> on the other hand, favoured five as the basic number. Yamaura<sup>18</sup> visualized rice as an allopolyploid derived from forms having five and seven pairs of chromosomes. From the results obtained with haploid rice, Hu<sup>4,5</sup> argued in favour of *O. sativa* being a secondary polyploid. The results of Morinaga and Fukushima,<sup>9</sup> Hirayoshi,<sup>3</sup> Shastry *et al.*,<sup>14</sup> Bouharmont,<sup>1</sup> Sen<sup>13</sup> and Katayama<sup>6</sup> however do not support this hypothesis.

In the present study, an attempt was made to understand the ploidy level in rice based on its radiobiological response.

Two subspecies of *O. sativa*, namely *indica* and *japonica* represented respectively by the varieties Taichung Native-1 and Taichung 65 were treated with several doses of gamma-rays and Ethylmethane sulfonate (EMS). The chlorophyll mutation frequency was estimated as percentage of plant and spike progenies segregating in the  $M_2$ . In  $M_3$  two types of populations were grown. First, the progenies of normal-looking plants occurring in the  $M_2$  families containing mutations were grown in separate family rows. Secondly, the progenies of  $M_2$  families in which no phenotypically detectable mutation occurred were grown in separate family rows.

Estimation of mutation frequency as measured by the percentage of families segregating for chlorophyll mutations in these two types of populations showed that the  $M_3$  families derived from families segregating for mutations in the  $M_2$  had more mutations than those derived from families which did not contain mutations in the  $M_2$ . However, on the whole, the mutation frequency in  $M_3$  was lower than in  $M_2$  (Figs. 1, 2, 3, 4). Thus, several of the phenotypically normal plants in segregating  $M_2$  lines must have been heterozygous for recessive mutations. An extremely low frequency of mutations realised in  $M_3$  in non-

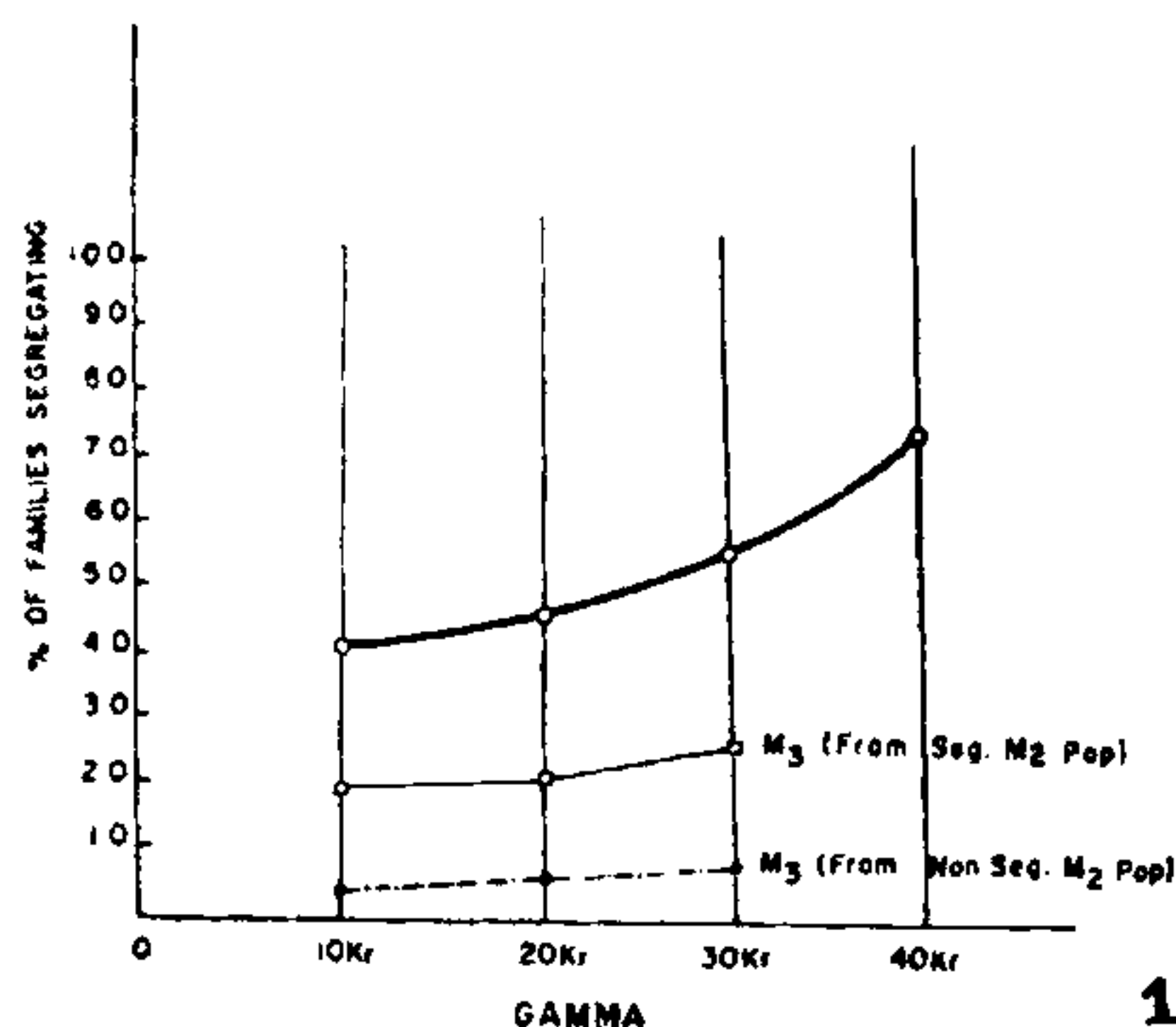
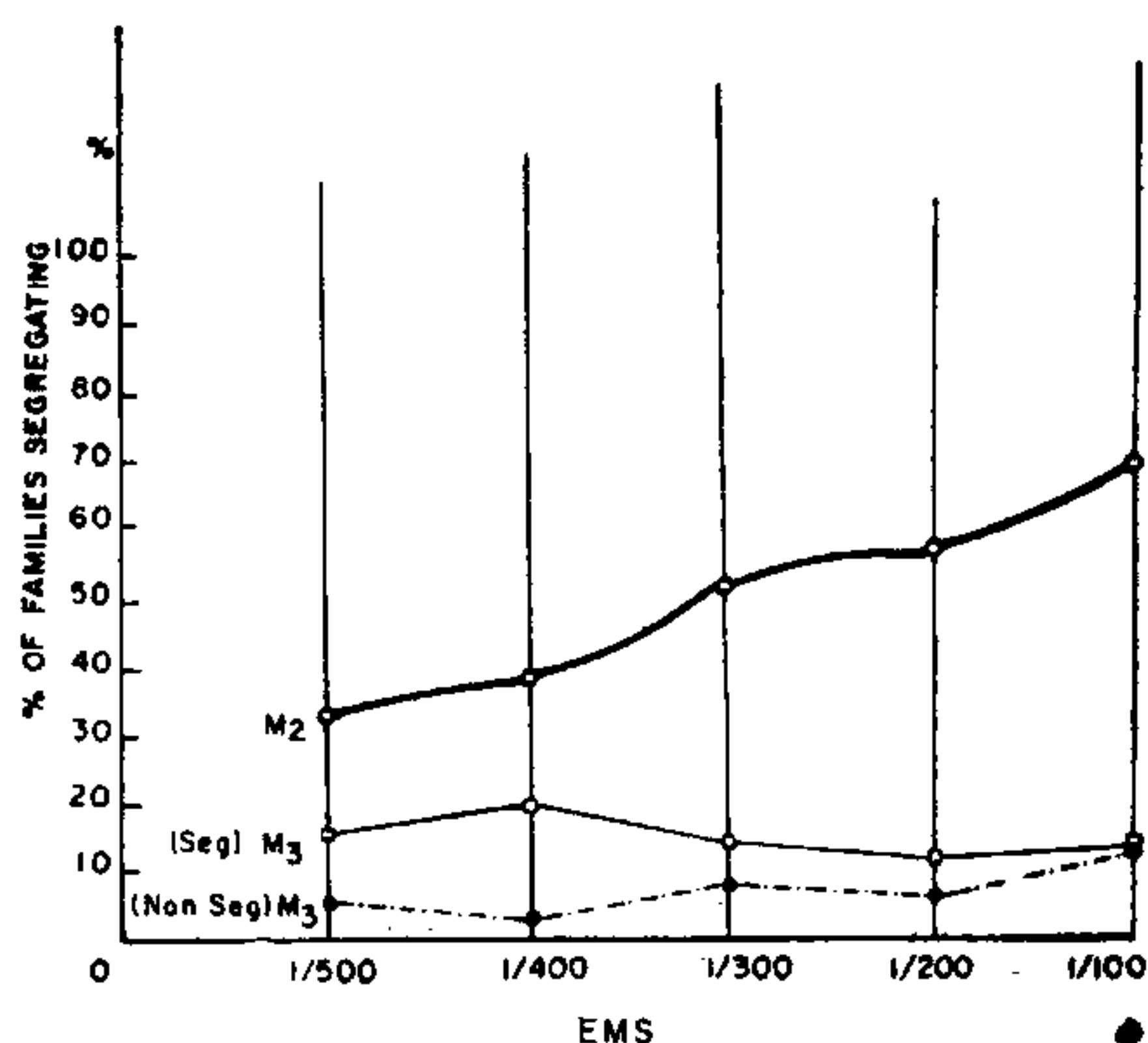
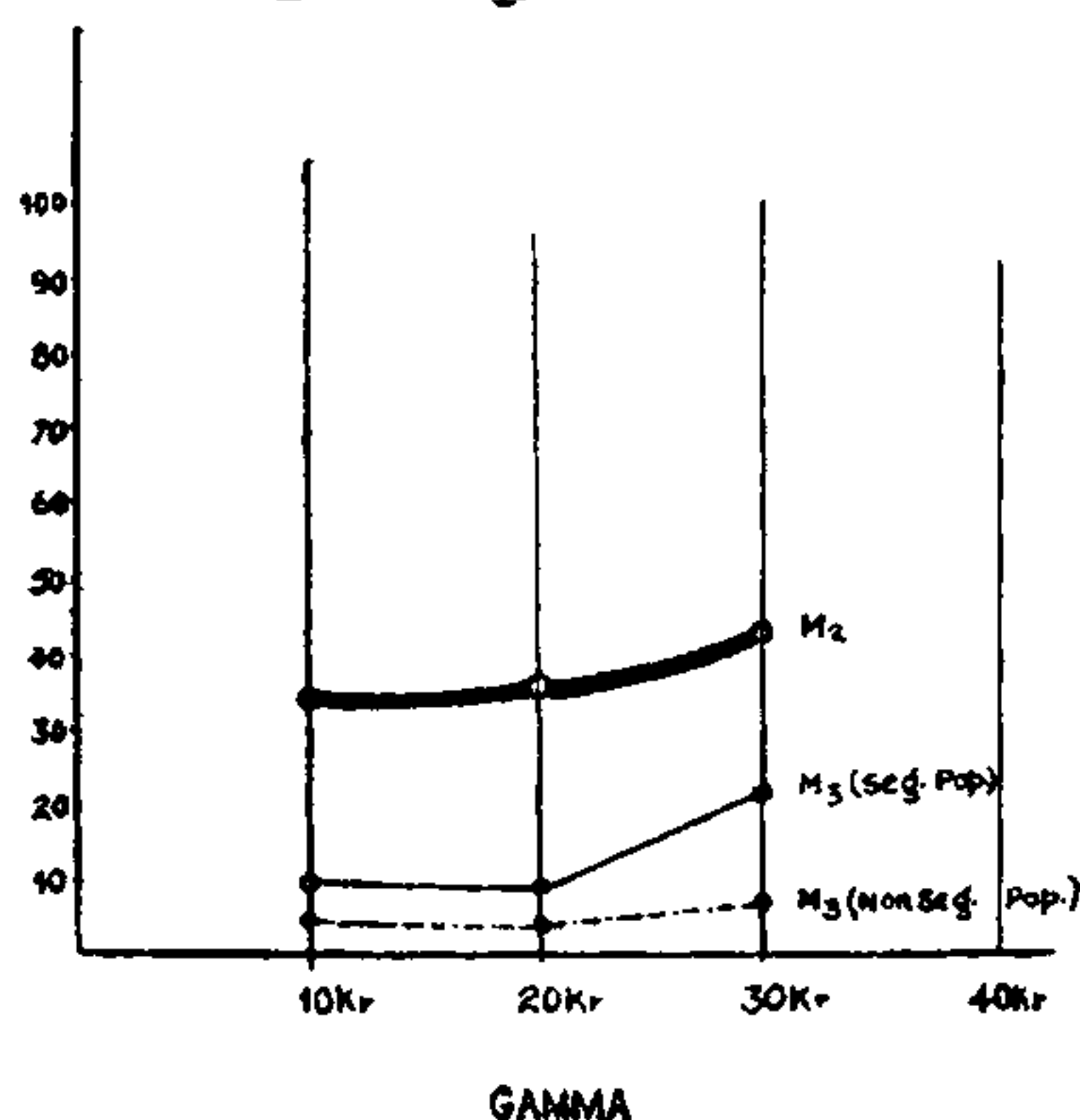
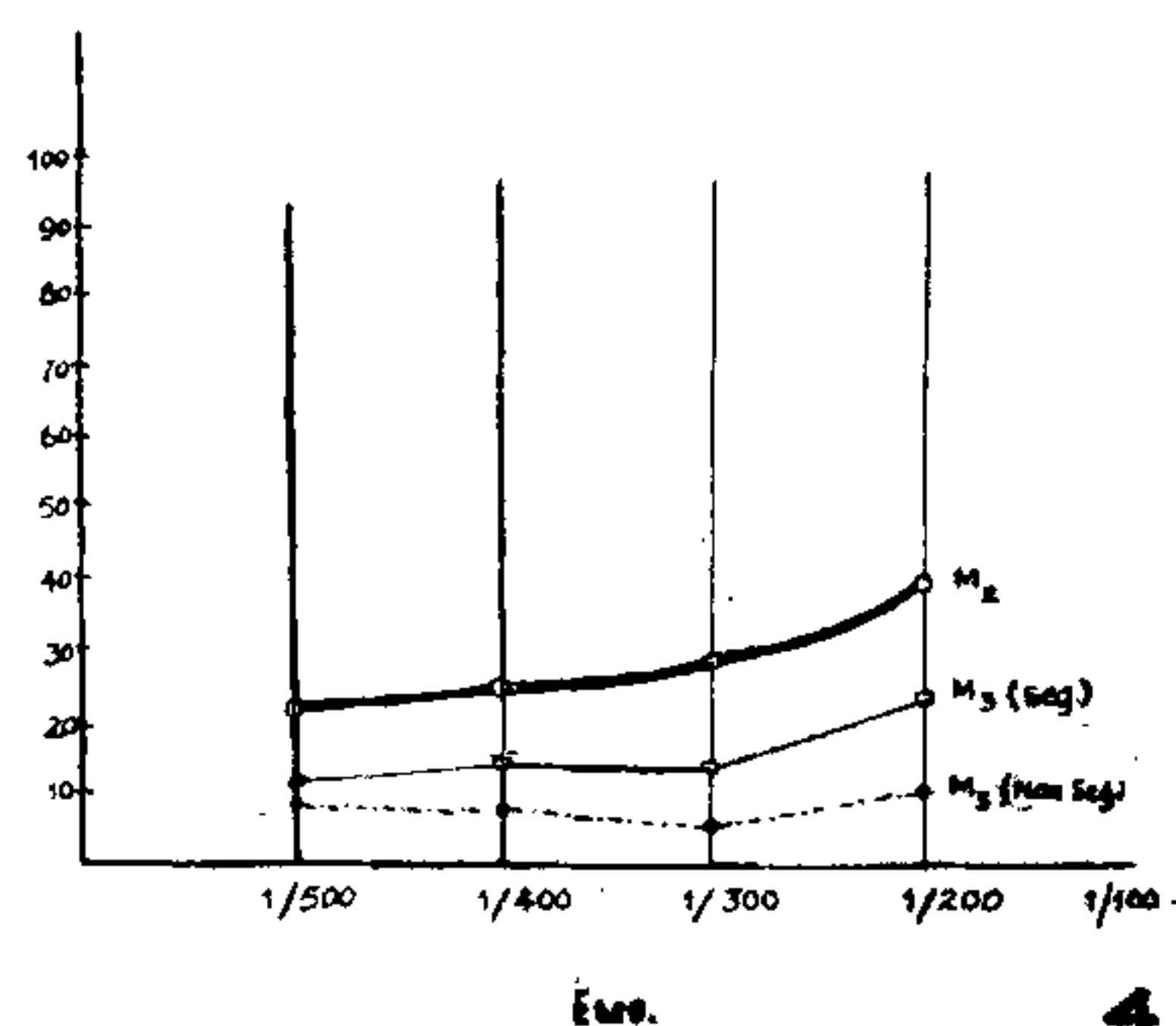
segregating lines suggests that rice behaves more like a diploid in this respect, since in polyploids, mutations find phenotypic expression more readily in later generations.<sup>15</sup>

A further approach to the study of the ploidy level was made through recurrent treatments with mutagens. Pooled seed samples of those plants which were normal looking in the  $M_1$  were subjected to two different doses of gamma radiation. The frequency of chlorophyll mutation as measured by the percentage of mutants in the total population was compared in the recurrently irradiated and the regular  $M_2$  populations. The data indicated that the mutation frequency was either unrelated or even reduced in recurrently irradiated material (Table I). Gaul<sup>2</sup> found that recurrent radiation treatments increase the frequency of mutation in polyploids and that the

TABLE I  
Frequency of chlorophyll mutations in recurrently irradiated Taichung Native-1 and Taichung-65

Variety	$M_1$ dose	Recurrent dose	Total number of seedlings	Number of chlorophyll mutants	% of chlorophyll mutants
Taichung Native-1	15KR	..	2280	25	1.006
( $M_1$ seeds)	15KR	15KR	1918	19	0.990
	30KR	..	1729	18	1.041
	30KR	30KR	1554	13	0.836
Taichung-65	10KR	..	2071	21	1.014
( $M_1$ seeds)	10KR	10KR	1345	17	1.263
	20KR	..	1367	18	1.316
	20KR	20KR	1163	15	1.289

mutation frequency increases with an increase in the number of radiation cycles. Swaminathan<sup>16,17</sup> working with *Gossypium* and *Triticum* demonstrated that different types of polyploids respond differently to recurrent irradiation. Had rice been a polyploid with homologous relationships among the constituent genomes, the chlorophyll mutation frequency following recurrent irradiation could have been expected to show a rise. The data on the other hand showed a reduction in the mutation frequency in the recurrently irradiated population. Thus, in its mutational-response pattern, *O. sativa* behaves like barley

FREQUENCY OF CHLOROPHYLL MUTANTS IN  
M<sub>2</sub> AND M<sub>3</sub> TAICHUNG NATIVE-1FREQUENCY OF CHLOROPHYLL MUTANTS IN  
M<sub>2</sub> AND M<sub>3</sub> TAICHUNG NATIVE-1FREQUENCY OF CHLOROPHYLL MUTANTS IN  
M<sub>2</sub> AND M<sub>3</sub> (TAICHUNG-65)FREQUENCY OF CHLOROPHYLL MUTANTS IN  
M<sub>2</sub> AND M<sub>3</sub> (TAICHUNG-65)

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4

FIGS. 1-4

or other diploids. If polyploidy had been involved in its phylogenetic history, either the parents must have had distinctly divergent genomes or else, a considerable degree of genetic diploidization must have occurred subsequent to its origin.

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