INDUCTION AND EARLY GENERATION SELECTION OF POLYGENIC MUTATIONS IN LENTIL (Lens culinaris Medik.)

By
ISHWAR SINGH SOLANKI

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Approved by:

Chairman .....
(Dr. B.Sharma)

Members: .....
1. (Dr.O.P.Govila)

.....
2. (Dr. N.Gupta)

.....
3. (Dr.H.P.Singh)

Dedicated

To My
Respected Parents
and
Brothers

WHOSE

ETERNAL LOVE HAS ALWAYS BEEN
A SOURCE OF
INSPIRATION
TO ME

Dr. B.Sharma
Head

Division of Genetics,
Indian Agricultural Research Institute,
New Delhi-110012

CERTIFICATE

This is to certify that the thesis entitled, " Induction and early generation selection of polygenic mutations in lentil (Lens culinaris Medik.)" submitted to the Post-Graduate School, Indian Agricultural Research Institute, New Delhi in partial fulfilment of the requirements for the degree of DOCTOR OF PHILOSOPHY IN GENETICS is a faithful record of bona fide research work carried by Shri Ishwar Singh Solanki under my guidance and supervision. No part of the thesis has been submitted for any other degree or diploma.

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(B.Sharma)
Chairman
Advisory Committee

August 6, 1991

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(I.S.Solanki)

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INTRODUCTION

Grain legumes occupy a unique position in world agriculture by virtue of their high protein content and capacity to fix atmospheric nitrogen. For developing countries like India, pulses constitute the major source of dietary proteins. In developed countries, grain legumes are also an important indirect source of protein, being animal feed of high biological value. They contain 20-30% protein in their seeds, which is 2 to 3 times more than in the cereals. The proteins from pulses are also nutritionally valuable because of higher lysine content than the cereal proteins. These two groups of crops have a complementary relationship in their amino acid composition and their combined intake can compensate,to a great extent, for their mutual amino acid deficiency.

Although a large area (about 25.8 million ha) is under different pulse crops in India, their production has remained practically stagnant for the last two decades. The available statistics indicate that the pulse production has ranged between 10.0 -14.5 million tonnes. The average yield of pulses in India is about 5.4 q/ha as against the world average of 8.1 q/ha. India contributed 14.0 million tonnes to the total world production of 58.6 million tonnes of pulses during 1988-89 (Anonymous, 1990). Since the growth in pulse production did not keep pace with the increasing population, the per capita availability of pulses has progressively declined. In general, pulses give lower yields than cereal crops (Jain, 1975). This led to the assumption that pulses may have lower genetic potential for yield than cereals (Boulter, 1973; Swaminathan, 1973).

Among the pulse crops, lentil has a history which is as old as the history of agriculture itself. Its cultivation started in the earliest Neolithic

farming village of the Near East about 7000-8000 years B.C. (Cubero, 1981). It is now one of the important pulse crops in the Indian subcontinent, being used as dal by majority of the people. Among all the pulses, lentil ranked fifth on the production map of India (1987) when it occupied 10,72,000 ha area with the production of 6,66,000 tonnes and average yield about 6.2q/ha (Anonymous, 1989). In spite of the obvious importance of lentil among pulses, little attention has been paid in the past to improve the yield potential of this crop. The low yield potential of the existing varieties and poorly managed farm practices are the main reasons for poor production level of lentil.

The poor yield performance of the existing pulse varieties is probably related to their evolutionary history. These crops have been traditionally grown under marginal conditions of moisture stress, low fertility and poor management. Therefore, pulses have been selected mainly for adaptation to low levels of management rather than for yield potential under better management. Natural selection has played a major role than human selection in determining their morphological, physiological and agronomic characters. Jain (1975) pointed out that in view of this past selection history, pulses have lost useful alleles as far as yield is concerned. Ho (1974) suggested that still enough genetic potential is present in most of the pulses. However, the lost variability must be regenerated through extensive hybridization of diverse genetic stocks collected from different parts of the world as well as induced mutations. Thus, creating new variability by induced mutagenesis becomes all the more important when the variability in the existing material is limited.

Recombination breeding in lentil is tedious. Emasculation and pollination are difficult operations due to tiny and delicate structure of flowers , which are major factors preventing rapid and successful hybridization in lentil.

Mutation breeding is another approach for improvement in this crop. Induced mutations can be used with advantage over conventional breeding procedures to rectify simple, specific undesirable traits in otherwise well adopted varieties without grossly disturbing its genetic constitution. Mutation breeding methodology needs to be sufficiently standardized for improvement of polygenic traits to gain general confidence and wide acceptance of its usefulness among the breeders so that experiments could be planned with reasonable expectations of success. Broad spectrum of genetic variability is a prerequisite for any successful breeding programme. Attempts to induce mutations in lentil have been quite successful in creating genetic variability. Besides the use of induced mutations in fundamental studies, induced mutagenesis can be used to create additional genetic variability for quantitative traits (Gregory, 1955; Scossiroli, 1968; Brock, 1967; Gaul, 1961b; Swaminathan, 1968).

The success of a mutation breeding programme depends not only on the quality of induced mutations, but also on the screening techniques to identify these mutations, which occur with a very low frequency among a large number of others of little breeding value. An attempt has been made here to develop standard screening techniques for micromutations affecting the polygenic system. In general, selection for quantitative traits, such as yield, should be preferably carried out in early generations because most of the desired combinations of favourable alleles are likely to be lost in advanced generations due to intensive or even no selection for other traits (Sneepe, 1977). However, after the studies of Brock (1965 a, b, 1967), it became a common practice to advance only normal looking M_2 plants to M_3 generation and apply the first cycle of selection not earlier than M_3. This results in increased volume of non-mutated

material and delay in isolation of promising variants. Consequently, the proclaimed advantage of rapid progress in breeding through mutation as compared to hybridization was lost. This probably acted as a discouraging factor for the workers to adopt micromutations as a tool for plant improvement on large scale, and most studies terminated at M_3 itself after demonstrating the increase in variance and genetic advance (Sharma, 1986). However, some experiments even demonstrated that selection in M_3 is more effective than in M_2 (Palenzona, 1966; Jana and Roy, 1973). This was, most probably, because the material already selected once in M_2 was confirmed with higher probability in subsequent generations (Ravi et al. , 1980). Even if the material selected in M_3 or later generations has higher probability of getting fixed as promising strains, there is no evidence to suggest that the frequency of promising mutations per se over the entire population is higher in M_3 than in M_2. Therefore, an attempt has been made to explore the possibility of selecting for polygenic variability in an early generations (M_2) following treatments with three mutagens: gamma-rays, ethylene imine (EI) and N-nitroso-N-ethyl urea (NEU).

In any mutation breeding experiment, the choice of material is very important because the crops differ in their response to mutagenic treatment (Sparrow et al., 1965). Several studies conducted on lentil have shown that this crop is highly sensitive and mutable. Therefore, lentil was considered suitable for the kind of analysis planned here. Thus, considering the economic importance of lentil and the tremendous potential of induced mutagenesis to generate mutations of economic value, the present study has been planned in Lens culinaris Med. with the following objectives :

1. To study mutagenic sensitivity and mutability of material under physical and chemical mutagenesis.
2. To decide the appropriate dose and estimate biologically comparable doses of mutagens under study.
3. To estimate and compare the effects (effectiveness and efficiency) of the mutagens under study (gamma-rays, EI, NEU) with special reference to their application in legumes.
4. To study the frequency and spectrum of induced macromutations and their characterization.
5. To study the nature and magnitude of micromutations affecting polygenic traits of economic value.
6. To generate genetic variability not normally present in the cultivar used as test organism.
7. To estimate heritability (H) and genetic advance (GA) in second and third mutagenized generations.
8. To estimate and compare selection response in M_2 and M_3 generations.
9. To develop suitable screening techniques for micromutations of economic importance.
10. To standardize the methodology of mutation breeding for polygenic traits.

REVIEW OF LITERATURE

The literature pertaining to different aspects of the present investigation is reviewed briefly under the following heads:

1. Mutagens utilized in the present investigation
2. Dose effect of mutagens
3. Parameters for estimation of mutagenic damage
4. Mutation frequency and spectrum
5. Mutagenic effectiveness and efficiency
6. Macromutations
7. Micromutations
8. Studies on heritability (h^2) and genetic advance (GA)
9. Early generation selection
10. Screening techniques for induced polygenic variability using different mutagens

1. Mutagens utilized

The term "mutation" for sudden heriditary changes in the evening primrose, Oenothera lamarckiana, was coined by the Dutch botanist, Hugo de Vries. Muller's (1927) discovery of the mutagenic effects of x-rays in Drosophila, subsequently confirmed in barley and maize by Stadler (1928), opened two important lines of investigation in mutation research. The first, concerned with the understanding of the nature of the gene, and second, tailoring the cultivated plants for higher productivity suited to diverse agroclimatic conditions. Goodspeed (1929) induced mutations in Datura and Nicotiana.

A wide range of physical and chemical mutagens have been used by

several investigators for inducing mutations in different crop plants. Although a fairly large number of mutagens have already been discovered and described, their number is continuously increasing. In practice, however, only a few radiations and chemicals are used more frequently for mutation induction in cultivated plants. A systematic study for evaluating the potential of induced mutations by physical and chemical mutagens for crop improvement in India was initiated in the mid-fifties (Swaminathan, 1957).

1.1 Physical mutagens

This group includes various kinds of radiations (ionizing and non-ionizing), but in the present investigation only gamma-rays, as a physical mutagen (ionizing radiation), has been used. Gamma-rays are the most commonly used physical mutagens for mutation studies, especially in plants (Sharma, 1977; Ravi et al., 1980; Dixit and Dubey, 1986a,b,c,d; Ravi and Minocha, 1987; Sharma, 1987; Mahla, 1988; Singh, 1988; Sinha, 1988; Pande and Raghuvanshi, 1988; Kalia and Gupta, 1989; Sarker and Sharma, 1989a,b). They being shorter wave-length radiations (10^{-13} to 10^{-11} cm), are capable of deep penetration in the plant tissues. They serve as a good check for comparison with other mutagens, because, unlike other ionizing radiations, facilities for gamma-irradiation are easily available, therefore, are used more frequently than others.

The effects of radiations (-rays) on the biological systems are direct as well as indirect. In the case of direct effects, energy is transferred to the gene molecule (DNA) directly by radiation. The direct effect of ionization on the DNA molecule includes rupturing of hydrogen bonds, linking of the nitrogenous bases, induction of breaks in one or both DNA strands, and cross-linking within as well as between the two DNA strands. However, the

indirect effect is mediated by free radical formation, the higher reactive radicals transfer their energy to other molecules. The irradiations lead to inhibition of mitosis, induce chromosomal oberrations, point mutations, and cause other effects like oxidation of double bonds, enzymatic inhibition and molecular polymerization.

1.2 Chemical mutagens

A large number of chemicals are known for their mutagenicity, but in the present investigation, only two alkylating agents, namely, ethylene imine (EI) and N-nitroso-N-ethyl urea (NEU) have been used. The first alkylating mutagens were discovered during the second world war: mustard gas and urethane. Though successful attempts to induce mutations by chemicals were made earlier (Morgan, 1911; Sakharov, 1932), yet Auerbach and Robson (1942) were the first to demonstrate mustard gas as a potent agent to induce mutations and chromosomal aberrations in Drosophila. Oehlker (1946) showed that urethane treatment could cause chromosomal breaks in Oenothera. In 1946, Rapoport demonstrated that formaldehyde, when mixed with food and fed orally to Drosophila, was mutagenic. Heslot (1959) demonstrated the mutagenic activity of ethylemethane sulphonate (EMS).

The use of mutagenic chemicals has increased significantly during the past decade. (Dixit and Dubey, 1986 a,b,c,d; Ravi and Minocha, 1987; Sharma, 1987; Mahla, 1988; Pande and Raghuvanshi, 1988; Singh, 1988; Sarker and Sharma, 1989 a,b). Out of the large number of different compounds known to be mutagenic, only a few are used in applied mutagenesis; the most popular and important ones are EMS, diethyl sulphate (DES), EI, NEU, NMU, sodium azide (SA), and other related chemicals.

1.2.1 Ethylene imine (EI)

It is a monofunctional alkylating agent with high degree of reactivity. It is an extremely reactive compound undergoing two major types of reactions (Fishbein et al., 1970): (i) ring opening reactions similar to those of ethylene oxide, and (ii) ring preserving reactions in which ethylene imine acts as a secondary amine.

The alkylating property of EI resides in the ethylenimonium ion, the free base which is responsible for the transport through membrane. It is a very potent, directly acting mutagen giving rise to both point mutations and chromosomal aberrations. The mechanism of mutation induction by ethylene imine is base substitution. Like other monofunctional agents, it lacks the ability to form cross links. EI has been shown to cause mutation in Drosophila (Rapoport, 1962; Alexander, 1967), Neurospora (Westergaard, 1957), wheat (Khvostova et al., 1965), barley (Ehrenberg et al., 1959, 1961) and peas (Singh, 1988).

1.2.2 N-nitroso-N-ethyl urea (NEU)

Nitroso ethyl urea (NEU: C_2H_5-N-NO-$CONH_2$) is also a monofunctional alkylating agent. The alkylating agents transfer alkyl groups to biologically important macromolecules under physiological conditions. Like other alkylating agents, NEU reacts specifically in DNA with the phosphate group and purine bases, particularly guanine (Freese, 1963). Alkylation of guanine at N_7 position is the initial major event in the pathway of mutation induction and chromosome breakage.

Out of all the chemical mutagens reported so far, the nitroso compounds have been found to be most effective (Rapoport, 1948, 1962, 1963).

Therefore, the chemicals belonging to this group have been named as "supermutagens" (Rapoport, 1966). In lentil (Dixit and Dubey, 1986; Sarker and Sharma, 1989a,b), peas (Singh, 1988) and barley (Swaminathan, 1969), nitroso-compounds have been reported to be most effective.

Nitroso-compounds are the most effective of all the alkylating compounds due to the presence of two different reactive groups in its molecule: the alkyl and nitroso groups. All the nitroso compounds give rise to the potent alkylating diazo-compounds at alkaline pH and to nitrous acid at acidic pH as their first degradation products (Kamra and Brunner, 1977). However, it is not clearly established whether direct alkylation of DNA or some indirect effects through production of diazo-compounds or nitrous compounds are responsible for induction of all the mutations obtained with them (Kamra and Brunner, 1977).

The chemical mutagens are specific in their action (Auerbach, 1965), whereas action of radiations is random. Sharma (1965), Blixt and Mossberg (1967) and Singh (1988) compared different mutagens in peas and concluded that certain chemical mutagens are more potent in inducing mutations than the physical mutagens. The same has also been reported by Sarker (1985) in lentil.

2. **Dose effect**

The tests for mutagenic effects of chemicals are almost as old as modern genetics (Auerbach, 1976). Dose in terms of applying a chemical mutagen to plant material is a measure not easily defined. It certainly involves the amount of mutagen (i.e its concentration) and the duration of treatment or life time of the compound. The dose required for a particular experiment depends on the desired effects and may be restricted by undesirable

effect of the treatment.

The physical and chemical mutagens cause three types of effects, i.e., physiological damage, gene mutations, and chromosomal aberrations. Gene and chromosomal mutations may be transferred from M_1 to the succeeding generations but physiological effects are generally restricted to the M_1 generation. Physiological effects are of varying nature, probably of both chromosomal as well as extra-chromosomal origin. Plant injuries due to mutagenic treatments can be measured quantitatively in various ways, e.g. germination percentage, seedling height, root length, plant survival, fertility reduction, leaf aberrations,and chlorophyll deficient chimeras.

The dose effect of mutagens on germination, plant growth, sterility and plant survival has been demonstrated by Sharma and Sharma (1983) and Sarker (1985) in lentil; Ehrenberg (1955), Blixt (1960), Mohan (1983) and Singh (1988) in Pisum; Rajput and Siddiqui (1982) in soybean, NaLampang and Janon (1982) in blackgram; Bala Ravi (1982) in pigeonpea; Patil and Bora (1961, 1973) in peanuts, and Santos (1965) in Vigna radiata. They observed a positive correlation between seedling injury and reduction in survival following treatment with different mutagens. Dose-dependent decline in germination was reported after treatment with NMU and gamma-rays in lentil (Sharma, 1977), EMS, NEU, SA and gamma-rays (Sarker, 1985), X-rays (Blixt et al., 1963) and chemicals (Migacheva, 1972) in peas, NEU in oats (Shevtsov, 1969), gamma-rays in pigeonpea (Bala Ravi, 1982), and sodium azide in mungbean (Mahapatra, 1983). Singh (1988) also observed dose-dependent decline in peas using NEU, EI and gamma-rays. At higher doses, the decline in germination was maximum with all the mutagens used. NEU was most effective, followed by EI and gamma-rays. Heringa (1964) observed more reduction in germination of pea with EMS than

with ionizing radiations. Similar dose-dependent reduction in germination, seedling height and fertility was reported by Wellensiek (1965), Selim et al. (1974) and Singh (1988) in pea; Singh and Chaturvedi (1980) in Vigna radiata; Nerkar (1970) in Lathyrus sativus; Hussein and Disouki (1976) in Phaseolus; Bhatia and Swaminathan (1963) in wheat; Sharma (1970) in barley, and Siddiq (1967) in rice.

Siddiq (1967) observed drastic reduction in germination and plant survival in rice following mutagenic treatments, which was more severe with NMU in comparison to gamma-rays, EMS and fast neutrons. Dixit and Dubey (1986) reported on the basis of seed germination, seedling height, leaves per seedling, seedling survival and sterility (in terms of seed set) in the M_1 and chlorophyll mutations in the M_2 that NMU was 2-5 times more efficient than gamma-rays. The combined treatments were also more efficient than gamma-rays alone. Chemical mutagens like EMS, NEU and NMU cause more reduction in pollen fertility than gamma-rays (Nerkar, 1970, in Lathyrus; Hussein and Disouki, 1976, in Phaseolus; Singh et al., 1978, in pearl millet; and Singh, 1988, in peas).

3. **Parameters for estimation of mutagenic damage**

The observations recorded in M_1 generation to estimate the damage caused by the mutagens to the genetic material are referred to as M_1 parameters. Many parameters are used for this purpose, such as germination, seedling height, root length, leaves per seedling, leaf aberrations, seedling survival, fertility, and chlorophyll-deficient chimeras. Only a few of these damage recording parameters, like seedling height and fertility percentage, are used frequently because of the convenience and precision in recording them. The phenomenon of leaf aberrations has attracted attention of many workers, as it makes possible the estimation of mutagenic effects, which may be more closely related to

gene mutations than the parameters of growth and fertility (Burn, 1954; Kaplan, 1954; Blixt et al.,1960, 1964, 1965; Zacharias and Ehrenberg, 1962).

3.1 Leaf aberrations

The term leaf aberration is used here for the deviating areas in the form of spots or sectors on the foliar structures, appearing as a result of treatment with mutagenic and chromosome-breaking agents. This phenomenon was first reported by Arntzen and Krebs (1925), but they paid little attention and described it simply as "a sickly look", which persisted for about four or five weeks and gradually disappeared thereafter.

Although the precise origin of the leaf spots is not known, some suggestions about their nature have been made. Kaplan (1954) studied the effect of X-irradiation on the pattern of leaf aberration in Glycine max under varied treatment conditions. The experiments showed dose-dependence of the average number of aberrations per leaf, in accordance with expectations if the leaf aberrations were a result of chromosomal aberrations. He showed that the number of leaf spots increased exponentially with dose and concluded that chromosomal aberrations were responsible for the induction of these spots. It was also noted that whilst there were many small leaf aberrations on the younger leaves of seedlings, they were fewer and larger on the older ones, and in the oldest they seemingly disappeared altogether.

Burn (1954) studied the mutational effect of x-rays in clover (Trifolium pratense). She noticed the occurrence of sharply defined sectors on the seedlings. In the later ontogenic stages, chlorophyll deficiencies became visible which might embrase almost the entire plant, and in atleast two cases, flower- color mutants were observed, displaying the same pattern as the primary chlorophyll deficient leaf aberrations. A further point of special interest is her observation of sudden leaf aberrations appearing on

the leaves late in the plants, that were entirely normal earlier.

Blixt et al. (1960, 1964) showed that leaf aberrations in Pisum were induced by the chemical mutagen EI, and the M_2 chlorophyll mutation rate was positively correlated with the leaf aberration frequency. This increased the value of leaf aberrations in the studies on induced mutagenesis.

After seed treatment many small leaf aberrations are descernible in the first leaf, and their number decreases thereafter, while their sizes increase with each consecutive leaf (Blixt et al.,1964), according to the number of cells of the respective leaves present in the embryo at the time of treatment. The results were similar when the mutagen was administered to the growing points later in the ontogenesis (Blixt and Gelin, 1965).

Positive correlation between leaf aberration frequency and mutation rate has been confirmed by Monti and Scarascia-Mugnozza (1964) for DES, by Monti (1968) for X-rays, by Speckman (1964) for EMS, and by Pipie (1970) for DES and EMS. This has also been found to be valid in maize (Ficsor, 1966). Some of the chlorophyll mutants registered in M_2 could be caused by a mechanism similar to that of leaf spots and streaks (Moutschen-Dahmen et al.,1959).

Zacharias and Ehrenberg (1962) found that densely ionizing radiations produce leaf aberrations proportional to the dose, sparsely ionizing radiation and ethylene oxide (EO) caused leaf aberrations almost proportional to the square of the dose, and neutrons were many times more effective than X-rays. The authors concluded that the most plausible explanation was that leaf aberration arose through changes in the genetic material. However, leaf spots are also induced by chemicals such as EMS and EI which induce chromosomal aberrations at much lower rate; this suggests that some other mechanism may also be involved in the induction of leaf spots. In the first leaves the size of the spot

is much smaller than in the latter formed leaves since different numbers of initial cells are responsible for the development of the consecutive leaves.

The leaf aberrations largely disappeared later in ontogenesis. Only those aberrations which constitute a part of the meristem will persist (Sharma and Rapoport, 1965). A comparison of the frequency of different color types of such persistent leaf aberrations with the chlorophyll mutation spectrum in M_2 showed a marked agreement (Blixt, 1965b). It was found that different agents induce different spectra of leaf aberrations as well as chlorophyll mutations.

It is now established that the development of leaf aberrations as a response to mutagenic treatment is characteristic of a very wide range of plant species (Blixt, 1965c) and, therefore, certainly not peculiar to the leguminous plants. It is probably a very general phenomenon.

Leaf-aberrations seem to be most easily induced in leguminous plants, which have comparatively fewer plastids, a fact, amongst others, which made it necessary to consider direct action on plastids also as one of the possible explanation for leaf-aberration induction. DNA is reported to be present in pea chloroplasts (Wilson, 1966).

The size of leaf-aberrations in Nicotiana partly follows a pattern different from that of Pisum (Dulieu, 1965 and 1970). This can possibly be explained on the basis of large differences in the size and degree of development of embryos in the seeds of the two species.

The effects of different chemical agents on leaf aberrations and other parameters recording mutagenic damage (growth inhibition, survival, etc.) were also not necessarily correlated, i.e. these effects could vary more or less independently of each other. Leaf aberration frequency was reported to be strongly correlated with the mutation rate (Blixt and Gelin, 1965).

At present, the pea is probably the only higher plant which meets the requirement of a high level of genetic information combined with reasonable convenience of handling; and the leaf aberrations make it further easy to obtain preliminary information about the initial mutagenic effects within a month (Blixt, 1967).

Full scale tests have been carried out with a number of substances using only leaf aberrations as a test system. The results showed the technique to be inexpensive, and relatively more reliable as compared with other tests (Blixt, 1967c).

In those plant species, where leaf aberrations are comparatively easily recorded, atleast in all dicotyledonous plants, it is possible to mass screen a large number of plants at the seedling stage on the basis of leaf aberrations, and use only their progenies to obtain large number of mutations. This might fill considerably the gap in our present information on spontaneous mutations (Blixt, 1972).

Debelyi et al. (1975) noted discoloration in pea leaves after gamma-ray and NMU treatments. The plants showing discoloration produced six times more mutations in M_2 than the normal ones. Similarly, a high positive correlation between M_1 spotting and mutation frequency in M_2 has been reported in peas (Debelyi and Bezhanidze, 1972). Sokolov (1975) also found more chlorophyll mutations in the progenies derived from variegated pea plants following EMS treatment. However, progenies of chimeral plants showed as many chlorophyll mutations as of the non-chimeral ones.

3.2 Sterility

Many reasons and sources have been assigned to the mutagen-induced reduction of reproductive ability. This may be caused by chromosomal aberrations, gene mutations, and physiological effects. The chromosomal changes are probably

the most important cause of mutagen-induced sterility. For breeding purposes, mutagenic treatments with lower sterility but higher frequency of vital mutations are desired.The radiation-induced sterility in M_1 generation is mainly caused by small or minute deficiencies (Gaul, 1963). There is evidence that radiation-induced M_1 sterility is partly transferred into later generations (Gaul and Mittelstenscheid, 1960). A large part of sterility is caused by physiological damage and consequently, not transferred to M_2. Little is known about the cause of chemically induced sterility. Only a part, though a larger one, of the EMS-induced sterility observed in the M_1 generation seems to have genetic origin (Gaul et al., 1966; Bender and Gaul, 1966, 1967). The other part may be caused by the physiological damage, and possibly also by the hydrolysis products. The genetical part of sterility is clearly inherited through subsequent generations.

It has been observed in barley that the rate of chlorophyll mutations in M_2 is independent of the degree of sterility of the M_1 spikes (Gaul, 1958). It has also been found that the mutation rate is the same in all the fertility classes including the fully fertile spikes. Similar results were reported by Bekendam (1961) in rice and by Hildering and Van der Veen (1966) in tomato. According to some reports, not only the mutation frequency is independent of the degree of M_1 sterility, but the spectrum of chlorophyll mutations also does not indicate any relation with M_1 spike sterility (Gaul, 1958, 1965b). Kivi (1965) reported maximum mutation frequency in M_2 generation of the group which was in 30-70% fertility range in M_1 . Ehrenberg et al.(1961), on the contrary, showed that spikes with different fertility levels have some evident differences in mutation rate. Walther (1970) found the highest number of induced chlorophyll mutations in population with medium fertility in barley.

Singh et al. (1972) reported high mutation rate in the fertility range of 42-50% irrespective of variety and treatment.

4. **Mutation frequency and spectrum**

Several investigations have been carried out in different crop plants by many workers to compare the mutation frequency and spectrum induced by different physical and chemical mutagens. With regard to mutation frequency and spectrum induced, chemicals are comparable to the physical mutagens used, or even better. For any successful mutation breeding programme, the selection of effective and efficient mutagen(s) is very essential in order to recover very high frequency of desirable mutations. It is a general opinion that the frequency of chlorophyll mutations scored in M_2 generation is a good indication of the total mutational effect (Mesken and Van der Veen, 1968). Therefore, in most cases, the frequency of chlorophyll mutants in M_2 generation was used as a test for judging the effectiveness of the mutagens used (Gottschalk, 1983). Mutagens have been found to show differences in the spectrum of chlorophyll mutations (Ehrenberg et al., 1959; Konzak et al., 1969; Swaminathan et al., 1962; Sharma, 1968; Sarker, 1985; Dixit and Dubey, 1968a; Singh, 1988; and Sarker and Sharma, 1989a). Auerbach (1967) reported that spectral changes could possibly be induced more by controlling the recovery process pattern rather than the primary process of mutation induction.

The chemical mutagens have been found to induce higher frequency of chlorophyll and viable mutations than physical mutagens in lentil (Sharma and Sharma, 1979a,b, 1981; Sarker, 1985; Dixit and Dubey, 1986a; Ravi and Minocha, 1987; and Sarker and Sharma, 1989a), peas (Blixt et al., 1958, 1963; Sharma, 1966; Monti, 1968; Mohan, 1983; and Singh, 1988), bread wheat (Goud, 1967b),and soybean (Baradjanegara and Umar, 1982). Chemical mutagens,

especially alkylating agents, in contrast to radiations, produce a wider spectrum of mutations (Swaminathan et al., 1962; and Singh, 1988).

Among chemical mutagens, nitroso-compounds have been found to induce more chlorophyll mutations than others. Alkylating agents, particularly NEU, were found to be the most effective among the mutagens studied (NEU, EMS, gamma-rays and SA) in inducing chlorophyll mutations in lentil (Sarker, 1985; and Sarker and Sharma, 1989a). They also reported that the mutation frequency was dose dependent for all mutagens studied and was in the order NEU>EMS>gamma-rays SA. Mutations of xantha and viridis types were induced more often than chlorina, whereas albina mutations were rare. Dixit and Dubey (1986c) reported NMU to be 2-5 times more effective than gamma-rays on the basis of M_1 seedling damage estimating parameters and chlorophyll mutations in M_2 generation. The combined treatments of NMU and gamma-rays were also more efficient than gamma-rays alone. However, in another study, these authors reported NMU and gamma-rays to be equally effective for inducing chlorophyll mutations, whereas NMU was found to induce more seedling (viable) mutations than gamma-rays.

Sharma (1965) compared the effect of NMU with various chemical and physical mutagens in peas and found that NMU induced the highest rate of mutations. Savin et al. (1968) reported higher chlorophyll mutation frequency induced by NMU than EMS, and NMU was found to induce more multiple mutations in barley. Marki and Bianu (1970) found that in flax, NMU and EMS were more effective than gamma-rays in inducing higher frequency and wider spectrum of chlorophyll mutations. Sahai (1974) reported in Phaseolus aureus (=Vigna radiata) NMU to be the most potent mutagen in inducing chlorophyll mutations. Sobchuk (1973) recorded a higher mutation frequency with NEU than with gamma-rays in peas. Shevtsov (1969)

demonstrated that NEU was more effective in inducing mutations than dimethyl sulphate (DMS) and EI. Bohmova (1980) recorded three -fold increase in chlorophyll mutation frequency in pea with NEU in comparison to NMU. Superiority of NEU among the chemical mutagens for inducing mutations in pea has also been demonstrated by Rybakov and Balashov (1971) and Kolotenkov (1975). Singh (1988) also demonstrated the superiority of nitroso-compound (NEU) over gamma-rays for inducing mutations in pea. The order of mutagenicity was NEU>EI>gamma-rays. Similar results were obtained in wheat, oats and barley by Dishler (1971). However, Desai and Bhatia (1975) reported that the frequency of chlorophyll and viable mutations was higher with NMU than with NEU. As regards viable mutations, EMS was found to be more effective than gamma-rays and NMU (Kawai, 1969; Prasad, 1972; Desai and Bhatia, 1975). Vasileva (1976) compared EI, EMS and DES in two varieties of pea and recorded highest mutation frequency with EMS and lowest with DES. Sidorova (1966) observed that the rate and spectrum of induced mutations in pea were affected by the mutagen as well as genetic architecture of the variety.

Dose-dependent effect of mutagens on the total mutation frequency and spectrum in lentil has been reported by Sharma and Sharma (1979); Ravi and Minocha (1987); Sarker (1985); and Sarker and Sharma (1989a). In peas, it has been reported by several workers. Rybakov and Balashov (1971) tested different concentrations of NEU, DEU, EI and DMS on eight pea varieties and hybrids. They found maximum number of M_2 mutants following treatment with 0.012% NEU and 0.06% EI. Ghosh et al. (1973) reported a linear relationship between mutagenic dose and chlorophyll mutation frequency. However, Pipie (1972) did not find any relationship between dose and mutation spectrum. Hussein et al. (1974) reported decline in mutation rate with increase in mutagenic

dose but spectrum remained unaffected. Maximum range of mutations with low concentrations of EMS and EI has been reported in peas (Vasileva, 1976) and lentil (Ravi and Minocha, 1987). Vo Hung (1974) did not find the highest dose to be always the most effective treatment in peas. Srivastava et al. (1973) reported lower doses of EMS to be less toxic than higher doses of MMS. Mehaudjiev (1974) reported increase in the number of useful mutations and decrease of lethal mutations with low dose of irradiation, followed by treatment with chemical mutagens. However, Khvostova et al. (1973) found phenotypically similar mutants induced by different treatments. Singh (1988) reported dose-dependent effect of mutagens on the total mutation frequency and spectrum. The frequency of macromutations, both chlorophyll and morphological, was highest at the highest dose of mutagens (NEU, EI and gamma-rays) used in the order: NEU > EI > gamma-rays. He also found increase in the number of useful mutations at the medium doses of chemicals and the highest dose of radiations. The direction and pattern of chlorophyll and morphological mutations have also been reported to be similar with the mutagens used. Similar results were reported in black gram (Kulshrestha and Singh, 1983). Nadarajan et al.(1982), on the other hand, recorded high frequency of chlorophyll mutations with medium dose in Cajanus cajan.

The pattern and direction of chlorophyll and morphological mutations have been found to be identical with different mutagens by various workers. However, many contradictory reports have also appeared for different mutagens. For example, Akhund-Zade (1979) found that N-nitroso-N-alkyl ureas are more effective in inducing chlorophyll mutations as well as those affecting quantitative traits, while Vo Hung (1974) recorded highest number of lethal mutations with

high doses of EMS. Dixit and Dubey (1986a) using NMU and gamma-rays in lentil reported that the two mutagens were equally effective for inducing chlorophyll mutations, while NMU induced more morphological mutations than gamma-rays. Similarly, Fillippetti et al.(1977) recorded high frequency of chlorophyll mutations after x-ray treatment, while morphological mutations were more frequent in the DES-treated material. Chlorophyll mutations of xantha type were more frequently induced by DES and those of chlorina type by x-rays. Mehaudjiev and Vasileva (1975) observed varietal difference in peas for mutations of different types. In the varieties, Voronezh and Romon 77, gamma-rays mainly induced chlorophyll mutations, whereas in Ramon 5 and Record, they induced mainly morphological mutations. Sharma (1970) treated the seeds of pea variety krupnoplodny G20 with gamma-rays, neutrons, EI, DES and NMU and noticed that NMU induced a large number of dominant mutations and its morphological mutation spectrum was considerably wider than eight other mutagens, and it also induced more useful mutations than other mutagens. Zenelov (1966) noticed higher frequency of foliage and shoot mutants in the irradiated material than in chemically treated. He further observed higher chlorophyll mutation frequency with chemicals than in the irradiated material. Popova (1981) noticed in peas that mutations most frequently affected characters like stem length, leaf and stipule shape, growth period and number of pods per peduncle. Shifrin (1972) reported that the frequency of morphological mutations in M_3 generation raised from the mutant M_2 families was three times as much as from nonmutant M_2 families. Favret (1960a) studied the effect of x-rays on EMS on the genes governing albinism in barley. He demonstrated that EMS affects selectively only one of the four genes, whereas x-rays affect all the four genes. The frequency of viridis

mutations was higher after chemical treatment as compared to those obtained with radiations, which produce albina mutations with high frequency.

Akhund-Zade and Khvostova (1966) reported maximum number of chlorophyll mutants with broad spectrum in EMS mutagenesis, followed by EI, gamma-rays and fast neutrons. Sidorova (1966) found positive correlation between the frequency as well as spectrum of chlorophyll and morphological mutations, i.e. wider the chlorophyll mutation spectrum, greater the range of morphological mutants.

Nilan (1967) reviewed the mutation rate and spectrum in pea and concluded that different agents yield different mutation spectra. However, there need not necessarily be a very close relationship between chemicals or between two agents from any of the mutagenic groups. He tested five mutagens, namely, x-rays, gamma-rays, EI, EMS and EO, and found that the agent with the most deviating mutation spectrum was EI. It was found that significant heterogeneity between mutagenic agents existed for xantha, chlorina and maculata types but not for chlorotica type. He found that EI induces very high frequency of chlorina, albina and chlorotescens types. However, the frequency of xantha mutations was the lowest with EI. Further, radiations induced high frequency of maculata type, while EO and EMS induced more of xantha mutations. He concluded that different agents may induce different spectra and the differences are quantitative rather than qualitative. This was also confirmed by the studies of Blixt et al. (1963), Blixt (1964b), and Singh (1988).

5. **Mutagenic effectiveness and efficiency**

Mutagenic effectiveness is a measure of the frequency of mutations induced by a unit dose of mutagen, whereas, mutagenic efficiency provides an

idea of the proportion of the mutations induced in relation to the total biological damage measured through lethality, sterility, etc. The value of any mutagen depends not only on mutagenic effectiveness, but also on its efficiency, or the mutation rate in relation to biological effects. Extensive studies on mutagenic effectiveness and efficiency of various physical mutagens have been carried out by Konzak et al.(1965).

Blixt (1964) compared the effectiveness and efficiency of gamma-rays and EI in pea and concluded that EI is more effective and efficient mutagen than gamma-rays at optimal doses.

Monti (1968) found DES to be more efficient and effective mutagen than x-rays in pea for both chlorophyll and morphological mutations.

Debelyi et al.(1975) recorded the highest number of mutated families in pea after NMU treatment than with EI and gamma-rays. Gamma-rays were also found to be less effective than EI and NMU in these experiments. Singh (1988) compared the efficiency and effectiveness of NEU, EI and gamma-rays in pea , and arranged them in the order, NEU > EI > gamma-rays.

Sharma and Sharma (1979) found that NMU was almost three times as effective as gamma-rays in lentil. The efficiency of NMU was also 1.5-2.0 times as much as of gamma-rays when chlorophyll, morphological mutations, or both were considered together.

Dixit and Dubey (1986a) reported that NMU and gamma-rays were equally effective for inducing chlorophyll mutations in lentil while NMU induced more seedling (viable) mutations; there was no synergistic effect from combined treatment. However, in another investigation, Dixit and Dubey (1986c) found NMU to be 2-5 times more efficient than gamma-rays. Their combined treatments were also more efficient than gamma-rays alone.

Ravi and Minocha (1987) reported EMS to be more efficient and effective than gamma-rays in lentil for the induction of chlorophyll and morphological mutations.

Sarker and Sharma (1989a) compared the effectiveness and efficiency of gamma-rays, EMS, NEU and sodium azide in lentil. They found NEU to be the most efficient and effective mutagen.

Nerkar (1977) studied the efficiency and effectiveness of gamma-rays, NMU and EMS in Lathyrus sativus and concluded that both effectiveness and efficiency did not have similar trend for a mutagen. The order of mutagens on the basis of effectiveness was NMU > EMS > gamma-rays, whereas the same mutagens were arranged on the basis of efficiency as gamma-rays > EMS > NMU. Both mutagenic effectiveness and efficiency were higher at low mutagenic doses.

Mahapatra (1983) studied mutagenic effectiveness and efficiency of gamma-rays, EMS, NMU and sodium azide (low pH) in green gram. He found sodium azide to be the most effective as well as efficient mutagen. However, Rathnaswamy and Kamalanathan (1978), observed that for both these parameters, gamma-rays were better than EMS.

Prasad (1972) compared the mutagenic effectiveness and efficiency of gamma-rays, EMS, NMG and MNG in Triticum durum and noted that NMU was the most effective and a reasonably efficient mutagen. Desai and Bhatia (1975) and Vo Hung (1974) found NMU to be superior to NEU for both efficiency and effectiveness in durum wheat. Ramulu (1970) observed highest mutagenic effectiveness at low doses of EMS, NEU and x-rays. He found that mutagenic efficiency of EMS was higher than that of NEU, probably due to high toxicity of NEU.

Several studies have been conducted in order to know the relationship of efficiency and effectiveness with the mutagenic dose. Many studies have shown that among the monofunctional mutagens, methylating agents are more toxic, hence can be used only at lower concentrations. Ethylating agents, being less toxic, can be applied at relatively higher concentrations to yield more mutations at equimolar concentrations. The methylating agents have been found to be more effective than ethylating mutagens (Minocha and Arnason, 1962, and Kamra and Brunner, 1977).

6. Macromutations

Those mutations which are easily identifiable on single plant basis are termed as macromutations. A series of phenotypic patterns in different crop plants have been studied with regard to their genetic backgrounds in the last three decades. Several different phenotypic patterns have been discussed (chlorophyll as well as morphological), where each pattern has a genetic background consisting of numerous genes and alleles with discrete effects.

6.1 Chlorophyll mutations

The chlorophyll mutations are of very little applied value in plant breeding, though conveniently used for estimating efficiency and effectiveness of mutagenic treatments and also widely used as a test system in experimental mutagenesis. They also have immense importance in horticultural and ornamental plants. The spectrum and frequency of chlorophyll mutations have been studied in lentil (Sharma and Sharma, 1979; Sarker, 1985; Dixit and Dubey, 1986a, 1986c; Ravi and Minocha, 1987; and Sarker and Sharma, 1989a), barley (Gustafsson, 1940, 1947; Gaul, 1960; Konzak et al., 1965), soybean (Krausse, 1983), wheat (Mackey, 1954; Chopra and Swaminathan, 1966), and pea (Nilan,

1967; Blixt et al., 1963; Blixt, 1968b, 1969b; Gattschalk, 1964; Sharma, 1965; Mohan, 1983; and Singh 1988).

Gustafsson (1941a) has given wide classification of chlorophyll mutations in barley. These classes were named as albina (A), viridis (V), xantha (X), alboviridis (Av), virido-albina (Va), albo-xantha (Ax), tigrina(T) and maculata (M). Most chlorophyll mutations are easily identified although in several cases their full expression depends on light intensity and temperature.

Tallenaar (1938) was the first to isolate a light green tobacco mutant after x-ray treatment. This was one of the very few chlorophyll mutants released for commercial cultivation.

The number of genes responsible for chlorophyll mutations was calculated by Gustafsson (1954) to be approximately 250-300 in barley. The classification and terminology of chlorophyll mutations in Pisum were developed by Lamprecht (1960) and Blixt (1961). They were of the opinion that a larger number of genes control chlorophyll synthesis in pea than in barley, which is reflected in the wider spectrum of chlorophyll mutations observed in pea. Blixt (1972) grouped chlorophyll mutations of pea in ten main types, viz., viridis, chlorotica, chlorina, xantha, albina, variomaculata, variegata, marginata, costata, and terminalis.

6.2 Morphological mutations

The mutations that can be identified either by naked eye or by use of simple screening procedures, can be either lethal or viable. Blixt (1972) has classified morphological mutations of pea on the basis of different plant parts affected as follows:

(a) Plant height: tall and dwarf.

(b) Growth habit: compact, bushy and ramosus (ram).

(c) Stem structure: slender (le cry la), fasciata (fa) and non-branching.

(d) Foliage: circular stipule (cist) , reduced stipule (st), curly leaves, waxless (wa, wb, wel, etc.), laciniata (lac), afila (af), acacia(tl), higher number of leaflets, cripsa (cri), rogue, cabbage leaf (calf), and leafy flower (lefl).

(e) Pod: concavum (con, co), latus (lat), thick pod wall, small pod, and beaded pods (p v).

(f) Seed: planatus (pla), corrugatus (foe), comprimere (com) , green seed (i), and wrinkled seed (r).

(g) Reproductive period : early, late, and sterile.

Many mutants affecting morphological features of lentil have been induced and characterized. Sharma and Kant (1975) reported a "funnel leaf" mutant in lentil. Sharma and Sharma (1978) induced the morphological mutants in lentil. Dixit and Dubey (1986a) reported seedling mutants with curled leaf apex, stunned growth, radicle hypertrophy, bi-lobed cotyledonary leaves, a'barren' leaf apex, folded leaflets and 'giant' seedlings (rapid hypocotyl growth followed by death). Dixit and Dubey (1986b) isolated three interesting mutants in lentil; one characterized by compact branching habit and reduced plant height and leaf size; second characterized by dwarfness (8-12cm against 28 cm in control), reduced leaf size, increased pod and seed number and yield, and early flowering; the third mutant was designated 'staggering mutant', characterized by closely arranged long branches spreading parallel to the ground for most of their length and finally turning upward with reduced branch and pod number, leaf and leaflet size, days to flowering, internode length and seed yield. They characterized these mutants in lentil obtained by gamma-rays and/or NMU treatments of seeds of the cultivar T36 (pink flowered). Dixit and Dubey (1986d) obtained two mutants, alba (white flowered) and tendrillar, in lentil. Ravi and Minocha (1987) induced a range of chlorophyll, and morphological mutants including

dwarf, compacted and large leaflet types. Sinha (1988) isolated a dwarf mutant (RPL-1) with gamma-rays in M_2. It bred true in M_3 and M_4 generations.

Similar reports on macromutations affecting morphological characters are also available in other pulse crops and cereals. Pipie (1975) obtained mutations in two varieties of pea following DES and EMS treatment, which affected internode length, thickness of main stem, number of branches, shape and size of leaves, flowers, fruits and seeds. Popova (1975) isolated 23 mutant lines following seed treatments of five pea varieties with NMU, NEU and EI. Out of the 23 mutant lines, 8 possessed economically valuable characters, such as, early ripening, open flower, determinate growth, late ripening and three pods per peduncle. Popova (1979) in another experiment, obtained mutants with determinate growth habit, altered growth period, lodging resistant and higher number of pods per peduncle following seed treatment of garden pea with EI. Gupta et al. (1981) obtained a dwarf mutant (MUP-1) with 23 days earliness over the parent variety T 163. Singh (1988) also induced and characterized many mutations affecting morphological features of pea. Patil (1966) obtained a true breeding mutant with modified foliaceous stipules in peanut. Nagada and Bassett (1982) isolated a dwarf mutant with 5.5% outcrossing following gamma-irradiation in Phaseolus vulgaris. Pande and Raghuvanshi (1988), using gamma-rays and EMS in Vigna radiata, isolated a dwarf mutant in M_2 which was true breeding in M_3. The mutant produces more pods per plant and seeds per pod, leading to higher seed yield. The mutant matured one week earlier than the control.

Gustafsson (1965) reported a useful macromutant in barley where plant height and straw stiffness, the length/breadth ratio and thickness of leaves, and ear density were affected simultaneously. Varughese and Swaminathan (1966) rectified a solitary defect of grain color in wheat variety Sonora-64, which was released as a new variety, Sharbati Sonara. Many useful dwarf mutants have

been isolated in wheat (Mackey, 1954), oats (Frey, 1965), and rice (Beachell, 1957).

7. **Micromutations**

Mutations affecting minor genes that can be isolated and fixed only by adopting biometrical procedures are called micromutations (Swaminathan, 1964). These can be identified and isolated in the form of increased variance at progeny or population level in M_2 and subsequent generations. The micromutations are of great importance in plant breeding.

Although, the term "polygene" was first proposed by Nilson-Ehle (1913), the significance of micromutations or polygenic mutations in evolution was recognized and stressed by Baur (1924), Stubbe (1959), and others. Morgan (1912) reported mutations with minor effects in Drosophila. However, in plants, micromutation was first reported in beans by Johannsen (1913) and the applied value of micromutations in plant breeding was emphasised by Knapp (1950). The polygenic theory of Mather (1941, 1943, 1954) involves two different genetic units for the phenotypic determination of traits in any organism: the "oligogenes", responsible for discontinuous variation and the "polygenes" responsible for characters with continuous variation. Any quantitative trait is a result of joint action of many single genes, whose individual contribution produces small effect at the phenotypic level, and of the environmental influences. Gaul (1965) was of the view that micromutations are useful in plant breeding for two reasons: (i) they might occur more frequently than macromutations, and (ii) they often do not affect vitality adversely as macromutations, because minute changes of physiological nature are less drastic.

The micromutations in plant breeding were best utilized in the

extensive and poineering work of Gregory (1956, 1961, 1965), Gaul (1961, 1965), Scossiroli (1965), Brock (1965b, 1967), Swaminathan (1969) and Lawrence (1968, 1975e). Gregory (1967) demonstrated that mutations affecting a quantitative trait of a crop can be induced by irradiation and phenotypic selection can accumulate positive mutations to produce better strains. Gaul (1965) treated seeds of four barley varieties with X-rays and demonstrated that the reduction in mean yield and increase in genetic variance depend on the dose applied. He further reported that even though the major part of induced genetic variability is in negative direction, a few lines surpassed the highest yielding control.

A few successful attempts have been made to induce polygenic mutations in pulses. In lentil, Sharma (1977) reported increase in variance for days to flowering, number of branches, pods and yield per plant in M_2 generation following gamma-rays and NEU treatments. However, variability for all these characters along with 100-seed weight increased further in M_3 generation, indicating the release of additional variability. Ravi et al. (1980) observed that mean of different quantitative characters of the treated population did not increase but the variance increased significantly. He noted greater selection advance for plant height, number of pods, primary branches and yield per plant in M_3 and M_5 than in M_2 generation. Kalia and Gupta (1989), following gamma-ray treatments, induced sufficient variation in various polygenic traits in both lentil types (bold and small seeded). The polygenic traits studied were seed yield, biological yield, harvest index and number of pods per plant, 100-seed weight, plant height, time to 50% flowering and time to maturity. The macrosperma type was found to be more radiosensitive. Sarker and Sharma (1989b) treated

seeds of cultivar, L3991 with gamma-rays, EMS, NEU and sodium azide. They reported higher variance for the characters studied viz., days to flowering, primary branches, peduncles and pods per plant, seeds per pod, 100-seed weight and seed yield per plant. Seeds per pod and 100-seed weight showed less variability in M_2 generation. Heterogeneity was observed among different M_2 families in each mutagenized population. On the basis of CV and mean, mutated families were identified as promising for multiple characters.

Abo-Hegazi (1973) treated seeds of five leguminous crops with gamma-rays to study the nature and magnitude of variation induced in M_1 generation. He noticed that CV increased for days to flowering, pod number, branches, plant height and seed yield per plant.

Khan (1970) irradiated seeds of gram with gamma-rays and reported mutations affecting plant height, branching, leaf size, pod size, and disease resistance. Mandal (1974) reported significantly higher variability (CV) in treated M_2 population for plant height, plant type, 100-seed weight, pods per plant, and seeds per pod. Muzeeb (1974) irradiated gram seeds with X-rays and recorded increase in variation for some morphological traits as well as yield components. Similarly, Rao (1974) found significant increase in overall inter- and intrafamily variances for seeds per pod, pods and yield per plant in chickpea. Shakoor and Haq (1980) noticed increased variance for quantitative characters in M_2 generation. Mutants selected in M_2 generation for grains per pod and pods and yield per plant were true breeding in M_3 generation. Kharkwal (1980) found many promising families in M_2 generation of gram having higher CV and mean for several characters of agronomic importance. Many of the families selected in M_2 were confirmed in M_3 on the basis of high character mean.

Rajput (1974) irradiated seeds of Vigna radiata with gamma-rays to study the nature and magnitude of polygenically induced variation. He found a shift in mean value following irradiation toward positive as well as negative direction for all the characters except pod length, which remained unchanged. NaLampang and Janon (1982) recorded significant increase in variability for branches and pods per plant, but plant height decreased significantly over the control in M_2 generation of black gram. Bhadra (1982) reported significant increase in variability for all the four characters studied, viz., number of bearing bunches, pods, seeds and yield per plant in blackgram. He selected many families in M_2 with higher CV and mean in comparison with the highest values in the control. Many of the families with higher mean were confirmed in M_3 as promising progenies for different characters. However, the CV values for all the traits under study increased.

Tickoo and Jain (1980) in mungbean reported increase in the overall and interfamily variance for six polygenic traits, viz., days to flowering, seeds per pod, pods per plant, 100-seed weight, yield per plant and harvest index in M_2 generation following treatment with EMS, HMU, HA and gamma-rays. They observed decrease in overall variance but increase in interfamily variance in M_3 and concluded that selection in M_2 is as effective as in M_3 and based on this, they isolated promising families in M_3 for many traits, particularly yield and pods per plant. Shakoor and Haq (1980) also observed higher variability (CV) for pods per plant, seeds per pod and 1000-seed weight in M_2 following mutagenic treatments. Sharma and Haque (1983) reported similar results for pods per plant, pods per cluster, grains per pod, and grain yield per plant with gamma-irradiation of two varieties of mungbean.

Rao (1974) found that the pattern of induced variability provides

considerable scope for selection within and between M_2 families in pigeonpea. As a result, Rao et al. (1975) selected plants in pigeonpea with higher harvest index by treating seeds with gamma-rays, EMS, NMU and HA. Nadarajan et al. (1982) reported that DES was more effective in increasing the pod number and seed size than gamma-rays.

Some information has also been generated on induced polygenic mutations in soybean. Raut et al. (1982) isolated several mutants with high yield, early maturity and determinate growth habit following treatment with gamma-rays, DES, EI and EMS. Upadhyaya and Singh (1979) recorded higher variability for all quantitative characters and shift in mean in both directions following mutagenic treatments. Baradjanegara and Umar (1982) observed higher variance for maturity, 100-seed weight and yield per plant, leading to effective selection for these traits in M_2 generation. Rajput and Siddiqui (1983) found that the seeds per pod, 100-seed weight and seed yield per plant decreased in irradiated population but the mean number of pods per plant shifted in both directions.

In groundnut, Sarma (1975) observed significant increase in overall variance and interfamily variance for various quantitative characters and concluded that pod weight, seed yield and number of secondary branches gave higher response to mutagenic treatment. Ojoma and Chhedda (1972) observed 1.2 to 8 times increase in genetic variance in M_3 of irradiated cowpea over control even without much change in character mean. Singh (1988) observed higher variance for days to flowering, pods per plant, seeds per pod, 100-seed weight and yield per plant leading to effective selection for these traits in M_2 and M_3 generations.

A large number of useful mutations have resulted as a result

of extensive work on induced polygenic variation in wheat (Bhatia and Swaminathan, 1962; Borojevic, 1965; Scossiroli, 1966a,b; Scossiroli et al. 1961; and Palenzona, 1963, 1964), barley (Gaul, 1961b; Ehrenberg et al., 1965; Goud, 1967a; Nilan et al., 1975), rice (Oka et al., 1958; Kao et al., 1960; Matsuo and Onozawa, 1961), oat (Krull and Frey, 1961; Frey, 1965), and maize (Gardner, 1968, 1969; Lonnquist et al., 1966).

Palenzona (1966) studied the progress of selection for three quantitative characters in wheat and concluded that selection in M_2 is less effective than in M_3 generation. Orlyuk (1972) and Maryushkin et al. (1977) found NEU to be the most effective mutagen in inducing genetic variability for polygenic traits as compared to gamma-rays and EI in wheat. Similar observations were reported by Minocha et al. (1970). Gill et al. (1974) induced polygenic variability by seed treatments with EMS and gamma- rays. They studied variability in M_3 and M_4 generations and found that the mean values either generally remained unaltered or shifted in negative direction. In rice, Oka et al. (1958) showed that mutations with positive and negative effects in relation to the control occur with equal frequency, and lower doses generate more variance. Jana and Roy (1973) observed considerable increase in variance for six characters in rice treated with EMS and EO. They observed shift in mean values towards the desired direction and found selection to be more effective in M_3 than in M_2 generation following gamma-irradiation. Tiwari et al. (1983) found in millet that variance for yield and its components increased significantly in M_2 and M_3 generations.

Donini et al. (1984) reviewed the work done on mutation breeding in different crops. They reported that, till 1982, 245 improved cultivars of

seed propagated crops have been developed by induced mutagenesis, out of which 146 are direct mutants and the remaining developed by utilizing induced mutants in hybridization programmes. Similarly, 254 improved cultivars of vegetatively propagated crops have been evolved using this technique.

The mean values of quantitative traits in the M_1 generation obtained from irradiated gametes (pollen) or dormant embryo (dry seeds) are generally lower than in untreated controls (Scossiroli, 1966a, b; Scossiroli et al., 1966; Heringa, 1964; Brock, 1965b, 1967; Gaul, 1965; Gill et al., 1974; Kulshrestha and Singh, 1983; and Rajput and Siddiqui, 1983). However, the difference between means of treated and untreated populations decreases in subsequent generations (Gardner, 1969). In a few instances, increase in character mean after mutagenic treatments has also been reported (Sharma and Saini, 1970; Enken and Sidorova, 1970; Kharkwal, 1980; Sharma and Haque, 1983), or it remains unaltered (Matsuo and Onozawa, 1961; Ojomo and Chheda , 1972; Rajput, 1974; and Ravi et al., 1980).

Dose effect on the magnitude of induced polygenic mutation was reported (Singh, 1988). On the one hand, it has been suggested that the dose causing maximum variability in one character was often not equally effective for other characters. Gaul (1965), on the other hand, found that the reduction in mean yield and increase in genetic variance depend on the dose applied. Generally, lower doses have been found to generate greater variability for polygenic characters (Oka et al.,1958; Kao, 1962; Scossiroli, 1965; Gill et al., 1974; and Ravi et al., 1980). However, in some studies, no relationship was found between the extent

of induced variation and mutagenic dose (Sharma, 1977). Also, some characters were reported to give better response to mutagenic treatments than others (Sarma, 1975; Sharma, 1977; NaLampang and Janon, 1982; Tickoo and Jain, 1980; Enken and Sidorova, 1970; Sharma, 1986; Kalia and Gupta, 1989; and Sarker and Sharma, 1989b).

8. **Heritability and genetic advance**

It is the degree of correspondence between the genotype and phenotype, i.e. the proportion of genotypic variance to the total phenotypic variance. The change caused by selection, which is the change in the mean genotypic level of a population, is referred to as selection advance. High heritability coupled with high genetic advance indicates the expected effectiveness of selection for the character under consideration.

Very little information is available on pulse crops regarding heritability and genetic advance under mutagenic treatments. In lentil, Sharma (1977) recorded higher GCV for all the quantitative characters studied except seed size in M_2, suggesting that a part of the variability recorded is genotypic which increased heritability and genetic advance (GA). The GCV, heritability (h^2) and GA remained unchanged for days to flowering, but these parameters displayed a general increase for number of branches and pods per plant, seed size (1000-seed weight), and seed yield per plant. Ravi et al. (1980) reported high heritability for pods per plant, followed by seeds and primary branches per plant. However, GA was highest for number of seeds per plant and pods per plant. They also reported higher gain from selection for various yield contributing traits. Dixit and Dubey (1985) reported the highest heritability for days to flowering while genetic

advance was highest for seed yield/plant. Sarker (1985) studied heritability and GA in M_2 and M_3 generations of lentil and observed highest h^2 for number of peduncles per plant, followed by days to flowering, 1000-grain weight and yield per plant. However, GA was highest for number of pods per plant, followed by peduncles and seed yield per plant in M_2 generation. In M_3 generation, the heritability and GA estimates were higher than in M_2 generation, but the trend regarding various characters was similar in both generations. Kalia and Gupta (1989), in both microsperma and macrosperma lentils, studied h^2 and GA in M_3 generation of irradiated material. He reported high h^2 and GA for most of the characters studied and found macrosperma type to be more radiosensitive.

In peas, Kaul (1978) studied plant height, days to maturity, seeds per pod, 1000-seed weight, yield per plant and seed protein content in two mutants of pea variety Bonneville and three mutants of Kashmir Local. He found high estimates of heritability for yield components and maturity period. Mohan (1983) estimated h^2 and GA in mutagenized population and recorded high heritability for pods and yield per plant, and demonstrated high response of these characters to selection in M_2 and M_3 generations. Singh (1988) also reported high h^2 for days to flowering, followed by 100-seed weight and seeds per pod, and high genetic advance (GA) for pods per plant, followed by yield per plant and seeds per pod. For the remaining characters, the estimates of h^2 and GA were comparatively lower.

In mungbean, Khan (1983) reported highest heritability for grain yield in the combined treatment (20 kR +0.01% HZ) as compared to irradiation or hydrazine (HZ) alone. Later, Khan (1984) studied the effect of several mutagenic treatments on heritability and GA for quantitative traits

in M_2 and M_3 generations and reported highest heritability for number of fertile branches in M_2 generation, but the genetic gain in M_3 was maximum for pods per plant. Bhamburkar and Bhalla (1983) estimated h^2 and GA in mutagenized blackgram populations for three generations and concluded that selection gain was conspicuous for all the yield contributing traits following HZ treatment. They also suggested that direct selection can be advantageous for seed size after HZ treatment individually as well as in combination with gamma-rays. Similar observations were reported in gram by Singh et al. (1973). Pathirana (1982), on the other hand, observed high h^2 only for 100-seed weight in groundnut in gamma-irradiated population, the other characters showing more or less equal and moderate estimates.

OKa et al. (1958) studied heritability of many polygenically controlled characters in irradiated population of rice and recorded high h^2 for some characters. They further pointed out that the populations developed after treatment with higher dose tend to give higher h^2 value. Saini and Sharma (1970) found higher estimates of h^2 and GA in combination of hybridization with irradiated than irradiation alone in rice. Jana and Roy (1973) studied the effect of EMS and EO on the heritability of six characters in rice. They noticed lower h^2 value than the predicted h^2 estimates in M_3 generation.

In wheat, Orlyuk (1972) found higher h^2 values for grains per spike, followed by grain yield and 1000-seed weight. Similar observations were reported by Sichkar et al. (1975). Gupta and Virk (1972) observed increase in the additive and nonadditive components of variance following irradiation. The GA realized from selection for yield was more than expected

in early generations. Kassem et al. (1976) studied the effect of mutagenic treatments on h^2 of specific traits and found them to be unique for each parent. The h^2 tended to be higher in the EMS treated population as compared to irradiated in both varieties used in the study. Mathur (1987) found high h^2 for yield components in irradiated wheat population, such as, number of spikelets and grains per spike. Moreover, irradiation of F_1 seeds in three crosses enhanced the h^2 estimates for spike length in addition to number of spikelets per spike and number of grains per spike. These results were also reflected in expected genetic advance computed for various populations.

9. **Early generation selection**

Conventionally it has been suggested that selection for polygenic traits should normally be practised in M_3 generation when the magnitude of variability is expected to be highest. Attempts have also been made to explore the possibility of selecting for polygenic variability in earlier (M_2) generation with a view to economise time and effort in selection.

A few attempts have been made to exercise selection in M_2 generation in the past (Brock and Latter, 1961; Brock and Andrew, 1965; Bhatia and Van der Veen, 1965; Shakoor et al., 1978; Mohan, 1983; Sarker, 1985; and Singh, 1988). However, Gupta and Swaminathan (1967) first suggested that different M_2 families should be analysed for the mean and variance of the character under consideration and the families showing higher mean and greater variance than the highest in the control should be selected. Similarly, Rao (1974) observed that considerable scope exists for selection between-and within M_2 progenies in gram. However, some experiments have demonstrated that selection in M_3 is more effective than in M_2

(Palenzona, 1966; Jana and Roy, 1973; and Kalia and Gupta, 1989).

A comparison of studies on selection in M_2 and M_3 generations revealed that in many cases the two generations may not differ much in respect of selection response in lentil (Sharma, 1977; Sarker, 1985), mungbean (Tickoo and Jain, 1980; Bhadra, 1982), gram (Rao, 1974; Kharkwal, 1983), peas (Mohan, 1983; Singh, 1988), and wheat (Scossiroli, 1968; Mathur, 1987). However, Sharma (1986) reviewing the work on mutation breeding in different crop plants, suggested that promising progenies can be identified with high degree of confidence in M_2 on the basis of mean and variance.

10. **Screening techniques for induced polygenic variability using different mutagens**

The main problem associated with the improvement of polygenic characters through mutational approach is non-availability of precise and efficient screening techniques to spot these mutations which occur with lower frequency in a large population. After the work of Brock (1965a, b, 1967), it became a normal practice to advance only normal looking M_2 plants to M_3 generation and apply the first dose of selection not earlier than M_3. This results in increased volume of nonmutated material and also reduction in the probability of isolation of promising variants.

Oka et al. (1958) adopted bulk population approach to isolate promising lines for heading date and plant height in mutagen-treated population in rice. They advanced material upto M_4 generation and applied the first dose of selection based on individual plant only in M_5 generation. This way, they were able to isolate some promising lines for different polygenic traits. Papa et al. (1961) practised selection for 5 polygenic traits in M_3 generation in soybean and used the 10 high yielding progenies

from each treatment for further evaluation. Selection for high yield was found effective in one variety but not in the other.

Borojevic (1965) studied the selection response of number of kernels per spike in wheat. He isolated 10 lines from each treatment in M_2 at random and from each line (intrafamily) spikes with the highest number of kernels were selected. Similar procedure was followed in M_3 and M_4 generations where five spikes were taken randomly from each line. This selection was effective for number of kernels.

Palenzona (1966) attempted selection for many polygenic characters of wheat in M_2 and M_3 generations and found selection in M_3 to be more effective than in M_2. Scossiroli (1968) on the other hand, did not observe any difference in selection response between M_2 and M_3 generations.

Gupta and Swaminathan (1967) studied selection response for number of secondary branches in Brassica compestris var. toria. They selected M_2 families on the basis of plot means and variance. The families having higher plot mean and variance in M_2 generation were selected and advanced to M_3 generation. The same procedure of selection was applied in M_3 also to identify promising families and ultimately succeeded in isolating many promising lines.

According to Gaul et al. (1969), only normal looking plants from M_2 generation should be advanced to M_3 generation for selection for higher yielding polygenic mutations. Selection was applied for the first time based on the results of M_4 generation for yield. Eight M_7 families from early selection and four families from late selection were compared in M_8. It was found that more high yielding mutants were isolated from early selections.

Ojomo and Chheda (1972) practised selection for grain yield on progeny basis in M_2 generation in cowpea. Equal number of plants were selected from each treatment in M_2 to raise M_3 generation. Twelve most promising lines were selected from each population based on the M_3 performance. These selections were tested in yield trial in M_4 generation. Many of these selections were found superior over control.

Jana and Roy (1973) studied response to selection for many polygenic traits, viz., tiller number, panicle length, number of sterile and filled grains per panicle, 100-seed weight, and grain in M_2 and M_3 generations in rice. Only those lines were selected and advanced to M_3 generation which showed significant deviation in mean values towards positive direction from the control. Seeds from each M_2 family were bulked by taking equal number of seeds from 50 random plants. A random sample from this bulk was taken to raise M_3 progeny. Many promising lines with higher mean value than control were detected following selection in M_3 after EMS treatment.

Gill et al. (1974) selected for heading date, 100-seed weight, and tiller number and yield per plant in M_2 and succeeding generations of barley. In M_2 generation, the plants were selected randomly. In M_3 generation, the top 5% progenies were selected and advanced to M_4 generation. Repeating the same procedure in M_4 and M_5, a number of early and high yielding lines were isolated. Sharma(1977) studied the selection response in M_2 and M_3 generations in lentil. The selection in M_2 as well as M_3 based on high mean and high variance lead to the isolation of promising families. He observed that the selection response in M_2 and M_3 generations varies from one character to another. The response to selection in positive direction in M_2 was greater for number of branches, pods and seed yield per plant.

Ravi et al. (1980) studied selection efficiency for four polygenic traits. In M_3 generation, raised from 10 normal looking M_2 plants in each treatment, the top 10% progenies were selected on the basis of higher character mean than control. A number of lines with desired characters were advanced from M_3 generation to raise M_4 generation, and suggested that selection should be started from M_3 generation for improvement in quantitative characters.

In mungbean, Bhadra (1982) practised inter-and intrafamily selection in M_2 and M_3 generations for many polygenic traits. In M_2 generation, promising progenies were identified on the basis of higher CV and mean. From each M_2 family 20% plants were selected to raise M_3 families. In M_3, only those families were selected which showed higher mean, but not CV than in control, as intrafamily variance is expected to decrease in M_3. This study lead to the conclusion that selection for various polygenic traits in M_2 is as effective as in M_3.

Zakri et al. (1983) studied the selection response for maturity period, lodging resistance and yield per plant in M_2 and M_3 generations in soybean. In the procedure adopted, they took two pods from each M_1 plants and bulked which gave rise to separate M_2 families. Selection of M_3 lines was carried out for yield, maturity period and lodging resistance, for which several lines were isolated.

Kharkwal (1983) suggested a selection technique for isolating promising families in M_2 and succeeding generations. According to him, the M_2 families of greater interest are those where the coefficient of variability (CV) has increased and simultaneously the mean value for the particular character has either increased or at least remained unchanged

in relation to the control. The other criterion was selection of the 5% progenies on the extreme side with positive variability of the frequency distribution curve. The effectivenss of this screening technique for micromutations was confirmed by the fact that a large number of superior micromutants with higher mean than control were isolated.

Mohan (1983) studied selection efficiency in M_2 and M_3 generations in peas. He also proposed that selection in M_2 should be based on higher mean and variance than in control. The selection response was found to be character specific and directly associasted with the genetic variability existing for a given trait. The extent of variability for polygenic traits in M_3 populations derived from the progenies segregating for macromutations in M_2 generation was found to be 1.4 to 3.2 times as high as in the unselected M_3 material raised from normal looking M_2 progenies. The character means in the macromutational M_3 populations were generally not affected adversely.

Sarker (1985) studied selection response for many polygenic characters in M_2 and M_3 generations of lentil, and suggested that in M_2 generation, promising families should be selected on the basis of higher CV and mean than the highest value recorded in the control for the character under consideration. In each progeny, two best looking plants were carried forward from M_2 to raise M_3 generation. In M_3, the main selection criterion was higher mean than highest value in control so as to identify promising families. He isolated many promising families with improvement in multiple characters. In peas, Singh (1988) followed the same procedure as Sarker (1985) but with different number of plants selected. From each progeny, three best looking plants were carried forward from M_2 to raise M_3 generation.

Mathur (1987) used higher mean and variance as the criterion for identifying promising families in M_2 generation of bread wheat. In M_3 also the same criterion was used to confirm the promising progenies. He isolated many progenies with higher mean value for all the polygenic characters studied, including grain yield per plant.

It appears from the above presentation that there is a definite scope for initiating the selection procedure in earlier generations. The technique of identifying the suspected promising plants or progenies needs to be perfected so as to increase the efficiency of selection, reduce the burden of carrying forward unmutated mass of plants, and save time and effort.

MATERIALS AND METHODS

The investigation reported was conducted at the Division of Genetics, Indian Agricultural Research Institute (IARI), New Delhi, during 1985-1988.

1. MATERIALS

1.1 Seed

The experimental material was the seed of a moderately bold seeded macrosperma variety of lentil, Precoz Selection (PS) of IARI origin, which was obtained after selection from Precoz, a macrosperma lentil originating from Northern Argentina, received through ICARDA (Acc.No. ILL-4605) in the International Summer Nurseries of 1982.

The other bold seeded varieties of the microsperma group, L4076 and Sehore 74-3(S74-3) were used as checks for comparison of yield in M_3 generation. The variety L4076 was also developed at IARI, New Delhi, and is suitable for cultivation in NWPZ and CZ. The variety S74-3 was developed at Sehore, Madhya Pradesh, and is suitable for cultivation in CZ.

1.2 Mutagens

Three mutagens: one physical, gamma-rays, and two chemcials, ethylene imine (EI) and N-nitroso-N-ethyl urea (NEU), were used for seed treatment. Sources of the mutagens and their mode of action are given in Table 1.

2. METHODS

2.1 Mutagenic treatments

Mature air-dried seeds with about 10-12% moisture content were used for mutagenic treatments. The details of the mutagenic treatments are given in Table 2.

Table 1. Sources and characteristics of mutagens used in the study

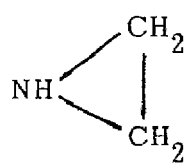
	Mutagen	Source	Description	Functional group	Mode of action
A.	Physical mutagen				
	1. Gamma-rays	A 1930 Ci ^{60}Co gamma cell installed in the Division of Genetics, IARI, New Delhi	Short wave electromagnetic radiation	-	Ionization
B.	Chemical mutagens				
	1. Ethylene imine (EI)	(Prof. I.A.Rapoport) Division of Chemical Genetics, Institute of Chemical Physics, Academy of Sciences, Moscow (USSR)	Monofunctional 	C_2H_5	Alkylation
	2. N-nitroso-N-ethyl urea (NEU)	-do-	Monofunctional C_2H_5-N-(NO)CONH$_2$	C_2H_5	Alkylation

Table 2. Mutagens and their doses (concentrations and durations)

Mutagen	Dose	No. of seeds treated	Duration	Treatment condition
Control	Plain water	500	6 h	Wet
Gamma-rays	5 kR	500	1 min	Dry
	10 kR	1000	2 min	Dry
	20 kR	1500	4 min	Dry
EI	0.005%	500	6 h	Soaking (400 ml)
	0.01%	1000	6 h	Soaking (500 ml)
	0.02%	1500	6 h	Soaking (600 ml)
NEU	0.005%	500	6 h	Soaking (400 ml)
	0.01%	1000	6 h	Soaking (500 ml)
	0.02%	1500	6 h	Soaking (600 ml)

2.1.1 Physical mutagen

Only one physical mutagen (gamma-rays) was used. The facility of Gamma Cell (1930 Ci ^{60}Co) installed in the Division of Genetics, IARI, New Delhi, was used for seed irradiation. Seeds of the test variety PS were irradiated with gamma-rays at the dose rate of 5 kR/min, using 500, 1000 and 1500 seeds for 5, 10 and 20 kR doses, respectively.

2.1.2 Chemical mutagens

Ethylene imine (EI) and N-nitroso-N-ethyl urea (NEU) were the two monofunctional alkylating agents used in this study. Samples of 500, 1000 and 1500 seeds were soaked in freshly prepared aqueous solutions of the respective concentrations of each mutagen for 6 h at 21°C with constant intermmittent

stirring at hourly intervals. Thenafter the seeds were thoroughly washed under running water to remove the superficial mutagen from seed surface. The seeds were sown in the field immediately after treatment, whereas seeds soaked in plain water for 6 h were used as control.

2.2 Experimental methodology

This investigation was extended over three cropping seasons. During first season (1985-86), M_1 was raised. In second (1986-87) and third (1987-88) seasons, M_2 and M_3 generations were raised. All three generations were grown in well prepared land at the Division of Genetics, IARI, New Delhi.

The experimental material in M_1, M_2 and M_3 generations was handled as described below.

2.2.1 M_1 generation

The M_1 generation was planted during winter (Rabi) of 1985-86. The control and treated seeds were sown in 4 m long rows with 30x5 cm spacing. The recommended agronomic and cultural practices were followed to raise a good crop.

2.2.1.1 Observations recorded in M_1 generation

The following M_1 parameters were recorded to estimate the mutagenic damage.

(i) **Germination**

The emergence of coleoptile at soil surface was taken as an indication of germination. The number of seeds germinated was recorded 20-25 days after sowing to determine germination percentage.

(ii) **Plant survival**

Plant survival was defined as a plant reaching maturity and producing

seeds. The survival percentage was calculated as the proportion of plants surviving till maturity out of the total number of seedlings germinated.

(iii) **Plant fertility**

The plants surviving in different treatments, including control, were harvested and threshed individually, and their seeds counted. Seeds per plant in different treatments were estimated by dividing the total number of seeds by the total number of plants in a particular treatment. Finally, relative plant fertility was computed by dividing the seeds per plant in a particular treatment by that of the control multiplied by 100.

(iv) **Leaf aberrations (a-sectors)**

The term leaf aberration is used as a name for the deviating areas in the form of spots or sectors on the foliage, which appear as a result of mutagenic treatment. After seed treatment, many small leaf aberrations (called a-sectors) are discernible in the first leaf, and thereafter their number decreases while their size increases with each consecutive leaf (Blixt et al.,1964). Therefore, observations on leaf variation were recorded from germination to 4-5 leaf stage of the plant. The entire material in each treatment was classified into two groups on the basis of a-sectors intensity henceforth called high and low seedling damage.

2.2.1.2 **Harvesting of M_1 generation**

The M_1 generation was harvested on single plant basis. The plants in each treatment, grouped on the basis of leaf aberrations, were further classified on the basis of fertility (seeds per plant). Thus, each treatment was divided into four groups.

(i) Low seedling damage and low fertility reduction (LL)

(ii) High seedling damage and low fertility reduction (HL)

(iii) Low seedling damage and high fertility reduction (LH)

(iv) High seedling damage and high fertility reduction (HH)

From each group, plants were taken to raise the M_2 generation. The progeny of each individual M_1 plant constituted one M_2 family.

2.2.2 M_2 generation

The individual M_1 plant progenies were sown in the field in separate M_2 progeny rows during rabi, 1986-87. The spacings between rows and plants were 30 and 5 cm, respectively. The recommended agronomic practices and plant protection measures were followed during the entire crop season.

2.2.2.1 Observations recorded in M_2 generation

(A) Macromutations

(i) Chlorophyll mutations

All the treated as well as control progenies were screened for chlorophyll mutations from emergence till the age of 4 weeks. The identification and classification procedures proposed by Lamprecht (Blixt, 1961, 1972; Yarnell, 1962) for pea, were followed. The frequency of chlorophyll mutations was calculated as percentage of mutated progenies/plants.

(ii) Morphological mutations

Throughout the entire growth period, all M_2 progenies were examined several times to detect viable mutations affecting various morphological attributes. The frequency of morphological mutations was also calculated as for the chlorophyll mutations.

(iii) Mutation frequency

The frequencies of chlorophyll and morphological mutations were estimated as follows:

(a) **M_2 family basis** (percentage of segregating M_2 progenies)

$$\text{Mutation frequency (\%)} = \frac{\text{No. of mutated progenies}}{\text{Total } M_2 \text{ progenies}} \times 100$$

(b) **M_2 population basis** (percentage of mutated M_2 plants or mutants)

$$\text{Mutation frequency (\%)} = \frac{\text{No. of mutants}}{\text{Total } M_2 \text{ plants}} \times 100$$

(iv) **Mutagenic effectiveness and efficiency**

Mutagenic effectiveness is a measure of the frequency of mutations induced by a unit dose of mutagen, while mutagenic efficiency gives an idea of the proportion of mutations in relation to the total biological damage measured through lethality, sterility, etc.

The parameters of mutagenic effectiveness and efficiency were estimated by the formula suggested by Konzak et al. (1965).

(a) Mutagenic effectiveness = Mf/tc or Mf/kR

(b) Mutagenic efficiency = Mf/S

Where, Mf= Percentage of M_2 families segregating for mutations (chlorophyll+ viable morphological).

t= Duration of treatment with chemical mutagen, h

c = Concentration of chemical mutagen, %

kR= Kilo Roentgen of physical mutagen

S = Sterility in M_1, %

(B) **Micromutations**

Observations were recorded on induced genetic variability for eight quantitative characters of economic importance. Only families with normal looking plants were included in the study. Those families which were showing segregation for macromutations (chlorophyll and morphological) were treated as a separate class. Five normal looking plants from each M_2 family that was

not segregating for macromutations and 5-10 normal looking plants from each segregating family for macromutations, depending on the availability of plants in a family, were choosen randomly to record observations on the following eight quantitative characters of economic value.

(i) **Days to maturity**

The maturity was calculated as the total number of days taken by a plant from sowing to the physiological maturity.

(ii) **Plant height**

The measurement from soil surface to the tip of the plant (cm) was considered as the plant height.

(iii) **Number of branches per plant**

The total number of fruiting branches per plant recorded at harvest.

(iv) **Number of clusters per plant**

The total number of effective clusters (pod bearing peduncles) per plant counted at harvest.

(v) **Number of pods per plant**

The total number of effective pods (containing seed) per plant recorded at harvest.

(vi) **Number of seeds per pod**

The total number of seeds per plant divided by total number of pods produced by a plant gave seeds/pod.

(vii) **100-seed weight**

100 seeds from each plant were counted and weighed; but in case of those plants where 100 seeds were not available, the total weight of seed harvested from each plant was used to determine the weight of 100 seeds (g).

(viii) **Seed yield per plant**

Total weight of the seed (g) harvested from a single plant.

2.2.2.2 **Selection in M_2 generation**

Selection was done at both interfamily and intrafamily levels.

(A) **Interfamily selection**

All those M_2 families were identified which showed higher CV for any one of the eight characters than the corresponding highest value in the control. These families were considered to be carrying induced mutations and their progeny means were compared with the highest control mean. From such analysis it was possible to detect some M_2 families having higher CV as well as mean for different characters. Such progenies were called "promising" M_2 families.

In case of days to maturity, increased CV and lower mean were considered to denote the promising families, as early maturity is dsirable. Further, more rigorous selection was applied to identify those M_2 families which showed higher CV and mean for more than one character (higher CV with lower mean for days to maturity). Such families were considered to be "exceptionally promising" for selection combining early maturity with high yield.

All the promising M_2 families (the families showing higher CV and better mean for one or more characters) and also the unselected M_2 families were advanced for further screening in the M_3 generation.

(B) **Intrafamily selection**

Intrafamily selection was practised simultaneously with interfamily selection. Three best plants were identified in each promising M_2 family. Finally, M_2 selected plants as well as those plants from the families not identified as

" promising" were used to raise M_3 generation. Thus, each M_3 family comprised offsprings of individual M_2 plants.

2.2.3 M_3 generation

The M_3 progenies were arranged in augmented block design along with three check varieties (one row each of untreated PS, L4076 and S74-3). A single row of 1 m length constituted one M_3 family. Row-to-row and plant-to-plant distances were 30 and 5 cm , respectively.

The M_3 generation was raised as single plant progenies of M_2 plants along with the corresponding controls (PS, L4076 and S74-3) to study micromutations in detail. Almost all M_2 families were advanced to M_3 generation except those showing very poor performance in respect of grain yield. The rejected families were also raised in M_3 to see if some of them performed better in M_3. In M_3 , only those families were harvested which showed uniformity without segregation for a major trait.

2.2.3.1 Observations in M_3 generation

The material in M_3 generation was classified into two broad groups, i.e. macromutation and nonmutated for macromutations, in two extreme groups (LL and HH) in each treatment. The remaining two groups (LH and HL) were not continued beyond M_2 generation in view of increased volume of experimental material. The progenies segregating for macromutations in M_3 were not considered for analysis of polygenic traits. Observations were restricted to the same eight quantitative characters as in M_2, taking five random plants from each family.

2.2.3.2 Selection of promising M_3 families

As the intrafamily variance was expected to decline in M_3 generation,

the comparison of mean values was considered as the most important criterion to estimate the effectiveness of M_2 selection. Therefore, the mean value of each M_3 family was compared with the highest mean value recorded in the control. Thus, an M_3 family having higher mean than the highest in the control was considered as "promising" to advance further.

Table 3. Population size in different generations

Treatment	No. of seeds treated	M_2 population		M_3 population	
		Families	Plants	Families	Plants
Control	500	100	500	237	1185
Gamma-rays	3000	742	2923	1083	5415
EI	3000	688	2902	1066	5330
NEU	3000	747	3171	1005	5025
Total of the experiment	9500	2277	9496	3391	16955

2.3 Statistical methods

The analysis of micromutations was done by using various statistical procedures. The data recorded in M_2 and M_3 generations on eight quantitative characters were subjected to the following statistical analyses.

2.3.1 Analysis of statistical parameters of induced variability in M_2 and M_3 generations

For each treatment and control, range and mean were computed on family and population basis. The magnitude of variability was estimated

on the basis of variance and coefficient of variation (CV) on family and population basis using the standard statistical procedures (Snedecor and Cochran, 1967).

The skeleton of analysis of variance is given in Table 4.

Table 4. Analysis of variance in M_2 generation

Source of variation	DF	MS	Expected MS	F value
Interfamily	(f-1)	V_{BF}	$\sigma^2_{WF} + n\,\sigma^2_{BF}$	V_{BF}/V_{WF}
Intrafamily	f(n-1)	V_{WF}	σ^2_{WF}	
Total	fn-1	-	-	-

where,

f = Number of families

n = Number of plants in each family

The observed F values were compared against the corresponding table values (Fisher and Yates, 1963).

The various statistical parameters for the analysis of induced variability were computed as follows:

Let x_{ij} be the value of the j^{th} plant in a sample drawn from the i^{th} family; f the total number of families; n_i the number of plants in the i^{th} family, and $N = \sum_{i=1}^{f} n_i$ the total number of plants under study, then various parameters are defined as follows :

(i) Total of the i^{th} family $(x_i.) = \sum_{j=1}^{n_i} x_{ij}$

(ii) **Family mean**

The character mean was calculated based on five random plants in a family.

Mean of the i^{th} family $(\bar{x}_{i.}) = \frac{1}{n_i} \sum_{j=1}^{n_i} x_{ij}$

(iii) **Population mean**

The character mean was calculated over all the plants studied in a treatment. In other words, it is the average mean value over different families in a particular treatment.

$$\text{Population mean} \quad (\bar{\bar{x}}) = \frac{1}{N} \sum_{i=1}^{f} \sum_{j=1}^{n_i} x_{ij}$$

(iv) **Intrafamily variance**

This refers to the variance for a character among the randomly selected plants of a family.

$$\text{Intrafamily variance } (i^{th} \text{ family}) = \frac{1}{n_i - 1} \left[\sum_{j=1}^{n_i} x_{ij}^2 - \frac{(x_{i.})^2}{n_i} \right]$$

(v) **Interfamily variance**

It is the variance for a character between different families of a single treatment.

$$\text{Interfamily variance} = \frac{1}{f-1} \left[\sum_{i=1}^{f} \frac{x_{i.}^2}{n_i} - \frac{1}{N} \left\{ \sum_{i=1}^{f} \sum_{j=1}^{n_i} x_{ij} \right\} \right]$$

(vi) **Population variance**

This refers to the interplant variance for a character averaged over all the families of a treatment.

$$\text{Population variance} = \frac{1}{N-1}\left[\sum_{i=1}^{f}\sum_{j=1}^{n_i} x_{ij}^2 - \frac{1}{N}\left\{\sum_i \sum_j x_{ij}\right\}^2\right]$$

(vii) **Intrafamily coefficient of variability**

Using the intrafamily variance estimates and progeny means for a particular character of a family, the intrafamily coefficient of variability is estimated as follows:

$$\text{Intrafamily CV} = \frac{\sqrt{\text{Intrafamily variance}}}{\text{Family mean}} \times 100$$

$$= \frac{\sqrt{\frac{1}{n_i-1}\left\{\sum_{j=1}^{n_i} x_{ij}^2 - \frac{(x_i.)^2}{n_i}\right\}}}{\frac{1}{n_i}\sum_{j=1}^{n_i} x_{ij}} \times 100$$

(viii) **Population coefficient of variability**

It was calculated using the population variance and population mean of a character in a particular treatment.

$$\text{Population CV} = \frac{\sqrt{\text{Population variance}}}{\text{Population mean}} \times 100$$

$$= \frac{\sqrt{\frac{1}{N-1}\left\{\sum_{i=1}^{f}\sum_{j=1}^{n_i} x_{ij}^2 - \frac{1}{N}\left(\sum_i \sum_j x_{ij}\right)^2\right\}}}{\frac{1}{N}\sum_{i=1}^{f}\sum_{j=1}^{n_i} x_{ij}} \times 100$$

(ix) **Standard error (SE)**

The term "standard error" of any estimate is a measure of the average magnitude of the difference between the sample estimates and population parameter taken over all possible samples of the same size from the population.

The standard error is estimated as given below :

$$SE = \frac{SD}{\sqrt{N}}$$

where, N= is the sample size

(x) **Test of significance for intrafamily variance in M_2 generation**

Individual family variance in M_2 generation was tested as given below:

$$F = \frac{V_1}{V_2}$$

where V_1 -- individual family variance to be tested,

V_2 -- the variance of the family showing highest variance in control.

The F values obtained were compared against the table values at n_1-1 and n_2-1 degrees of freedom, and 1 and 5% levels of significance.

(xi) **Bartlett's test of homogeneity of variances**

The comparison of error variances between families provides a rough idea of the relative magnitudes of genetic variability among the families. However, it is necessary to carry out the test of homogeneity of error variances before making the comparison, since differences in genetic variability could be assumed to exist only if significant heterogeneity between error variances is revealed by the test.

The intrafamily variance in mutation breeding experiments is attributed to genotypic plant-to-plant differences as well as environmental variations. The use of Bartlett's test here can confirm whether genotypic plant-to-plant differences are significant. At the same time, this test can also testify whether different families in the treated population are significantly different on the basis of their variances.

The test is conducted as follows:

Let there be n families with their individual variances as S_1^2, S_2^2, S_3^2, ------S_n^2 based, respectively, on K_1, K_2, -----K_n degrees of freedom. From these values $\bar{S}^2$ is calculated by the following formula:

$$\bar{S}^2 = \frac{1}{\sum_1^n Kr} \left(\sum_1^n Kr \quad Sr^2 \right)$$

The quantity, $\chi'^2 = \left\{ \left(\sum_1^n Kr \right) \log_e \bar{S}^2 - \sum_1^n Kr \log_e Sr^2 \right\}$ is distributed approximately as χ^2 with (n-1) degrees of freedom but is slightly biased upwards. It can be effectively corrected by dividing with the correction factor

$$C = 1 + \frac{1}{3(n-1)} \left\{ \sum_1^n \frac{1}{Kr} - \frac{1}{\sum_1^n Kr} \right\}$$

The quantity χ'^2 /C obtained is compared against the table value of χ^2 at n-1 degrees of freedom; if the value is significant then the variances are concluded to be significantly heterogeneous.

2.3.2 **Estimation of genetic parameters in M_2 and M_3 generations**

(i) **Genotypic coefficient of variation (GCV)**

This was estimated as follows :

$$\text{Genotypic coefficient of variation} = \frac{\sqrt{\sigma_g^2}}{\bar{X}} \times 100$$

where σ_g^2 — genotypic variance, and $\bar{X}$ — the population mean.

(ii) **Phenotypic coefficient of variation (PCV)**

PCV was estimated as follows:

$$\text{Phenotypic coefficient of variation} = \frac{\sqrt{\sigma_p^2}}{\bar{X}} \times 100$$

where σ_p^2 — phenotypic variance, and $\bar{X}$ — the population mean.

(iii) **Heritability**

Heritability in broad sense (h^2) was computed as the ratio between the interfamily variance (σ^2_{BF}) and the total phenotypic variance (σ^2_T) :

$$h^2_{(bs)} = \frac{\sigma^2_{BF}}{\sigma^2_T} \times 100$$

where $\sigma^2_T = \sigma^2_{BF} + \sigma^2_{WF}$

$$\sigma^2_{BF} = \frac{V_{BF} - V_{WF}}{n}$$

$$\sigma^2_{WF} = V_{WF}$$

σ^2_{BF} — interfamily variance

σ^2_{WF} — within family variance

(iv) **Genetic advance**

The expected genetic gain (GA) due to selection was estimated as percentage of mean :

$$GA = \frac{\sqrt{\sigma^2_T} \times h^2_{(bs)} \times K}{\bar{X}} \times 100$$

where K — selection differential (for 5% selection pressure, K = 2.06), and $h^2_{(bs)}$ — heritability in broad sense.

2.3.3 Field layout in M_3 generation

The M_3 families were compared for induced polygenic variability in each treatment in augmented block design (Federer, 1956), where each block had different test progenies along with three rows of the control varieties (one row each of PS, L4076 and S74-3). The analysis of variance for each character was done separately as follows:

Table 5. Skeleton of analysis of variance of augmented block design in M_3 generation

Source of variation	DF	MS	F value
Block	(b-1)	-	
Entries (Control+new progenies)	(V_b+V-1)	V_{vs}	
Control varieties	(V_b-1)	V_v	
New progenies and control vrs new progenies	V	V_s	
Intra block error	$(V_b-1)(b-1)$	E_e	
Total	$(\mu-1)$		

where V_b-- No. of check varieties, v -- No. of new progenies/test progenies, b -- No. of blocks, and n -- No. of new/test progenies in each block. Then, no. of plots in each block,

$$\mu = b(V_b+n)$$
$$= bV_b+bn$$
$$= bV_b+v$$

Various standard errors under augmented block design were estimated as follows:

(i) SE for testing difference between two check variety means :

$$SE_{(1)} = \sqrt{\frac{2E_e}{b}}$$

where E_e is the error mean square.

(ii) SE for testing difference between two new progenies' means when both are in the same block :

$$SE_{(2)} = \sqrt{2E_e}$$

(iii) SE for testing difference between two new progenies' means when they are in different blocks:

$$SE_{(3)} = \sqrt{2E_e \left(1 + \frac{1}{V_b}\right)}$$

(iv) SE for testing difference between the check variety and a progeny (strain) under comparison :

$$SE_{(4)} = \sqrt{E_e \left(1 + \frac{1}{b} + \frac{1}{V_b} + \frac{1}{bV_b}\right)}$$

EXPERIMENTAL RESULTS

The main findings of the present investigation generation-wise are presented below.

1. Observations in M_1 generation

The immediate effects of mutagenic treatments on genetic material were measured in terms of reduction in germination, plant survival and seed fertility as compared to control (untreated) in M_1 generation.

1.1 Germination

The results presented in Table 6 and Fig. 1a show that all the mutagenic treatments significantly reduced germination as compared to control. In general, chemical mutagens had more drastic effect (EI 68.9 - 87.0% and NEU 65.3 -83.1% germination) than gamma-rays (79.1 - 91.1% germination). Among the chemical mutagens, NEU showed more severe effect than EI. Reduction in germination was linearly dose dependent with increasing dose of all mutagens (Fig. 1a). Maximum reduction (only 65.3% germination) was observed with the highest dose NEU (0.02%), which was comparable to the highest dose of EI (0.02%), giving 68.9% germination. Similarly with gamma-ray treatments, the maximum reduction (79.1% germination) was observed with the highest dose (20 kR). The lowest doses of both chemicals (0.005%) also caused comparable damage (EI 87.0% and NEU 83.1% germination), while the lowest dose of gamma-rays (5 kR) caused still less damage (91.1% germination).

1.2 Plant survival

The results on plant survival (Table 6, Fig. 1b) indicate that all the mutagenic treatments decreased plant survival drastically. Plant survival also showed trend similar to germination: chemicals caused more drastic reduction in

Table 6 Effect of mutagens on germination, plant survival and seed fertility in M_1 generation

Treatment	Relative, %		
	germination	plant survival	seed fertility
Control	100.0	100.0	100.0
Gamma rays			
5 kR	91.1	82.2	76.5
10 kR	85.5	74.6	72.6
20 kR	79.1	58.2	65.2
EI			
0.005%	87.0	76.2	74.0
0.01%	77.0	61.8	70.5
0.02%	68.9	47.2	64.7
NEU			
0.005%	83.1	73.2	72.3
0.01%	73.3	55.6	68.9
0.02%	65.3	44.0	62.6

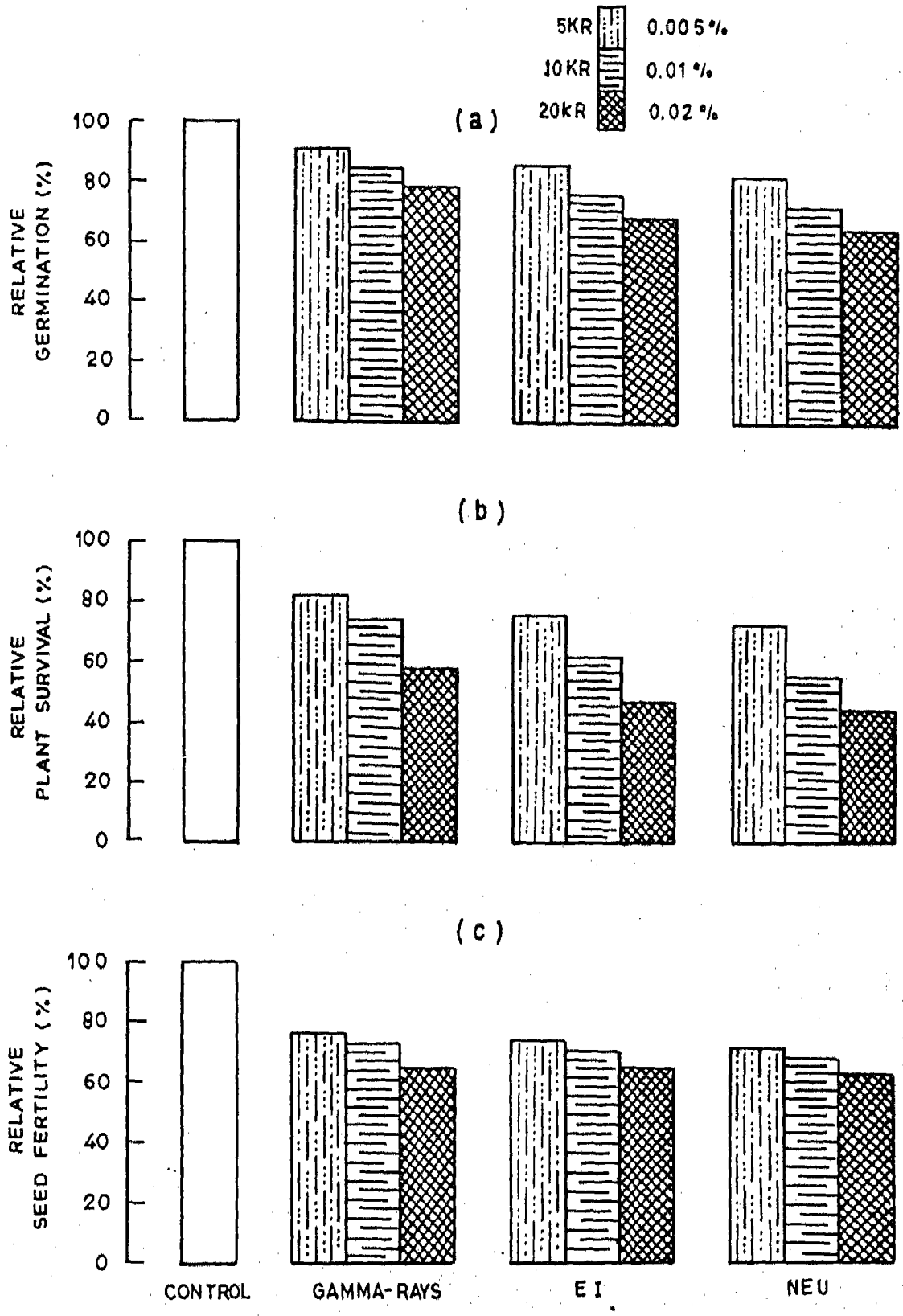


Fig. 1. EFFECT OF MUTAGENS ON GERMINATION (a), PLANT SURVIVAL (b) AND SEED FERTILITY (c) IN M1 GENERATION

plant survival (EI 38.3% and NEU 42.4%) than radiation (gamma-rays 28.3%). Among the chemicals, NEU caused more post-germination lethality (42.4%) than EI (38.3%). The maximum reduction in plant survival was observed with the highest dose of NEU (0.02%) and minimum with the lowest dose of gamma-ways: the relative survival was 44.0 and 82.2%, respectively. The highest doses (0.02%) of EI and NEU had a more or less comparable effect causing 47.2 and 44.0% survival, respectively. Reduction in plant survival was linearly dose dependent with increasing dose of all mutagens (Fig. 1b).

1.3 Seed fertility

Observations on seed fertility (Table 6, Fig. 1c) also revealed that mutagenic treatments caused high level of sterility as compared to control. Among the mutagens used, NEU reduced seed fertility to the maximum extent (32.1% reduction), followed by EI (30.3%) and gamma-rays (28.6%). In general, fertility decline was dose dependent with all the three mutagens (Fig. 1c). In the treated material, seed fertility ranged between 62.6 - 76.5% of control (taken as 100%). The maximum fertility decline was recorded with the highest dose of NEU (0.02%), followed by EI (0.02%): 37.4 and 35.3%, respectively, while medium dose of gamma-rays (10 kR) and lowest doses of EI and NEU (0.005%) caused comparable reduction in seed fertility (27.4, 26.0 and 27.7%, respectively).

Comparative biological doses

In general, a perusal of Table 7 revealed some definite patterns regarding the various biological parameters recorded in M_1 generation.

(i) NEU was most effective, followed by EI (medium damage) and gamma-rays (least damaging) in respect of all the biological parameters studied.

(ii) Dose dependent relationship was noticed with all the three mutagens.

Table 7 Comparative biological doses on the basis of M_1 parameters

Treatment	Relative, %		
	germination	plant survival	seed fertility
Gamma rays 10 kR (intermediate)	85.5	74.6	72.6
EI 0.005% (lowest)	87.0	76.2	74.0
NEU 0.005% (lowest)	83.1	73.2	72.3
EI 0.02% (highest)	68.9	47.2	64.7
NEU 0.02% (highest)	65.3	44.0	62.6

(iii) In general, the biological damage caused by the medium dose of gamma-rays (10 kR) was comparable with that of the lowest doses of EI and NEU (0.005%), in respect of all the biological parameters studied.

(iv) The highest doses of EI and NEU (0.02%) caused a comparable biological damage.

The biologically comparable doses are most appropriate for comparing the genetic effects of various mutagens, and their efficiency and effectiveness at comparable levels of damage.

2. Observations in M_2 generation

2.1 Macromutations

The treated as well as untreated (control) materials (Appendix I) were screened visually for macromutations at different stages of plant growth in M_2 generation.

2.1.1 Chlorophyll mutations

The frequency of chlrophyll mutations mutagen-wise is presented in Appendix II. A detailed analysis of the frequency of chlorophyll mutations is given in Appendix III, and their frequency treatment-wise and damage group-wise, is summarized in Tables 8 and 9, respectively. A study of Appendix II shows the overall frequency of chlorophyll mutations (5.5% M_2 progenies and 0.51% plants mutated). All three mutagens induced high frequency of chlorophyll mutations. The untreated (control) material did not have any chlorophyll mutation. NEU was the most effective mutagen, inducing chlorophyll mutations in 6.3% M_2 progenies and 0.65% plants, followed by EI (5.4% and 0.48% mutated progenies and plants, respectively) and gamma-rays (4.7% and 0.4%). The general trend of chlorophyll mutation frequency with different mutagens was NEU $\geq$ EI $\geq$ gamma-rays (Fig.2).

Dose - dependent relationship was observed in the case of gamma-rays

Table 8 Frequency of chlorophyll mutations in M_2 generation

Treatment	Percentage of mutated	
	progenies	plants
Control	-	-
Gamma rays		
5 kR	4.3	0.34
10 kR	4.7	0.39
20 kR	5.2	0.46
Overall	4.7	0.40
EI		
0.005%	4.8	0.40
0.01%	6.1	0.59
0.02%	5.4	0.46
Overall	5.4	0.48
NEU		
0.005%	5.6	0.53
0.01%	7.4	0.88
0.02%	6.0	0.54
Overall	6.3	0.65
Overall experiment	5.5	0.51

Table 9 Frequency of chlorophyll mutations in different damage groups in M_2 generation

Treatment	Percentage of mutated	
	progenies	plants
Control	-	-
Gamma rays		
LL	2.8	0.22
LH	3.9	0.32
HL	5.5	0.42
HH	7.0	0.65
Overall	4.7	0.40
EI		
LL	2.8	0.28
LH	4.7	0.40
HL	6.3	0.55
HH	8.0	0.71
Overall	5.4	0.48
NEU		
LL	4.3	0.47
LH	5.6	0.61
HL	7.2	0.67
HH	8.1	0.87
Overall	6.3	0.65
Overall experiment	5.5	0.51

(5 kR $\geq$ 10 kR $\geq$ 20 kR) whereas, for chemicals, the medium dose (0.01%) was found to be most effective for inducing chlorophyll mutations. The highest chlorophyll mutation frequency was recorded with the medium dose (0.01%) of NEU (7.4% and 0.88% mutated progenies and plants, respectively), and lowest with the lowest dose (5 kR) of gamma-rays (4.3% and 0.34%). Within the chemical treatments, the lowest doses produced chlorophyll mutations at the lowest rate.

Significant group differences with regard to induction of chlorophyll mutations were observed with all the mutagens and their doses. The highest frequency was recorded in HH group (high seedling damage coupled with high sterility in M_1), and the lowest with group LL (low damage at both stages). Among the intermediate groups, HL (high seedling damage, low sterility) carried more chlorophyll mutations than LH (low seedling damage, high sterility) (Fig.3).

2.1.1.1 **Types of mutations**

The chlorophyll mutations scored in M_2 generation were described and classified in accordance with the modified classification of Blixt (1972). The spectrum of chlorophyll mutations induced by different treatments, and damage group-wise, is given in Appendix IV and Appendix V, respectively.

(i) **Albina**

Seedlings emerged completely or nearly white, lethal, died within two week of germination.

(ii) **Xantha**

Seedlings yellow, high pale yellow or orange , died within 15 days, few survived even up to flowering stage.

(iii) **Chlorina**

Seedlings emerged greenish yellow and started dying within 15-20 days

after germination, few survived a little longer without seed setting.

(iv) **Viridis**

Light green, fully viable and more or less normally productive (Plate 1).

2.1.2 Morphological mutations

The overall frequency of morphological mutations in this study was 4.6% mutated progenies and 0.45% plants mutated in M_2 generation (Appendix II). Their frequency in different treatments and damage groups is given in Appendix VI, and their frequency mutagen-wise and damage group-wise pooled over all the treatments of a mutagen, is summarized in Tables 10 and 11, respectively. The pattern of morphological mutations was similar to that of chlorophyll mutations with regard to the mutagens, doses and groups of mutagenic damage. The overall trend of induction of morphological mutations with different mutagens was in the order of NEU $>$ EI $>$ gamma-rays (Fig.2). Dose - dependent relationship (Fig. 4) was very conspicuous (5 kR $>$ 10 kR $>$ 20 kR) for induced morphological mutations with gamma-rays, while with chemicals the medium dose (0.01%) was again found to be most effective, as the highest frequency of morphological mutations was recorded with this dose of NEU, followed by that of EI. Similar to chlorophyll mutations, distinct differences between various groups of mutagenic damage were noted with regard to the frequency of morphological mutations. In general, the groups could be arranged in the sequence HH $>$ HL $>$ LH $>$ LL on the basis of mutation rate (Fig. 3).

2.1.2.1 Types of mutations

The mutations affecting different morphological features of the plant were grouped according to the classification proposed by Blixt (1972). The relative spectrum of morphological mutations induced by different mutagens, treatments and their damage groups, is presented in Appendices VII, VIII and

Table 10 Frequency of morphological mutations in M_2 generation

Treatment	% Mutated	
	progenies	plants
Control	-	-
Gamma rays		
5 kR	3.4	0.31
10 kR	3.9	0.37
20 kR	4.4	0.42
Overall	3.9	0.37
EI		
0.005 %	3.5	0.35
0.01 %	5.5	0.52
0.02 %	4.0	0.39
Overall	4.3	0.42
NEU		
0.005 %	5.2	0.47
0.01 %	5.9	0.66
0.02 %	5.5	0.54
Overall	5.5	0.56
Overall experiment	4.6	0.45

Table 11. Frequency of morphological mutations in different damage groups in M_2 generation

Treatment	Percentage of mutated	
	progenies	plants
Control	-	-
Gamma rays		
LL	2.1	0.16
LH	3.3	0.32
HL	4.5	0.45
HH	6.0	0.55
Overall	3.9	0.37
EI		
LL	2.7	0.25
LH	3.5	0.35
HL	4.7	0.49
HH	6.4	0.60
Overall	4.3	0.42
NEU		
LL	3.4	0.36
LH	5.0	0.47
HL	6.1	0.61
HH	7.4	0.77
Overall	5.5	0.56
Overall experiment	4.6	0.45

IX, respectively.

(a) **Mutations affecting plant growth**

A very high proportion (24.6%) of induced morphological mutations affected growth habit (Appendix VII).

(i) **Compact**

Mutations with highly condensed and short internodes, induced in maximum numbers (8.3%) by gamma-rays (Plate 2).

(ii) **Bushy**

Plants with profuse branching, mostly induced by NEU (11.5%).

(iii) **Prostrate**

Plants with the branches spreading on the ground, induced most frequently (10.4%) by gamma-rays.

(b) **Mutations affecting foliage**

These mutations appreared with the highest frequency (42.3%) among the total morphological mutations (Appendix VII). Such mutations were induced most frequently by gamma-ray treatments.

(i) **Narrow leaf**

Leaflets with reduced breadth, with consequent reduction in surface area of the leaf. They occurred most frequently (14.6%) in gamma-irradiated populations.

(ii) **Broad leaf**

Leaflets with increased length and breadth, increasing the surface area of the leaf. Their maximum frequency was observed in populations treated with gamma-rays.

(iii) **Rogue**

Leaflets smaller with acute apex. Flower and pod also reduced (Plate 3). They were observed with almost equal frequency in the populations treated with

all three mutagens.

(iv) **Curly leaf**

Plants with curly and deformed lamina, reduced fertility, sometimes completely sterile. They were observed most frequently in EI treated populations.

(v) **Laciniata**

Leaflets transformed into a funnel-shaped structure. Gamma-rays did not induce this mutation at all. Among chemicals, NEU (6.4%) was more effective than EI (4.9%).

(vi) **Tendrilled leaf/ Tendrillar**

Leaflets transformed into tendrils, sometimes plants bear few leaflets (Plate 4). They were observed with almost equal frequency with gamma-rays and NEU (6.3 and 6.4%, respectively) whereas , EI induced them relatively less frequently (4.9%).

(c) **Mutations affecting plant height**

Among all the morphological mutations, the relative proportion of mutations affecting plant height was 15.6%. Majority of these mutations were isolated from EI treated populations, followed by NEU and gamma-rays.

(i) **Tall**

Plants 40% taller than the normal plants were considered as tall. They were observed with maximum frequency (9.8%) in EI treated populations, followed by gamma-rays (6.2%) and NEU (5.1%).

(ii) **Dwarf**

Plants with 40% reduction in height than the normal were considered as dwarf. The maximum frequency of dwarf mutations was observed in EI (11.5%) treated populations, followed by NEU (7.7%) and gamma-rays (6.2%).

(d) **Mutations affecting maturity**

The relative frequency of mutations influencing flowering behaviour and maturity period was fairly high (17.6% of total morphological mutations), next only to the mutations affecting growth habit (24.6%).

(i) **Early mutations**

Only those events were considered as early mutations which showed at least 1-2 weeks earliness in maturity than the control (Plate 5). They appeared frequently in all three mutagenized populations. On an average, 9.6% of the morphological mutations were early. Their frequency was highest in the EI treatments (11.5%), followed by the irradiated (10.4%) and NEU treated (7.7%) populations.

(ii) **Late mutations**

Those plants were considered late where maturity was delayed by atleast 1-2 weeks than the normal plants in control (118.5 days). Among morphological mutations, their proportion was 5.3 %. They appeared with highest frequency in irradiated populations (8.3%), followed by NEU (5.1%) and EI (3.3%) mutagenized populations.

(iii) **Sterile mutations**

Morphologically normal as well as abnormal plants with completely sterile flowers (no seed setting) were included in this group (Plate 6). They formed the smallest group among the mutations affecting maturity. Their maximum frequency was recorded in EI mutagenized populations (3.3%), followed by NEU (2.7%) and gamma-ray treated (2.1%) populations.

2.1.3 **Mutation frequency**

The frequency of total macromutations (chlorophyll + morphological) in M_2 generation is presented in Table 12, and their frequency in different

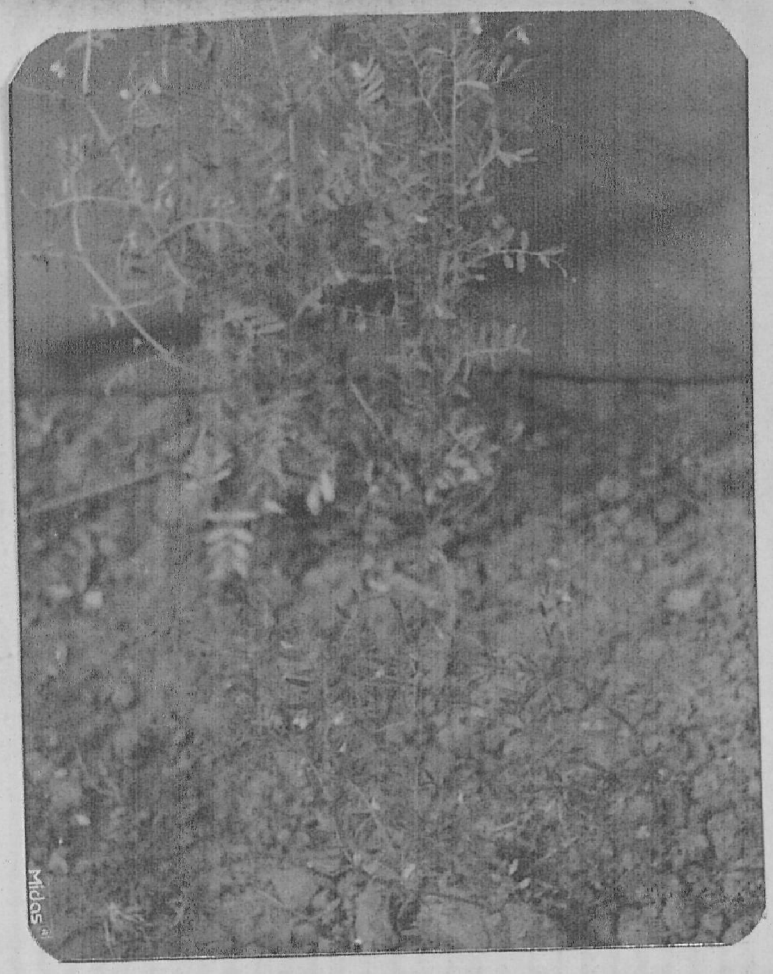


PLATE 1. A VIRIDIS MUTANT

PLATE 2. A COMPACT MUTANT

PLATE 3. A ROGUE MUTANT

PLATE 4. A TENDRILLAR MUTANT

PLATE 5. AN EARLY MUTANT

PLATE 6. A STERILE MUTANT

damage groups pooled over all the doses of a mutagen is summarized in Table 13. A study of Table 12 shows that all three mutagens induced high frequency of macromutations. The untreated (control) material did not yield any macromutation. The chemical mutagens induced a higher frequency (9.7 - 11.8% mutated progenies; 0.90 - 1.21% mutants) of macromutations than radiation (8.6% mutated progenies, 0.77 % mutants). NEU was the most effective mutagen in inducing the macromutations with 11.8% mutated M_2 progenies and 1.21% plants, followed by EI (9.7% and 0.90% mutated progenies and plants, respectively) and gamma-rays (8.6% and 0.77%). The general trend of macromutation frequency with different mutagens was NEU $>$ EI $>$ gamma-rays.

Dose-dependent relationship was observed in the case of gamma-rays as a corresponding increase in macromutation frequency was obtained with increase in dose (Table 12, Fig. 4). For chemicals, the medium dose (0.01%) was most effective for inducing macromutations. The highest macromutation frequency was recorded with the medium dose of NEU (13.3% and 1.54% mutated progenies and plants, respectively), followed by the medium dose of EI (11.6% and 1.11%) and the highest dose (20 kR) of gamma-rays (9.6% and 0.88%). The lowest frequency of macromutations was recorded with the lowest dose (5 kR) of gamma-rays (7.7% mutated M_2 progenies and 0.65% plants), followed by the lowest dose (0.005%) of EI (8.3% and 0.75% mutated progenies and plants, respectively) and NEU (10.8% and 1.0 %).

Significant group differences with regard to the induction of macromutations were observed with all the mutagens (Table 13) and their doses (Appendix X). With all the mutagens, highest frequency of macromutations was recorded in HH group, and the lowest with LL group. Among the two

Table 12. Frequency of macromutations in M_2 generation

Treatment	Percentage of mutated	
	progenies	plants
Control	-	-
Gamma rays		
5 kR	7.7	0.65
10 kR	8.6	0.76
20 kR	9.6	0.88
Overall	8.6	0.77
EI		
0.005%	8.3	0.75
0.01%	11.6	1.11
0.02%	9.4	0.85
Overall	9.7	0.90
NEU		
0.005%	10.8	1.00
0.01%	13.3	1.54
0.02%	11.5	1.08
Overall	11.8	1.21

Table 13 Frequency of macromutations in different damage groups in M_2 generation (pooled over doses of a mutagen)

Treatment	Percentage of mutated	
	progenies	plants
Control	-	-
Gamma rays		
LL	4.9	0.39
LH	7.2	0.65
HL	10.0	0.88
HH	13.0	1.20
Overall	8.6	0.77
EI		
LL	5.5	0.53
LH	8.2	0.76
HL	11.0	1.04
HH	14.4	1.31
Overall	9.7	0.90
NEU		
LL	7.7	0.83
LH	10.6	1.07
HL	13.3	1.28
HH	15.5	1.61
Overall	11.8	1.21

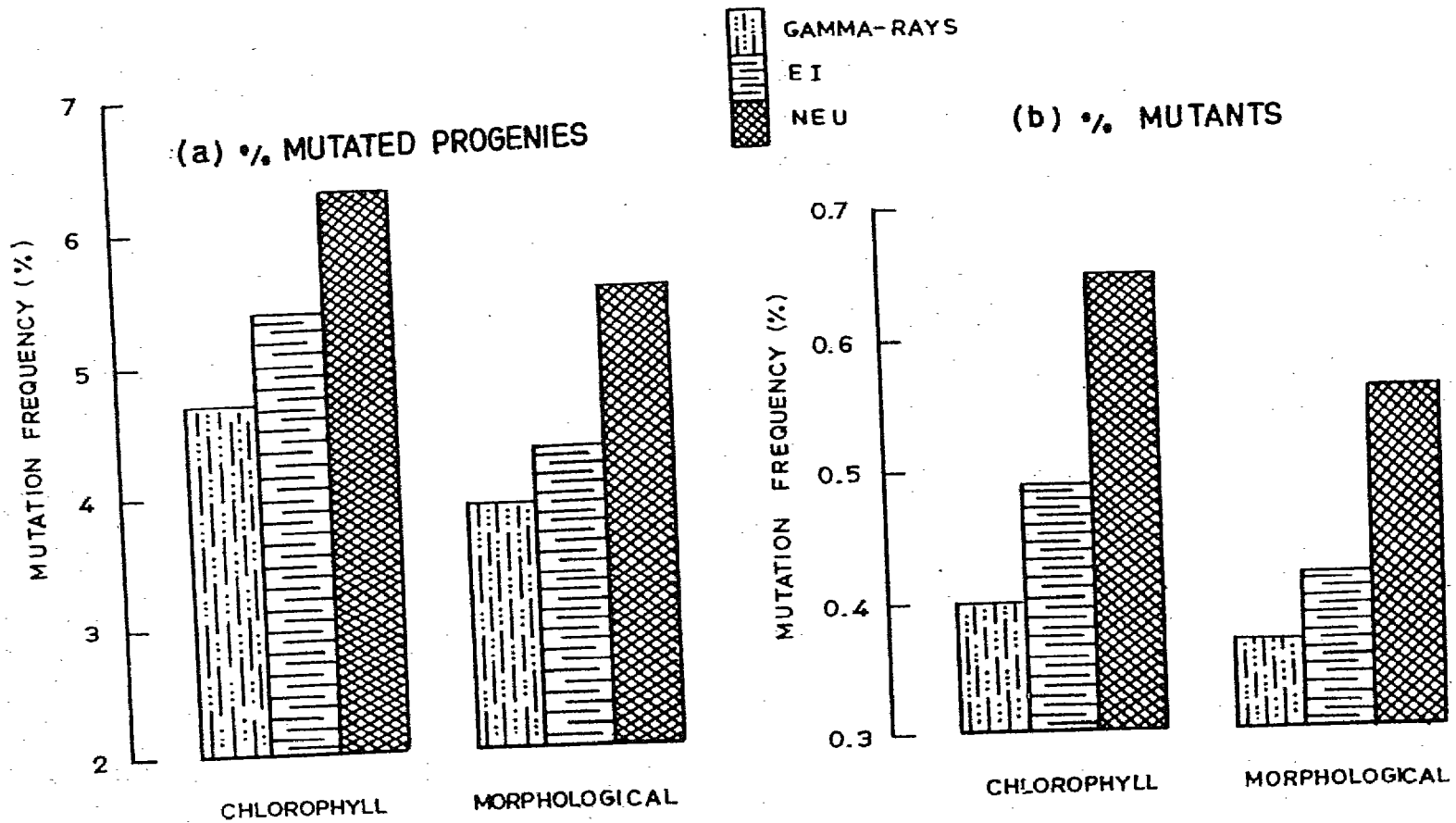


Fig. 2. MACROMUTATION FREQUENCY IN M_2 GENERATION

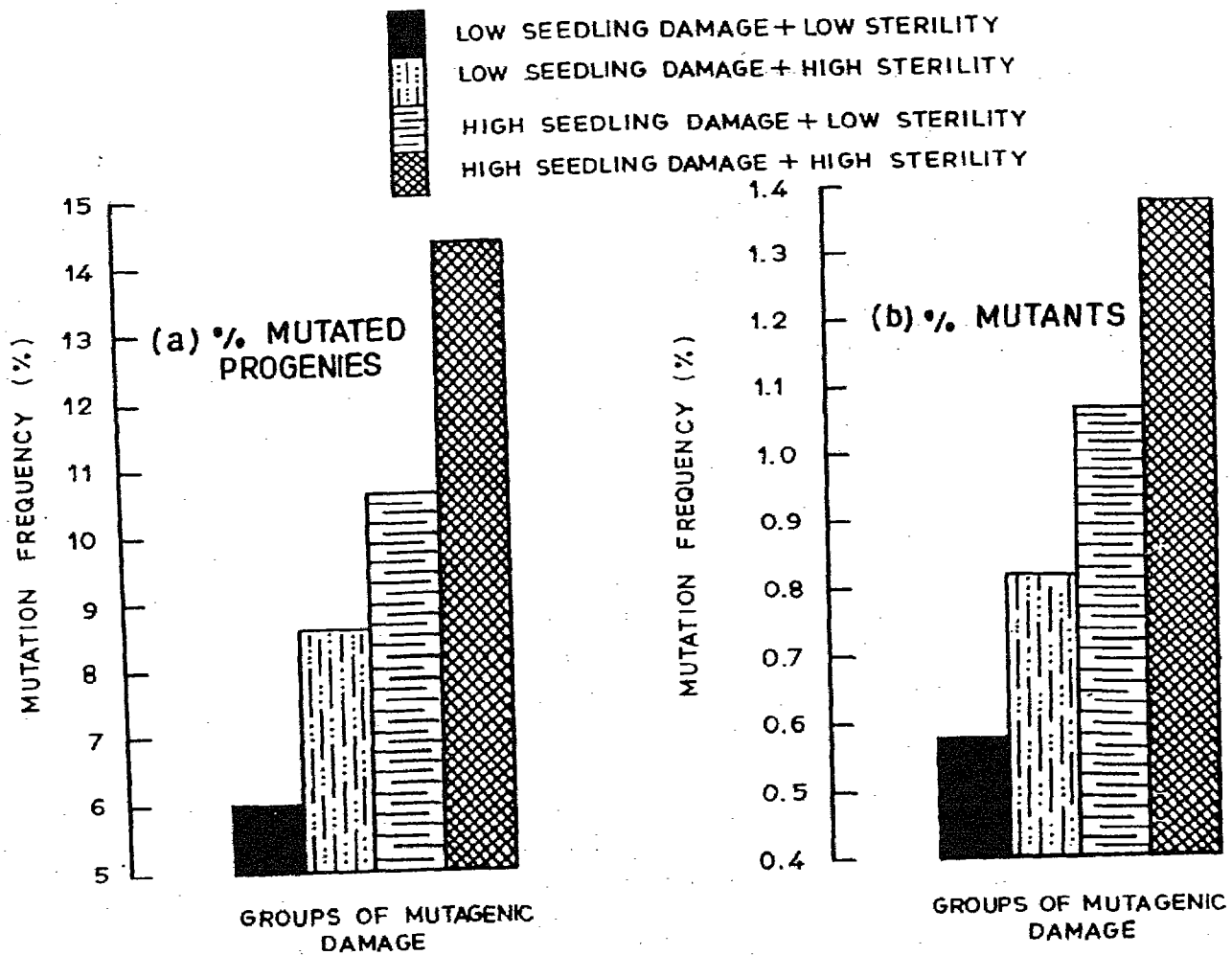


Fig. 3. TOTAL MUTATION FREQUENCY IN DIFFERENT GROUPS OF MUTAGENIC DAMAGE

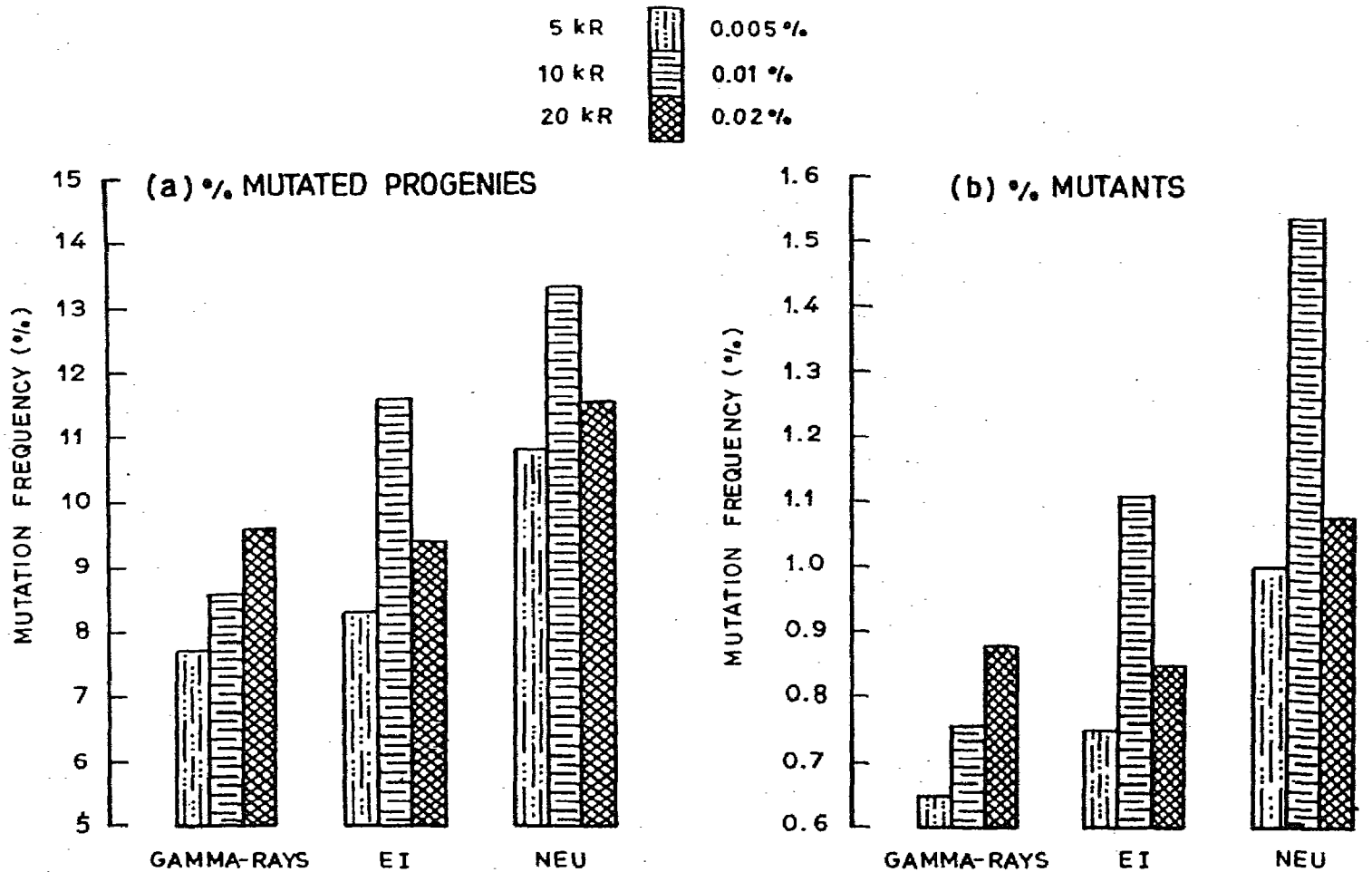


Fig.4. DOSE EFFECT OF MUTAGENS IN M_2 GENERATION (TOTAL MUTATIONS)

intermediate groups, HL carried more macromutations than LH. The highest mutation frequency was observ ed in HH group of NEU (15.5% mutated progenies and 1.61% mutated plants), followed by HH of EI (14.4% and 1.31% mutated progenies and plants, respectively) and gamma-rays (13.0% and 1.2%). The lowest mutation frequency was recorded in LL group of gamma-rays (4.9% and 0.39% mutated progenies and plants, respectively). Next higher were LL groups of EI (5.5% mutated progenies and 0.53% plants) and NEU (7.7% and 0.83%). In general, the groups were arranged in the sequence HH > HL > LH > LL.

2.1.3.1 **Mutation spectrum**

The detailed spectrum of macromutations induced is presented in Table 14 and Appendix XI. The chemical mutagens induced a wider spectrum of macromutations than ionizing radiations. In case of chemical mutagens, both NEU and EI induced the widest spectrum of macromutations with all the 18 mutation types recorded in this experiment, accounting for 42.1% and 32.8% of the total mutations, respectively. Gamma-rays with 17 mutation types accounted for 25.1% of the total mutations recorded. In general, chlorophyll mutations were induced more easily (53.1% of all macromutations) than the morphological mutations (46.9%). Some chlorophyll mutations were induced more frequently than others: viridis 19.3%, xantha 18.5% and chlorina 11.3% of all the macromutations, whereas, the albina were induced with the lowest frequency (4.0% of total mutations). At the same time, viridis were induced most frequently by EI (25.2% of all mutations), xantha by gamma-rays (25.0%) and chlorina by NEU (13.7%). Albina mutations were induced with comparable frequency by gamma-rays (5.0% of all the macromutations) and the chemical treatments (EI 3.8% and NEU 3.6%). This shows preferential

Table 14 Spectrum of macromutations (%) induced by different mutagens

Mutation type	Control	Gamma rays	EI	NEU	Total mutations	
					No.	%
Albina	-	5.0	3.8	3.6	16	4.0
Chlorina	-	11.0	8.4	13.7	45	11.3
Xantha	-	25.0	16.0	16.7	74	18.5
Viridis	-	11.0	25.2	19.6	77	19.3
Compact	-	4.0	3.1	3.0	13	3.2
Bushy	-	3.0	4.6	5.4	18	4.5
Prostrate	-	5.0	3.1	3.6	15	3.8
Narrow leaf	-	7.0	3.8	5.4	21	5.3
Broad leaf	-	4.0	2.3	3.6	13	3.2
Rogue	-	3.0	3.1	3.0	12	3.0
Curly leaf	-	3.0	3.8	3.6	14	3.5
Laciniata	-	-	2.3	3.0	8	2.0
Tendrillar	-	3.0	2.3	2.4	10	2.5
Tall	-	3.0	4.6	3.0	14	3.5
Dwarf	-	3.0	5.3	3.0	15	3.8
Early	-	5.0	5.3	4.2	19	4.8
Late	-	4.0	1.5	2.4	10	2.5
Sterile	-	1.0	1.5	1.2	5	1.3
		100(25.1)	131(32.8)	168(42.1)	399	100.0

induction of certain mutations with some mutagens than with others, although only in quantitative terms. Among the different damage groups, HH was most effective quantitatively for inducing a wider spectrum of chlorophyll mutations (Appendix V). In general, chlorophyll mutations (53.1%), and mutations affecting foliage (19.6%), growth habit (11.5%) and maturity (8.6%) occurred more frequently. Among the morphological mutations, narrow leaf mutations (5.3% of the total) appeared most frequently, followed by early and bushy mutations (4.8% and 4.5%, respectively). Dwarf, prostrate and curly leaf mutations were next in total frequency (3.8%). Sterile and laciniata mutations appeared with the lowest frequency (1.3% and 2.0% of all the macromutations, respectively). Relative mutagen- dependent differences in the specificity of induction of morphological mutations were also noted. Mutations affecting maturity (10.0% of total mutations) appeared more frequently with gamma-rays, whereas EI induced more mutations for plant height (9.9%). NEU, on the other hand, induced more mutations affecting foliage (21.0% of total mutations), and was found equally effective as gamma-rays for inducing mutations affecting growth habit (12.0%). Like chlorophyll mutations, there was no definite trend in the spectrum of morphological mutations in relation to the groups of mutagenic damage and doses (Appendix IX).

2.1.4 **Mutagenic effectiveness and efficiency**

Mutagenic effectiveness and efficiency have been estimated based on mutated M_2 progenies (Table 15).

2.1.4.1 **Mutagenic effectiveness**

Mutagenic effectiveness is an index of genotypic response to various doses of a mutagen. The effectiveness of the mutagens tested in the present

Table 15 Comparative mutagenic effectiveness and efficiency

Mutagen	Sterility (%)	Total mutated progenies (%)	Mutagenic effective-ness	Mutagenic efficiency
Gamma rays	28.6	8.6	0.7	0.31
EI	30.3	9.7	138.6	0.33
NEU	32.1	11.8	168.6	0.38

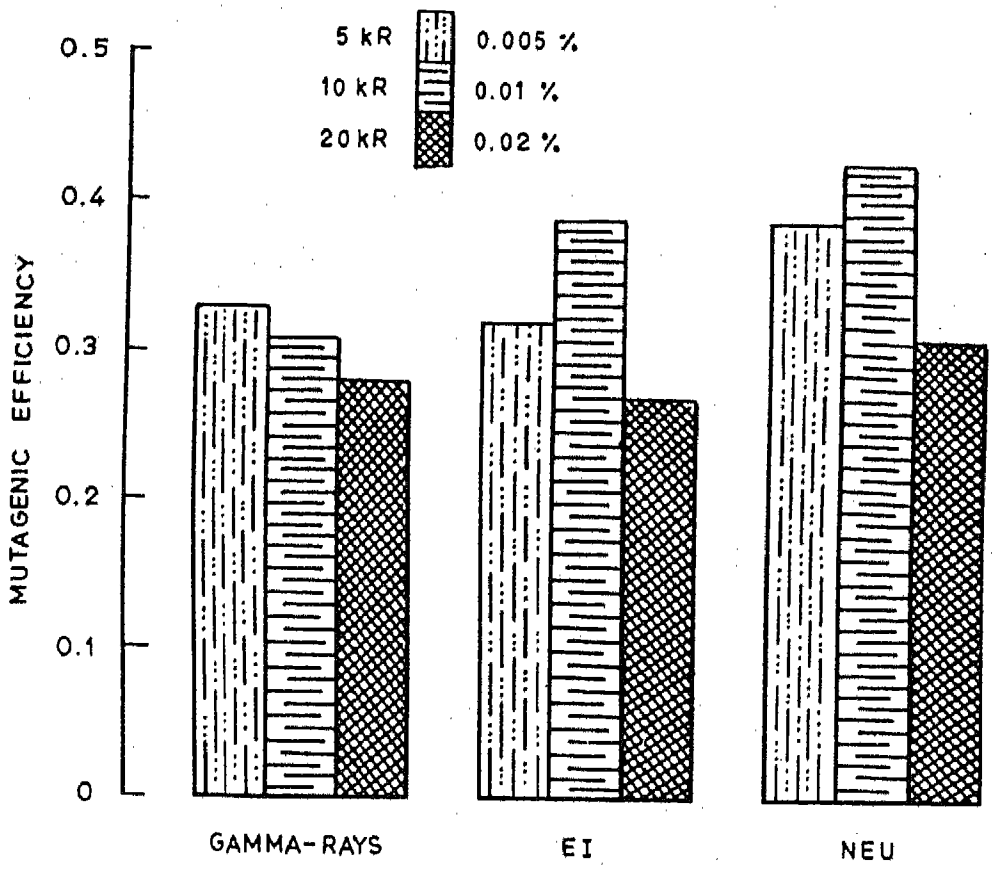


Fig. 5 MUTAGENIC EFFICIENCY ON THE BASIS OF SEED FERTILITY

study differed considerably. Among the mutagens used, chemicals were found to be more effective than radiation (gamma-rays). The mutagenic effectiveness of NEU was the highest (168.6), followed by EI (138.6) and gamma-rays (0.7). Thus, NEU was 1.2 and 241 times more effective than EI and gamma-rays, respectively. Similarly, EI was nearly 200 times more effective than gamma-rays.

2.1.4.2 **Mutagenic efficiency**

Mutagenic efficiency is a measure of mutation rate in relation to the biological damage measured as lethality, sterility, etc., in M_1 generation. Among the mutagens tested, NEU was the most efficient mutagen (0.38), followed by EI (0.33). Gamma-rays were the least efficient (0.31) mutagen (Fig.5). Thus, NEU was 1.23 and 1.06 times more efficient than gamma-rays and EI, respectively.

2.2 **Micromutations**

The total size of M_2 population in various treatments in M_2 generation has already been described (Table 3 and Appendix XII). The M_2 progenies derived from single M_1 plants were raised as separate rows in unreplicated completely randomized design (CRD). The data recorded on five random plants for eight quantitative characters, viz., days to maturity, plant height, branches per plant, pod clusters per plant, pods per plant, seeds per pod, 100-seed weight and seed yield per plant, were analysed statistically.

2.2.1 The results on polygenic mutations are presented character-wise.

2.2.1.1 **Days to maturity**

The range, population mean, variance, standard deviation (SD) and and coefficient of variation (CV) for days to maturity are presented in Table 16

Table 16 Range, population mean, variance, SD and CV for days to maturity in different damage groups in M_2 generation

Damage group	Range	Mean	Variance	SD	CV
Control	116.4 - 121.0	118.5	2.2	1.5	1.3
Gamma rays					
LL	115.0 - 129.0	124.6	2.7	1.6	1.3
LH	114.6 - 129.5	125.2	3.9	2.0	1.6
HL	115.0 - 132.0	125.6	6.6	2.6	2.0
HH	114.1 - 134.0	123.8	7.4	2.7	2.2
Overall	114.1 - 134.0	124.8	6.2	2.5	2.0
EI					
LL	114.2 - 131.8	122.5	4.8	2.2	1.8
LH	114.4 - 133.7	122.4	8.9	3.0	2.4
HL	114.2 - 134.0	124.5	12.5	3.5	2.8
HH	113.0 - 136.8	121.9	13.6	3.7	3.0
Overall	113.0 - 136.8	122.2	10.2	3.2	2.6
NEU					
LL	114.0 - 128.0	121.2	3.8	1.9	1.6
LH	114.6 - 124.7	120.3	6.9	2.6	2.2
HL	114.0 - 125.3	119.4	9.0	3.0	2.5
HH	114.5 - 130.0	120.5	14.5	3.8	3.2
Overall	114.0 - 130.0	120.4	10.5	3.2	2.7

and Appendix XIII. The range of maturity duration increased(113.0 -136.8 days) in all the mutagenized populations as compared to the control (116.4 -121.0 days). The mean number of maturity days shifted in positive direction (towards lateness) in all the treated populations as compared to control. The increase in mean maturity time had no relationship with the nature of mutagens, doses or groups of M_1 damage. However, a wider range was observed with medium doses of chemical mutagens, especially in the HH group. The magnitude of induced variability was also measured through estimates of variance, SD and CV. The variability , as indicated by these parameters, increased in all the treated populations as compared to control. However, the LL groups of 5 and 10 kR were exceptions, where the variability was less than in the control. The chemical mutagens caused greater variability than radiations. Among the chemical mutagens, NEU was more effective than EI. The highest dose of radiation (20 kR) and medium doses of the chemicals generated maximum variability for days to maturity. Among the groups of damage, HH had the widest range of variability (CV 2.2 - 3.2%), with few minor exceptions to this trend. The groups were arranged as HH $\succ$ HL $\succ$ LH $\succ$ LL in order of induced variability for maturity days (Table 16).

The analysis of variance (ANOVA), genotypic and phenotypic coefficients of variation (GCV, PCV), heritability and genetic advance (GA) for days to maturity are presented in Table 17. A perusal of the data shows that the groups of damage differ significantly with all the mutagenic treatments irrespective of dose. The group HH showed highest inter family variance. The arrangement of groups was HH (19.5-52.2) $\succ$ HL (13.9-45.6) $\succ$ LH (10.4-40.1) $\succ$ LL (8.4-23.7). The interfamily variance was significant in all the treated populations. Among the mutagens, NEU showed the highest interfamily variance

Table 17 Analysis of variance, components of variation, heritability and genetic advance for days to maturity in M_2 generation

Statistical parameter	Treatment	Control	Gamma rays			EI			NEU		
			5 kR	10 kR	20 kR	0.005%	0.01%	0.02%	0.005%	0.01%	0.02%
Variance											
between groups		-	527.6**	537.8**	490.9**	236.5**	1129.9**	381.9**	499.5**	1460.0**	388.7**
between families within treatment		4.0	12.9**	18.3**	23.2**	32.4**	29.7**	20.9**	18.6**	38.4**	20.1**
within group	LL	-	8.4**	11.0**	16.5**	17.3**	23.7**	11.9**	8.7**	21.3**	12.9**
	LH	-	10.4**	14.4**	21.2**	30.9**	26.6**	19.1**	16.3**	40.1**	15.0**
	HL	-	13.9**	22.9**	26.0**	33.5**	31.7**	26.1**	22.0**	45.6**	19.3**
	HH	-	19.5**	24.1**	32.0**	51.2**	37.9**	29.7**	26.7**	52.2**	34.2**
within family		1.8	2.9	2.8	3.2	4.4	6.7	6.4	5.1	7.9	5.6
GCV		0.6	1.1	1.4	1.6	1.9	1.7	1.4	1.4	2.0	1.4
PCV		1.3	1.8	1.9	2.2	2.5	2.7	2.5	2.3	3.1	2.4
Heritability		19.6	41.7	53.2	56.1	56.5	40.7	31.6	35.0	43.7	34.7
Genetic advance		0.5	1.5	2.1	2.5	2.9	2.3	1.6	1.7	2.8	1.7

** Significant at 1% level

(18.6 - 38.4), followed by EI (20.9 - 32.4) and gamma-rays (12.9 - 23.2). Dose-dependent increase in interfamily variance was recorded with gamma-rays, but not with the chemicals. For instance, among the radiation treatments, maximum interfamily variance (23.2) was recorded with the highest dose (20 kR), while EI gave highest interfamily variance (32.4) at the lowest (0.005%) and NEU (38.4) at the medium (0.01%) dose. Variance between groups was highly significant in all the mutagenic treatments.

All the treated populations had higher PCV for maturity time (1.8 - 3.1%) than 1.3% in the control. Similarly, (GCV) was also higher in all the mutagenized populations (1.1 - 2.0%) than in the control (0.6%). The heritability estimates (31.6 - 56.5%) in all the treated popultions were higher than in control (19.6%). Hertability increased with increasing dose of gamma-rays but not in chemicals. The change in heritability was also not mutagen dependent. The GA increased in the treated populations (1.5 - 2.9% as against 0.5% in the control).

Development of early varieties of crop plants is the prime objective of the breeders. Therefore, the M_2 families of greater interest are those which have higher CV and lower mean number of maturity days than the corresponding highest CV and lowest mean in the control. Thus, the families with higher CV than the highest value of control can be treated as mutated progenies with confidence. The relative frequency of mutated families (Appendices XXI, XXIX and XXX) shows that, depending on the extent of mutagenic damage, the frequency of mutated families in various damage groups ranged from 7.0 - 34.1% . As regards the mutagens used, NEU had the highest frequency of mutated families (23.3%), followed by EI (20.7%) and gamma-rays (19.7%). Dose-dependent increase in the frequency of mutated

families was noted in this study, and the highest doses of all the mutagens induced mutations in the highest proportion of families. The highest percentage of mutated families was 21.6, 23.1 and 24.9% with gamma-rays, EI and NEU, respectively with 20 kR dose in gamma-rays and 0.02% of chemicals. Among the groups of damage, HH showed superiority over others. The M_2 families with high CV and lower number of days to maturity were advanced to the next generation for confirmation and detailed analysis.

2.2.1.2 **Plant height**

Table 18 shows the range, population mean, variance, SD and CV for plant height in different damage groups over doses in different mutagens in M_2 generation, whereas Appendix XIV shows the same parameters in different treatments in M_2 generation. The range for plant height increased in all the treated populations (17.0 - 43.6 cm against 24.4 - 36.2 cm in the control). The widest range for plant height was recorded in the NEU mutagenized population (17.0 - 43.0 cm), followed by EI (19.8 - 43.6 cm) and gamma-ray (20.2 - 43.5 cm) treated populations. Among the groups of mutagenic damage identified in M_1, HH (17.0 - 43.6 cm) showed the widest range, followed by HL (18.3 - 43.0cm), LH (24.0 - 43.5cm), and LL (25.4 - 43.4) in all the mutagens under study. Dose-dependent increase in range was noted. The highest dose of all the mutagens induced the widest range. The population mean shifted slightly towards higher plant height in all the damage groups, except the HH group of NEU where it decreased slightly (26.7cm as against 30.3cm in control). The maximum plant height was recorded with gamma-rays (32.2cm), followed by EI (32.0cm) and NEU (30.6cm) mutagenized populations. With regard to different damage groups, the trend was LL $\succ$ LH $\succ$ HL $\succ$ HH, i.e. group LL had the maximum and HH the minimum plant height in a particular mutagen.

Table 18 Range, population mean, variance, SD and CV for plant height in different damage groups in M_2 generation

Damage group	Range	Mean	Variance	SD	CV
Control	24.4 - 36.2	30.3	11.6	3.4	11.2
Gamma rays					
LL	25.4 - 43.2	33.9	17.5	4.2	12.3
LH	24.3 - 43.5	32.1	19.8	4.4	13.9
HL	22.3 - 42.1	31.9	24.9	5.0	15.6
HH	20.2 - 40.3	30.8	27.4	5.2	17.0
Overall	20.2 - 43.5	32.2	22.6	4.8	14.8
EI					
LL	26.2 - 43.4	34.3	20.2	4.5	13.1
LH	24.0 - 40.6	32.6	22.3	4.7	14.5
HL	19.8 - 41.7	30.3	29.4	5.4	17.9
HH	19.9 - 43.6	30.1	35.4	5.9	19.8
Overall	19.8 - 43.6	32.0	26.8	5.2	16.2
NEU					
LL	25.4 - 43.0	32.6	19.5	4.4	13.5
LH	24.0 - 42.9	32.2	26.2	5.1	15.9
HL	18.3 - 43.0	31.0	35.4	5.9	19.2
HH	17.0 - 42.7	26.7	43.0	6.6	24.6
Overall	17.0 - 43.0	30.6	31.0	5.6	18.2

Maximum plant height was recorded with the lowest doses of mutagens, but plant height decreased gradually with increasing dose. Therefore, dose-dependent depression in plant height was noted with all the mutagens. The trend for increase in height was gamma-rays > EI > NEU. The magnitude of induced variability was measured by variance, SD, and CV. The estimates of all these statistical parameters increased in the treated populations as well as the damage groups than control. Among the mutagens tested, NEU showed the maximum variance, SD and CV, followed by EI and gamma-rays. The increase in the magnitude of these parameters was also dose related. The highest estimates of these parameters were recorded with the highest dose of gamma-rays (20 kR) and medium doses (0.01%) of NEU and EI. Among the groups of mutagenic damage, HH showed the highest variance (27.4 - 43.0), SD (5.2 - 6.6) and CV (17.0 -24.6), followed by respective values of variance, SD and CV in HL, LH and LL.

The ANOVA, components of variation, heritability and GA (Table 19) showed that the damage groups differed significantly in all the treated populations. Among the groups of mutagenic damage, HH showed the highest interfamily variance (39.9 - 103.2) with all the three mutagens, followed by HL (37.8 - 85.4), LH (37.3 -84.7) and LL (32.9 - 62.5). It is also evident that interfamily variances were significant with all the mutagens and their doses, which was non-significant in the untreated (control) population. The magnitudes of GCV (6.4 - 11.0%) and PCV (13.9 - 19.5%) were higher in the treated populations than in the control (4.5% and 11.2%, respectively). The heritability estimates were also higher in all the treated populations (21.4 - 34.8%) as against 16.4% in the control. Higher GA (6.1 -12.8%) was recorded in the mutagenized populations (3.8% in the control).

Table 19 Analysis of variance, components of variation, heritability and genetic advance for plant height in M_2 generation

Statistical parameter	Treatment	Control	Gamma rays			EI			NEU		
			5 kR	10 kR	20 kR	0.005%	0.01%	0.02%	0.005%	0.01%	0.02%
Variance											
between groups		-	154.8**	287.1**	948.0**	628.1**	2115.6**	461.4**	757.5**	2163.6**	2150.0**
between families within treatment		19.2	37.5**	47.0**	56.1**	60.5**	69.7**	45.8**	51.0**	83.7**	70.8**
within group	LL	-	35.3**	35.1**	48.5**	52.8**	62.5**	32.9**	38.8**	58.8**	56.2**
	LH	-	37.3**	38.0**	52.9**	57.4**	65.4**	39.7**	39.2**	84.7**	62.6**
	HL	-	37.8**	44.0**	54.5**	62.1**	74.2**	56.3**	44.3**	85.4**	71.6**
	HH	-	39.9**	68.1**	65.6**	68.4**	80.2**	60.2**	81.2**	103.2**	92.7**
within family		9.7	16.0	17.5	16.1	16.5	22.7	17.3	16.5	25.2	23.3
GCV		4.5	6.4	7.6	8.8	8.9	9.7	7.7	8.4	11.0	10.4
PCV		11.2	13.9	15.1	15.3	15.1	17.9	15.4	15.4	19.5	19.4
Heritability		16.4	21.4	25.1	33.2	34.8	29.3	24.7	29.3	31.7	29.0
Genetic advance		3.8	6.1	7.8	10.5	10.9	10.8	7.8	9.3	12.8	11.6

** Significant at 1% level

Appendices XXII, XXIX and XXX show the proportion of mutated families. Among different mutagens, the range of mutated families was 16.0 - 23.7% (Appendix XXII). The highest percentage of families mutated for plant height was obtained with NEU (20.7%), followed by EI (19.7%) and gamma-rays (19.5%). The increase in the percentage of mutated families was dose-dependent. All the mutagens gave the highest frequency of mutated families with their highest doses. The trend of mutated families in the groups of mutagenic damage was HH $>$ HL $>$ LH $>$ LL. The families with higher CV and higher mean than the highest in the control were advanced to next generation for further investigation.

2.2.1.3 **Fruiting branches per plant**

The range, population mean, variance, SD and CV for number of fruiting branches per plant (Table 20 and Appendix XV) show that the range for branches per plant exceeds the limits of control (9.8 - 21.8) in both directions. The range in the treated populations was 4.0 - 61.0 branches per plant. Among the mutagens tested, NEU showed the widest range for branches per plant (4.7 - 61.0), followed by EI (4.3 - 56.2) and gamma-rays (4.0 - 50.0). All mutagens showed the widest range at their highest doses. Among the groups of mutagenic damage, HH with all the mutagens studied showed the widest range, followed by HL, LH and LL. The mean number of branches per plant increased in all the mutagenized populations. No dose-dependence was observed with regard to mean, except in the case of NEU where the mean increased with the increase in dose. In case of gamma-rays, the highest dose was found to be the most effective, whereas the medium dose of EI was more effective than other doses of this mutagen. Among different damage groups, HH showed the highest mean followed by HL, LH

Table 20 Range, population mean, variance, SD and CV for total fruiting branches per plant in different damage groups in M_2 generation

Damage group	Range	Mean	Variance	SD	CV
Control	9.8 - 21.8	13.4	32.0	5.6	42.2
Gamma rays					
LL	4.0 - 31.3	13.3	61.8	7.9	59.1
LH	4.4 - 43.0	14.3	71.8	8.5	59.3
HL	5.7 - 43.5	15.6	96.3	9.8	62.9
HH	5.2 - 50.0	19.6	166.8	12.9	65.9
Overall	4.0 - 50.0	15.8	99.9	10.0	63.3
EI					
LL	4.8 - 30.6	15.6	69.9	8.4	53.6
LH	5.4 - 35.0	16.7	89.0	9.4	56.5
HL	6.0 - 39.0	18.0	107.2	10.4	57.5
HH	4.3 - 56.2	18.8	144.7	12.0	64.0
Overall	4.3 - 56.2	16.7	100.3	10.0	60.3
NEU					
LL	7.8 - 40.0	17.8	82.3	9.1	51.0
LH	5.5 - 39.8	18.9	106.6	10.3	54.6
HL	5.5 - 42.3	20.0	127.5	11.3	56.5
HH	4.7 - 61.0	21.6	160.0	12.6	58.6
Overall	4.7 - 61.0	19.6	119.1	10.9	55.7

and LL. The magnitude of induced variability was measured by variance, SD, and CV. Among the chemical mutagens, the maximum increase in the estimates of these parameters (except CV) was found with NEU. The maximum CV was observed with gamma-rays (63.3%), followed by EI (60.3%) and NEU (55.7%). Gamma-rays occupied third position after NEU and EI in respect of induced variability. The range of CV in mutagenized populations was 48.7 -74.8% as against 42.2% in the control. Among the groups of M_1 damage, HH showed maximum increase in variance, SD and CV with all three mutagens studied (Table 20). In respect of variability, the groups were arranged in the sequence: HH > HL > LH > LL.

The ANOVA, GCV, PCV, heritability and GA (Table 21) revealed that the groups of M_1 damage were significantly different in all the treated populations, and the HH group showed maximum interfamily variance (153.6 -374.4), followed by HL (134.3-346.2), LH (119.7-293.3) and LL(89.3-209.1) in all the mutagenic treatments. The interfamily variance ranged from 124.8 to 296.3 (48.4 in the control) and was significant in all the treated populations. The highest value of interfamily variance was noted with 0.02% NEU (296.3) and minimum (124.8) with 5 kR gamma-rays. The increase in interfamily variance for branches per plant was dose-dependent. The highest interfamily variance was noted at the respective highest doses of the mutagens studied. The treated populations showed higher PCV (54.8-64.7%) than control (42.2%). The GCV in the treated populations also increased to 23.4-33.8% as compared to 15.1% in the control. Heritability increased (18.4-27.8%) in the mutagenized populations by a significant margin (12.8% in control). The estimates of GA in the mutagenized populations ranged from 20.8 to 36.8% of mean, as compared to 11.1% in the control.

Table 21 Analysis of variance, components of variation, heritability and genetic advance for branches per plant in M_2 generation

Statistical parameter	Treatment	Control	Gamma rays			EI			NEU		
			5 kR	10 kR	20 kR	0.005%	0.01%	0.02%	0.005%	0.01%	0.02%
Variance											
between groups		-	1285.6**	3486.9**	2017.1**	1474.5**	1977.8**	1875.3**	1507.1**	3630.9**	1601.7**
between families within treatment		48.4	124.8**	139.4**	267.0**	152.0**	195.8**	225.6**	179.3**	223.0**	296.3**
within group	LL	-	103.6**	89.3^{NS}	158.0**	108.7**	132.0**	141.2**	146.9**	182.6**	209.1**
	LH	-	119.7**	123.0**	164.9**	156.7**	197.7**	222.7**	151.6**	192.3**	293.3**
	HL	-	134.3**	134.3**	346.2**	161.5**	210.9**	272.0**	185.0**	208.2**	302.7**
	HH	-	153.6**	213.3**	368.6**	182.5**	230.0**	274.9**	222.1**	344.5**	374.4**
within family		27.9	58.8	63.4	110.5	70.0	80.8	77.1	78.8	88.0	105.3
GCV		15.1	23.4	28.5	30.4	24.1	28.0	33.8	24.9	26.8	29.0
PCV		42.2	54.8	64.7	64.6	55.3	59.8	64.2	55.2	55.3	56.2
Heritability		12.8	18.4	19.3	22.1	19.0	22.2	27.8	20.3	23.5	26.6
Genetic advance		11.1	20.8	25.7	29.5	21.7	27.2	36.8	23.1	26.8	30.8

** Significant at 1% level

NS Non-significant

The estimates of frequency of mutated families (Appendices XXIII, XXIX and XXX) show that the proportion of mutated families for number of branches per plant ranged from 8.8 to 35.0%. Among the mutagens used, NEU showed the highest frequency of mutated families (13.0 - 35.0%), followed by EI (13.0 - 33.3%) and gamma-rays (8.8 -29.3%). Dose-dependent increase was noted in mutation frequency. The highest doses of all three mutagens were found most effective. The damage groups also differ for percentage of mutated families. The four groups of damage were arranged in the following order on the basis of frequency of mutated progenies: HH > HL > LH > LL

2.2.1.4 **Pod clusters per plant**

The range, population mean, variance, SD and CV for effective clusters per plant in different damage groups and different mutagenized populations of all three mutagens are presented in Table 22 and Appendix XVI. The damage groups in all three mutagens over different doses showed a trend for increasing values of all these statistical parameters (Table 22). The range for cluster/plant increased from 14.4-54.6 in control to 7.0-152.3 in the mutagenized populations. The increase in range was maximum in the HH group of 0.01% NEU (9.3-152.3) and minimum in the LL group of 5 kR gamma-rays (12.5 - 56.7). All the mutagenic treatments except 5 kR gamma-rays, shifted the population mean in the positive direction (higher number of clusters per plant). Maximum population mean was recorded with 0.01% NEU (35.5) and minimum with 5 kR gamma-rays (24.3). The magnitude of genetic variability, measured as variance, SD and CV, increased considerably in the treated populations (CV 60.0 - 82.5%) over the control (CV 45.2%). Among the mutagens used, NEU gave the highest values of variance, SD and

Table 22 Range, population mean, variance, SD and CV for clusters per plant in different damage groups in M_2 generation

Damage group	Range	Mean	Variance	SD	CV
Control	14.4 - 54.6	25.0	127.7	11.3	45.2
Gamma rays					
LL	8.8 - 69.7	24.4	277.5	16.7	68.3
LH	10.0 - 78.8	26.4	343.8	18.5	70.2
HL	11.6 -113.3	29.9	489.5	22.1	74.0
HH	8.3 -128.7	32.1	584.9	24.2	75.3
Overall	8.3 -128.7	28.8	431.3	20.8	72.1
EI					
LL	8.3 - 66.7	23.5	247.4	15.7	66.9
LH	9.2 - 80.6	25.9	334.0	18.3	70.6
HL	8.8 -120.3	30.7	513.8	22.7	73.8
HH	8.4 -135.3	33.2	629.3	25.1	75.6
Overall	8.3 -135.3	28.5	436.3	20.3	73.4
NEU					
LL	9.3 - 72.7	29.8	365.9	19.1	64.2
LH	7.0 - 91.7	32.0	510.2	22.6	70.6
HL	7.0 -126.8	33.8	685.2	26.2	77.4
HH	7.4 -152.3	35.7	850.0	29.2	81.7
Overall	7.0 -152.3	33.3	618.2	24.9	74.7

CV for clusters per plant, followed by EI and gamma-rays. Dose-dependent increase in variability was recorded with all the three mutagens. The two chemicals showed highest magnitude of variance, SD and CV at their medium doses, while the highest dose of gamma-rays (20 kR) was most effective in this respect. As can be seen from Table 22, the maximum variability was recorded in the HH group of mutagenic damage, followed by HL, LH and LL groups of all the three mutagens.

The ANOVA, GCV, PCV, heritability and GA (Table 23) revealed that the groups of M_1 damage were significantly different in all the treated populations, and the HH group showed maximum interfamily variance (705.4 - 2524.3), followed by HL (547.3 - 1734.7), LH (421.9 - 1398.9) and LL (416.5 - 1040.3) in all the mutagenic treatments. The interfamily variance ranged from 535.4 to 1556.6 (178.1 in the control), and was significance in all the treated populations at 5% or 1% levels of significance. The highest value of interfamily variance (1556.6) was noted with 0.01% NEU, and minimum (535.4) with 5 kR gamma-rays. The increase in interfamily variance for clusters per plant was dose-dependent. The highest interfamily variance with chemicals was noted with medium doses of chemicals and the highest dose (20 kR) of gamma-rays. The treated population showed higher PCV (66.7 - 79.1%) than control (45.2%). The GCV also increased from 31.0 - 40.8% in the treated populations compared to 14.2% in the control. The heritability increased by a significant margin to 18.9 -28.7% in the mutagenized populations over 9.9% in the control. The estimates of GA ranged from 28.0 to 44.8% of mean, as against 9.2% in the control.

The frequency of mutated families (Appendices XXIV, XXIX and XXX)

Table 23 Analysis of variance, components of variation, heritability and genetic advance for clusters per plant in M_2 generation

Statistical parameter	Treatment	Control	Gamma rays			EI			NEU		
			5 kR	10 kR	20 kR	0.005%	0.01%	0.02%	0.005%	0.01%	0.02%
Variance											
between groups		-	1794.4**	4733.0**	25367.0**	6609.8**	31937.9**	12534.9**	31871.9**	42138.0**	22133.8**
between families within treatment		178.1	535.4**	753.6**	1127.6**	645.5**	1053.6**	893.1**	965.6**	1556.6**	1177.1**
within group	LL	-	416.5**	485.8**	758.6**	447.3**	687.4**	495.8**	649.1**	1040.3**	854.6**
	LH	-	421.9**	695.9**	766.7**	452.8**	922.9**	794.1**	809.8**	1398.9**	1176.8**
	HL	-	547.3**	760.6**	1207.3**	676.8**	1353.6**	1085.8**	1138.2**	1734.7**	1401.6**
	HH	-	705.4**	1060.1**	2030.2**	1206.7**	1468.3**	1215.8**	1620.5**	2417.9**	2524.3**
within family		115.1	247.4	312.6	425.6	271.5	372.1	325.1	395.1	516.6	424.1
GCV		14.2	31.2	31.6	38.5	31.0	40.8	37.4	34.1	40.6	38.7
PCV		45.2	71.9	67.4	77.4	66.7	79.1	73.5	72.1	75.8	75.6
Heritability		9.9	18.9	22.0	24.8	21.6	26.8	25.9	22.4	28.7	26.2
Genetic advance		9.2	28.0	30.5	39.5	29.7	43.5	39.2	33.3	44.8	40.8

** Significant at 1% level

for clusters per plant ranged from 14.0 - 38.9%. Among the mutagens used, NEU showed the highest proportion of mutated families (27.8%), followed by EI (26.3%) and gamma-rays (24.1%). Dose-dependent increase in the frequency of mutated families was noted. The highest doses of all three mutagens were the most effective. Group differences for percentage of mutated families were also recorded. The four groups of mutagenic damage were arranged in the following order on the basis of mutated progenies: HH $>$ HL $>$ LH $>$ LL.

2.2.1.5 **Pods per plant**

Table 24 and Appendix XVII show the range, population mean, variance, SD and CV for pods/plant in M_2 generation. The mutagenic damage groups pooled over all the doses of a particular mutagen show increasing trend in order of HH $>$ HL $>$ LH $>$ LL with regard to all the statistical parameters analysed (Table 24). The range for pod number increased in all the treated populations (10.0 - 208.6 as against 22.4 - 74.8 pods/plant in the control). The widest range for pods per plant was recorded in the NEU-mutagenized populations (10.0 - 208.6 pods/plant), followed by EI (12.8 -198.8) and gamma-rays (13.3 - 182.0). Dose-dependent increase in the range was evident. Both chemical mutagens gave the widest range of pod number with medium doses, and gamma-rays with the highest dose (20 kR). The population mean shifted slightly towards higher pod number in all the mutagenized populations, except 5 kR gamma-rays, where it decreased slightly (43.0 pods/ plant), as compared to the control (45.0 pods). Among the mutagens studied, maximum increase in mean pod number/plant was noted with NEU (59.1), followed by EI (52.8) and gamma-rays (51.2). Medium doses of all three mutagens were the most effective in increasing the pod number (54.0 -62.2).

Table 24 Range, population mean, variance, SD and CV for pods per plant in different damage groups in M_2 generation

Damage group	Range	Mean	Variance	SD	CV
Control	22.4 - 74.8	45.0	590.5	24.3	54.0
Gamma rays					
LL	16.0 - 91.8	44.7	859.5	29.3	65.6
LH	15.4 -140.7	47.0	1076.1	32.8	69.8
HL	15.0 -151.3	52.8	1397.3	37.4	70.8
HH	13.3 -182.0	58.9	1967.4	44.4	75.3
Overall	13.3 -182.0	51.2	1419.7	37.7	73.6
EI					
LL	15.4 - 99.8	46.2	1030.3	32.1	69.5
LH	15.0 -145.5	48.5	1190.0	34.5	71.1
HL	14.4 -174.3	54.8	1617.6	40.2	73.4
HH	12.8 -198.8	61.6	2266.9	47.6	77.3
Overall	12.8 -198.8	52.8	1556.8	39.5	74.8
NEU					
LL	14.7 -102.5	52.5	1210.6	34.8	66.3
LH	10.0 -150.4	57.7	1712.0	41.4	71.7
HL	16.2 -181.4	62.6	2293.1	47.9	76.5
HH	12.8 -208.6	66.0	2736.3	52.3	79.3
Overall	10.0 -208.6	59.1	2020.7	45.0	76.1

The mutagenic damage groups increased podding intensity in the order HH > HL > LH > LL. The SD and CV for pods/plant increased as a result of mutagenic treatment. Among the mutagens tested, NEU showed the highest values of variance, SD and CV, followed by EI and gamma-rays. The increase in these parameters was dose-related, and highest estimates of these parameters were obtained with the highest dose of gamma-rays (20 kR) and medium doses of NEU and EI (0.01%). Among the groups of mutagenic damage HH had the highest values of variance (1967.4-2736.3), SD (44.4-52.3) and CV (75.3 - 79.3%), followed by corresponding values of these parameters in HL, LH and LL (Table 24).

The ANOVA, components of variation, heritability and GA (Table 25) showed that the groups differed significantly among themselves and in all the treated populations. The HH group of mutagenic damage showed the maximum interfamily variance, followed by HL, LH and LL. This trend was consistent with all the three mutagen used in this study. It can also be seen that the interfamily variances were significant with all the mutagens and their doses, while it was nonsignificant in the untreated (control) population. The magnitudes of GCV (31.8 - 43.4%) and PCV (66.9 - 79.8%) were higher in the treated populations than in the control (18.8% and 54.1%, respectively). So were the heritability estimates (19.5 - 31.3%) in treated materials as against 12.1% in the control. The higher values of GA (29.4 -50.0%) in the mutagenized populations (13.5% in control) indicate the possibility of improvement for podding intensity through selection.

Appendices XXV, XXIX and XXX give an idea about the percentage of mutated families: 17.5 - 45.0% mutated for this character. The highest percentage of mutated families for podding intensity was obtained with NEU

Table 25 Analysis of variance, components of variation, heritability and genetic advance for pods per plant in M_2 generation

Statistical parameter	Treatment	Control	Gamma rays			EI			NEU		
			5 kR	10 kR	20 kR	0.005%	0.01%	0.02%	0.005%	0.01%	0.02%
Variance											
between groups		-	14413.6**	18648.1**	61331.4**	23230.1**	59217.4**	95530.6**	50443.9**	130737.5**	91800.9**
between families within treatment		876.5	1758.2**	2849.2**	3488.1**	2419.8**	4049.6**	3165.4**	3510.0**	5229.2**	3977.1**
within group	LL	-	1246.5**	2149.2**	2331.1**	1853.1**	3251.4**	2135.2**	2601.2**	3911.1**	2463.1**
	LH	-	1624.1**	2455.8**	2529.3**	2077.5**	3635.4**	3713.5**	2746.6**	4116.9**	2776.1**
	HL	-	1706.2**	3072.6**	4242.5**	2678.1**	3802.7**	3775.7**	4013.5**	5887.2**	3642.7**
	HH	-	2330.2**	2695.8**	5044.3**	3280.5**	6342.2**	3905.9**	6663.4**	7716.7**	6181.5**
within family		519.0	795.2	1093.7	1208.1	983.8	1309.6	1155.9	1361.0	1595.2	1364.1
GCV		18.8	32.3	34.2	40.6	31.8	43.4	39.2	36.8	43.3	39.2
PCV		54.1	73.2	69.4	77.5	66.9	79.8	77.1	75.0	77.4	74.5
Heritability		12.1	19.5	24.3	27.4	22.6	29.5	25.8	24.0	31.3	27.7
Genetic advance		13.5	29.4	34.7	43.8	31.1	48.5	41.0	37.1	50.0	42.5

** Significant at 1 % level

(33.4%), followed by EI (32.3%), and gamma-rays (29.9%). The increase in the percentage of mutated families followed a definite dose-dependent pattern. All three mutagens gave the highest frequency of mutated families at their respective highest doses. The groups of mutagenic damage were again arranged in the order of HH $\succ$ HL $\succ$ LH $\succ$ LL in this regard. The families having higher CV and mean than the highest values in the control were advanced to M_3 generation for confirmation and detailed observations.

2.2.1.6 **Seeds per pod**

The study of range, population mean, variance, SD and CV for seeds per pod in different groups of mutagenic damage (Table 26) and treatments (Appendix XVIII) in M_2 generation showed that the range for seeds/pod crossed the limits of control (1.1 - 1.6) in both the directions. The increase was more in the positive direction (i.e. higher seed number per pod). The range in the treated populations was 1.0 - 2.2 seeds/pod for all the three mutagens under study. Gamma-rays showed the widest range at the highest dose (20 kR), EI at the lowest dose (0.005%), and NEU at its medium dose (0.01%). The mean seed number per pod increased in all the treatments, except in 5 kR gamma-rays and 0.02% EI. Both the chemical mutagens gave the highest number of seed/pod at their medium doses, whereas in case of gamma-rays, the highest dose was most effective. Variance, SD and CV for this character also increased in all the mutagenized populations as compared to control. The two chemicals showed maximum increase in these statistical parameters, and among them NEU had an edge over EI at least for CV. The CV in the mutagenized populations varied from 17.4 - 22.6% as against 17.2% in the control. Among the groups of M_1

Table 26 Range, population mean, variance, SD and CV for seeds per pod in different damage groups in M_2 generation

Damage group	Range	Mean	Variance	SD	CV
Control	1.1 - 1.6	1.3	0.05	0.22	17.2
Gamma rays					
LL	1.0 - 1.9	1.4	0.06	0.25	17.9
LH	1.0 - 2.1	1.4	0.06	0.25	17.9
HL	1.0 - 2.1	1.4	0.07	0.27	19.7
HH	1.0 - 2.2	1.5	0.09	0.30	20.4
Overall	1.0 - 2.2	1.4	0.07	0.26	19.3
EI					
LL	1.0 - 1.7	1.3	0.06	0.25	18.4
LH	1.0 - 2.1	1.3	0.06	0.25	19.3
HL	1.0 - 2.1	1.4	0.08	0.28	20.2
HH	1.0 - 2.2	1.5	0.10	0.30	21.8
Overall	1.0 - 2.2	1.4	0.08	0.28	20.1
NEU					
LL	1.1 - 1.9	1.4	0.06	0.25	17.5
LH	1.0 - 2.0	1.4	0.06	0.25	17.9
HL	1.0 - 2.1	1.5	0.08	0.28	19.2
HH	1.0 - 2.2	1.5	0.11	0.30	21.7
Overall	1.0 - 2.2	1.4	0.08	0.28	20.2

damage, HH carried maximum increase in variance, SD and CV irrespective of mutagens and their doses, and also when pooled over all the doses of a particular mutagen. The groups of mutagenic damage were arranged in the sequence: HH > HL > LH > LL.

The ANOVA, GCV, PCV, heritability and GA (Table 27) revealed that the variance between groups of M_1 damage was highly significant in all the treatments. Variance within LL group was non-significant in all the treatments except 0.01% EI. Three such cases (5 kR gamma-rays, 0.005% and 0.02% NEU) were observed in the LH group of damage. The HH group showed maximum interfamily variance (0.12 - 0.20) for seeds per pod, followed by HL (0.10 - 0.14), LH (0.09 - 0.13) and LL (0.07 - 0.12). The inerfamily variance ranged from 0.10 to 0.14 (0.06 in control). The interfamily variances were significant with all the mutagens and their doses (non-significant in control). The magnitudes of GCV (6.3 - 8.5%) and PCV (18.5 - 20.6%) were higher in the treated populations than in control (4.2% and 17.2%, respectively). The heritability estimates were also higher in all the treated populations (10.5 - 17.7% as against 6.0% in control). Genetic advance also increased (4.4 - 7.4%) in the mutagenized populations (2.1% in control).

Appendices XXVI, XXIX and XXX give an idea about the percentage of mutated families for seeds/pod. The range of mutated families was 9.6 - 14.6% in different treatments. The highest percentage of families mutated for seeds per pod in different treatments was obtained with NEU (11.4-14.6%), followed by EI (10.8 - 13.9%) and gamma-rays (9.6 - 12.0%). The increase in percentage of mutated families was dose-dependent, except with 0.01% EI. All the mutagens gave the highest frequency of mutated progenies in M_2 at their respective highest doses. The trend of mutated families in the groups

Table 27 Analysis of variance, components of variation, heritability and genetic advance for seeds per pod in M_2 generation

Statistical parameter	Treatment	Control	Gamma rays			EI			NEU		
			5 kR	10 kR	20 kR	0.005%	0.01%	0.02%	0.005%	0.01%	0.02%
Variance											
between groups		-	0.33**	4.78**	0.46**	0.62**	0.28**	3.82**	2.88**	0.99**	1.77**
between families within treatment		0.06	0.11**	0.11**	0.14**	0.10**	0.13**	0.11**	0.12**	0.13**	0.11**
within group	LL	-	0.10^{NS}	0.07^{NS}	0.10^{NS}	0.09^{NS}	0.12**	0.08**	0.10^{NS}	0.11^{NS}	0.09^{NS}
	LH	-	0.10^{NS}	0.09**	0.13**	0.10**	0.12**	0.12**	0.10^{NS}	0.12**	0.10^{NS}
	HL	-	0.11**	0.14**	0.13**	0.10**	0.13**	0.12**	0.12**	0.13**	0.13**
	HH	-	0.13**	0.14**	0.20**	0.12**	0.15**	0.13**	0.16**	0.17**	0.15**
within family		0.05	0.06	0.06	0.07	0.06	0.07	0.06	0.06	0.08	0.07
GCV		4.2	7.7	7.6	8.5	6.3	8.0	7.7	7.8	6.7	6.5
PCV		17.2	20.2	18.5	20.6	20.1	20.2	20.4	19.1	20.0	20.5
Heritability		6.0	14.3	16.3	17.7	11.2	15.6	14.3	16.5	11.2	10.5
Genetic advance		2.1	6.0	6.3	7.4	4.4	6.5	6.0	6.4	4.6	4.4

* Significant at 5% level
** Significant at 1% level
NS Non-significant

of mutagenic damage was HH > HL > LH > LL. The mutated families having higher CV and mean than the highest values in the control were advanced to the next generation for further confirmation.

2.2.1.7 **100-Seed weight (seed size)**

Table 28 and Appendix XIX give the range, population mean, variance, SD and CV for 100-seed weight in different damage groups pooled over all the doses of different mutagens and treatments in M_2 generation. The range for 100-seed weight increased from 2.7 - 3.6g in control to 1.3 - 4.6g in the mutagenized populations. The maximum increase in range for 100-seed weight was recorded in the HH group of damage of 0.01% EI (1.3 - 4.6g) and minimum in the LL group of 5 kR gamma-rays (2.2 - 4.0g). Almost all the mutagenic treatments shifted the population mean in positive direction (higher seed size). Only with 5 kR gamma-rays, 0.02% EI and NEU, the population mean was equal to that in the control (3.1g). The highest population mean was observed with the highest dose of gamma-rays, lowest dose of EI and medium dose of NEU. The order of mutagens on the basis of population mean was gamma-rays > EI > NEU. The magnitude of genetic variability, measured as variance, SD and CV, increased in the treated populations (CV 18.3 - 31.6%) over the control (17.7%), except in the LL group of 10 kR gamma-rays where it decreased slightly to 16.1%. Dose-dependent increase in variability for 100-seed weight was recorded with three mutagens, with the maximum variability induced by their highest doses. The highest dose of gamma-rays induced maximum variability for 100-seed weight among all the treatments. Among the groups of mutagenic damage, the highest magnitude of variability was recorded in the HH group, followed by HL, LH and LL in all the three mutagens (Table 28).

Table 28 Range population mean, variance, SD and CV for 100-seed weight in different damage groups in M_2 generation

Damage group	Range	Mean	Variance	SD	CV
Control	2.7 - 3.6	3.1	0.3	0.5	17.7
Gamma rays					
LL	2.0 - 4.4	3.6	0.4	0.6	17.7
LH	1.7 - 4.3	3.4	0.5	0.7	21.7
HL	1.5 - 4.5	3.1	0.6	0.8	25.6
HH	1.3 - 4.6	3.0	0.7	0.9	28.5
Overall	1.3 - 4.6	3.3	0.6	0.8	24.4
EI					
LL	1.9 - 4.2	3.4	0.4	0.7	19.5
LH	1.7 - 4.4	3.3	0.6	0.8	23.7
HL	1.4 - 4.4	3.1	0.7	0.8	26.4
HH	1.3 - 4.6	3.0	0.8	0.9	29.8
Overall	1.3 - 4.6	3.2	0.7	0.8	26.0
NEU					
LL	1.9 - 4.2	3.4	0.5	0.7	20.2
LH	1.8 - 4.4	3.3	0.5	0.7	22.3
HL	1.7 - 4.4	3.1	0.6	0.8	25.0
HH	1.5 - 4.6	3.1	0.7	0.8	26.7
Overall	1.5 - 4.6	3.2	0.6	0.8	23.6

Table 29 shows ANOVA, components of variation, heritability and GA for 100-seed weight in M_2 generation. Variances between families within LL group of five treatments (5 kR of gamma-rays, 0.005% and 0.01% of EI and 0.005% and 0.02% of NEU), and also within group LH of 0.005% NEU were non-significant. However, variances between different damage groups, and also interfamily variances with different treatments were significant at 1 or 5% levels. Interfamily variance in the control was non-significant. Among the groups of mutagenic damage, HH showed highest magnitude of interfamily variance (1.1 -2.2) followed by HL (1.0 - 1.8), LH (0.7 - 1.4) and LL (0.6 - 1.0) consistently with all the mutagens and their doses. The magnitudes of GCV (9.2 - 13.2%) and PCV (22.1 - 27.6%) were higher in all the treatments than in the control (4.6% and 17.7%, respectively). The heritability estimates were also higher in the treatments (17.1 - 25.6%) than in the control (6.7%). Genetic advance also increased over control (2.4%) as a result of mutagenic treatment (7.8-13.7%).

Appendices XXVII, XXIX and XXX give an idea about the percentage of M_2 mutated families. The range of mutated families for 100-seed weight was 10.2 - 16.5% in different treatments of all the three mutagens. The highest percentage of families mutated for 100-seed weight was obtained with NEU (14.9%), followed by EI (12.9%), and gamma-rays (11.8%). The increase in proportion of mutated families was dose dependent. All the mutagens gave the highest frequency of such M_2 families at their respective highest doses. The trend of mutated families in the groups of mutagenic damage was HH $>$ HL $>$ LH $>$ LL. The promising families (those having higher CV and higher mean than the highest value of control) were advanced

Table 29 Analysis of variance, components of variation, heritability and genetic advance for 100-seed weight in M_2 generation

Statistical parameter	Treatment	Control	Gamma rays			EI			NEU		
			5 kR	10 kR	20 kR	0.005%	0.01%	0.02%	0.005%	0.01%	0.02%
Variance											
between groups		-	4.8**	8.5**	32.7**	11.6**	18.1**	26.5**	4.9**	28.9**	7.3**
between families within treatment		0.4	0.9**	1.0**	1.6**	1.0**	1.3**	1.2**	0.8**	1.2**	1.1**
within group	LL	-	0.7^{NS}	0.7**	1.0**	0.9^{NS}	0.9^{NS}	0.9*	0.6^{NS}	1.0**	0.9^{NS}
	LH	-	0.9**	1.0**	1.4**	0.9**	1.1**	1.1**	0.7^{NS}	1.1**	1.0**
	HL	-	1.0**	1.2**	1.8**	1.1**	1.4**	1.4**	1.1**	1.4**	1.3**
	HH	-	1.1**	1.6**	2.2**	1.4**	1.7**	1.4**	1.2**	1.5**	1.4**
within family		0.3	0.4	0.4	0.6	0.5	0.6	0.6	0.4	0.5	0.5
GCV		4.6	10.2	10.8	13.2	10.1	12.1	11.2	9.2	11.9	11.2
PCV		17.7	22.3	22.5	26.7	23.0	26.4	27.6	22.1	23.5	25.0
Heritability		6.7	20.5	23.2	25.3	18.2	20.9	17.4	17.1	25.6	19.7
Genetic advance		2.4	9.6	10.6	13.7	8.8	11.3	9.7	7.8	12.4	10.1

* Significant at 5% level
** Significant at 1% level
NS Non-significant

to the next generation for further analysis.

2.2.1.8 **Seed yield per plant**

The statistical parameters (range, population mean, variance, SD and CV) for seed yield per plant (Table 30 and Appendix XX) indicate that all the mutagenic treatments effectively increased the range of plant productivity over the control (1.0 - 4.1g), the widest (0.6 - 10.2g) being for 0.01% NEU and the narrowest (0.6 - 8.2g) for 5 kR gamma-rays. Among the groups of mutagenic damage, HH (0.4 - 10.2g) showed the maximum increase in the range of seed yield in all the mutagenic treatments, followed by HL (0.7 - 8.2g), LH (0.4 - 6.2g) and LL (0.5 0 6.0g). The population mean yield increased in all the mutagenized populations except the LL group of 10 kR gamma-rays where slight decrease in mean yield per plant was observed (1.9g). The mean seed yield of treated populations increased with increasing dose. The highest mean with chemicals was observed at medium doses (2.7 and 2.5g with NEU and EI, respectively), but with gamma-rays (2.6g) at the highest dose (20kR). Among the mutagens, NEU (2.6g) was most effective in increasing seed yield, followed by EI and gamma-rays (2.4g). Among the damage groups, HH (2.5 -3.7g) was most effective, followed by HL (2.3-3.3g), LH (1.9 - 2.4g) and LL (1.7-2.4g), in increasing grain yield. The variability recorded in terms of variance, SD and CV increased considerably in the treated populations as compared to the control. The range of CV among the treated populations was 67.3-95.6%, as compared to 66.8% in the control population. Among the mutagens tested, chemicals (NEU followed by EI) generally showed higher estimates of all these parameters of variability (except CV which was higher in EI) than gamma-rays. Dose-dependent increase in variability

Table 30 Range, population maen, variance, SD and CV for seed yield per plant in different damage groups in M_2 generation

Damage group	Range	Mean	Variance	SD	CV
Control	1.0 - 4.1	2.0	1.9	1.4	66.8
Gamma rays					
LL	0.6 - 5.2	2.0	2.2	1.5	74.2
LH	0.6 - 5.5	2.2	3.1	1.8	80.0
HL	1.0 - 7.9	2.6	4.8	2.3	83.6
HH	0.7 - 8.7	2.8	5.9	2.6	87.0
Overall	0.6 - 8.7	2.4	4.0	2.0	83.8
EI					
LL	0.5 - 4.3	2.1	2.3	1.5	73.7
LH	0.6 - 5.8	2.1	3.2	1.8	84.4
HL	0.7 - 7.9	2.6	5.1	2.3	85.6
HH	0.8 - 9.9	2.9	6.8	2.6	91.1
Overall	0.5 - 9.9	2.4	4.3	2.1	86.1
NEU					
LL	0.5 - 6.0	2.2	2.9	1.7	78.1
LH	0.4 - 6.2	2.2	3.3	1.8	82.6
HL	0.7 - 8.2	2.9	5.8	2.4	84.1
HH	0.4 -10.2	3.5	8.7	2.9	85.0
Overall	0.4 -10.2	2.6	4.9	2.2	83.9

for seed yield per plant was also observed with all the three mutagens. Medium doses of chemicals (0.01%) showed maximum variability for seed yield, whereas gamma-rays caused maximum variability at the highest dose (20kR). As regards the groups of mutagenic damage identified in M_1, HH again showed its superiority over all others with respect to the magnitude of variability (giving highest variance, SD and CV).

The ANOVA, components of variation, heritability and GA for seed yield per plant in M_2 generation are presented in Table 31. The ANOVA showed signficant differences between the groups of mutagenic damage as well as different families within the mutagenic treatments. Interfamily variances within LL group of 5 kR gamma-rays and 0.005% EI were non-significant, whereas all other groups of mutagenic damage showed significant interfamily variances. The HH group was far superior over all other groups (8.9-16.8), followed by HL (6.6-12.8), LH (4.5-8.9) and LL (2.9-7.4). The interfamily variances ranged from 6.3 (5 kR gamma-rays) to 11.1 (0.01% NEU) as compared to 2.0 in control. The increase in interfamily variance was dose-dependent with all three mutagens. The chemicals showed the highest interfamily variance (NEU 11.1 and EI 9.6) at the medium doses, whereas gamma-rays induced maximum interfamily variance (7.3) at the highest dose (20 kR). The GCV varied from 34.4% to 43.8% in the treatments as against 9.6% in the control, and PCV from 78.7% to 94.0% in different treatments as compared to 66.9% in the control population. Very high increase was recorded in heritability (15.6-27.5%) and genetic advance (30.2-46.6%) as a result of mutagenic treatments over control (2.1% and 2.8%).

Appendices XXVIII, XXIX and XXX show mutated families in the

Table 31 Analysis of variance, components of variation, heritability and genetic advance for seed yield per plant in M_2 generation

Statistical parameter	Treatment		Control	Gamma rays			EI			NEU		
				5 kR	10 kR	20 kR	0.005%	0.01%	0.02%	0.005%	0.01%	0.02%
Variance												
	between groups		-	44.3**	124.9**	27.0**	94.7**	162.7**	141.3**	147.9**	213.1**	158.1**
	between families within treatment		2.0	6.3**	6.7**	7.3**	6.6**	9.6**	7.7**	7.5**	11.1**	9.6**
	within group	LL	-	3.2^{NS}	4.0*	5.6**	2.9^{NS}	5.9**	5.1**	5.4**	7.4**	7.2**
		LH	-	4.5**	5.1**	6.1**	5.8**	8.9**	6.4**	6.6**	8.1**	8.3**
		HL	-	6.7**	7.7**	8.2**	6.6**	10.6**	8.6**	8.7**	12.8**	9.4**
		HH	-	9.8**	10.4**	9.1**	12.4**	16.8**	15.8**	8.9**	15.3**	16.7**
	within family		1.8	3.3	3.2	3.3	3.1	3.6	3.3	3.5	3.8	3.9
GCV			9.6	36.9	34.9	34.4	36.1	43.8	37.3	35.8	43.2	41.1
PCV			66.9	94.0	83.4	78.7	85.6	87.5	82.3	81.6	83.0	85.5
Heritability			2.1	15.6	18.2	20.0	18.1	24.7	20.6	19.3	27.5	22.8
Genetic advance			2.8	30.2	30.9	32.1	31.6	44.6	34.8	33.0	46.6	40.4

* Significant at 5% level

** Significant at 1% level

NS Non significant

range of 15.8 - 42.5% for seed yield/plant. Among the mutagens tested, NEU induced highest frequency of mutated families (30.9%), followed by EI (27.7%) and gamma-rays (27.0%). The increase in percentage of mutated families was also dose dependent. The highest frequency of such families 33.3, 29.4 and 28.6% mutated families was obtained with the highest doses of all the three mutagens in the order: NEU $\succ$ EI $\succ$ gamma-rays. Among the groups of mutagenic damage, HH carried maximum concentration of mutated families in all the mutagenic treatments employed. In this respect, the damage groups could be arranged in the sequence: HH $\succ$ HL $\succ$ LH $\succ$ LL. The families with higher CV coupled with higher mean than the highest value in the control were advanced to M_3 generation for the confirmation of their behaviour and further selection.

2.2.2 Summary of M_2 results on micromutations

On the basis of the above analysis a few general trends can be identified about induction of micromutations. The range of the eight characters studied increased in all the treatments over the control. The population means also increased marginally over the control level. The variability, measured through the estimation of variance, SD and CV in the mutagenized as well as treated populations, in general, increased considerably in all the treated populations. The comparison of CV of all the eight characters revealed that seed yield per plant showed maximum variability (CV 84.6), followed by pods per plant (74.8), whereas minimum variability was induced for days to maturity (CV 2.4). The remaining five characters, i.e. no. of clusters and branches per plant, 100-seed weight, seeds per pod and plant height, showed little or intermediate increase in variability in decreasing order.

The analysis of variance showed that, with few exceptions, interfamily variance was significant for all the treated populations and non-significant for control for all the eight characters studied. Both GCV and PCV increased as a result of mutagenic treatments. Among the characters studied, seed yield per plant showed highest PCV, followed by pods per plant. However, GCV was considerably low for both the characters. The correspondence between GCV and PCV was maximum for days to maturity and the minimum for seeds per pod; other characters showing intermediate relationship between these parameters. The heritability was highest, average over all the treatments, (43.7%) for days to maturity, followed by plant height (28.7%), pods per plant (25.8%), clusters per plant (24.1%), branches per plant (22.1%), 100-seed weight (20.9%), yield per plant (20.8%), and seeds per pod (14.2%). The highest value of GA (39.8% of mean) was recorded for pods per plant and lowest (2.1%) for days to maturity.

The overall CV of each M_2 progeny was used to identify the frequency of mutated families. The chemical mutagen NEU was most efficient in producing such families for all the eight characters studied. The lowest number of families mutated for micromutations was recorded following gamma-ray treatments, and EI was intermediate. Among the characters studied, pods per plant was the most mutable character, followed by seed yield and clusters per plant. Branches per plant, days to maturity and plant height were comparable with medium mutability, whereas 100-seed weight and seeds per pod were least mutable characters.

2.2.2.1 **Dose effect**

The lowest magnitude of variability was induced with the lowest

dose of all the three mutagens without any exception. Generally, maximum variability (expressed as range, variance, SD and CV) for all the characters was induced by the medium doses of chemicals (0.01%) and the highest dose of gamma-rays (20 kR). The frequency of mutated families was maximum with the highest doses of all the three mutagens, followed by the medium and lowest doses.

2.2.2.2 **Mutation frequency in relation to mutagenic damage**

Among the four groups of mutagenic damage in M_1, HH (high rate of leaf aberrations and high sterility) carried maximum variability for all the eight characters. The general pattern of mutation induction was in the order of HH $>$ HL $>$ LH $>$ LL. The frequency of mutated families was also highest in the HH group, followed by HL, LH and LL.

2.2.3 **Test of significance of difference**

All the families treated as mutated showed significantly higher F values at 1 or 5% levels. The Bartlett's test was used to determine whether the families in the treated populations were significantly different on the basis of their individual variances (intrafamily variance). With a few exceptions, the χ^2 values in each treated population were significantly high for all the eight characters at 5 or 1% levels with n-1 degrees of freedom (Appendix XXXI).

2.2.4 **Screening of promising families**

Although a large number of families were identified as mutated (with higher CV) for the characters studied, all of them are not expected to be of equal selection value. The mutated families for each character were further divided into three groups, i.e. , mutated families with higher, unchanged and lower mean than that of control (Appendices XXI-XXVIII).

The character means of the mutated families were compared with the highest family mean in control in each treatment for rigorous selection. Only those families were considered promising which had higher CV and mean than the highest of control progenies.

The families with higher CV and unchanged mean were in greater number than the mutated families with lower or higher mean in each treatment (Appendices XXI - XXVIII). The proportion of mutated families with higher mean was not the same as with lower mean for all the eight characters under study. As stated earlier (*cf.* Materials and Methods), the mutated progenies with higher CV and mean shifted in the desired directions were treated as "promising" progenies for the purpose of selection. Among the mutagens tested, NEU was most effective in this respect as it induced the highest frequency (3.1% each for 100-seed weight and seeds/pod to 13.3% for pods/plant) of promising families for all the characters, followed by EI (2.4% to 12.2%) and gamma-rays (2.1% to 10.6%). The highest dose of gamma-rays (20 kR) gave higher frequency of promising families than the medium and lower doses (Appendix XXXII). However, the chemicals induced highest frequency of promising families with medium doses (0.01%) which were comparable with their highest doses (0.02%). The groups of mutagenic damage were arranged in the following order with regard to frequency of promising families: HH $>$ HL $>$ LH $>$ LL (Table 32).

The proportion of mutated families promising for multiple characters are shown in Table 33 and 34. It can be seen that the proportion of promising families varied from 17.6% with 5 kR gamma-rays to 30.0% following 0.01% NEU treatment. Similarly, the proportion of promising families with multiple characters varied from 57.6% (5 kR gamma-rays) to 71.4%

Table 32 Percentage of promising families for various characters in different groups of mutagenic damage pooled over all treatments in M_2 generation

Group	Total families studied	Days to maturity	Plant height	Branches/ plant	Clusters/ plant	Pods/ plant	Seeds/ pod	100-seed weight	Seed yield/ plant
LL	591	2.2	1.5	2.5	4.7	6.6	0.7	1.0	5.1
LH	543	5.0	3.9	4.6	7.7	9.4	2.2	2.8	8.1
HL	506	7.9	6.5	7.7	11.3	13.0	4.3	5.1	12.5
HH	537	11.0	8.8	11.0	14.3	16.2	6.5	7.3	16.0
Overall	2177	6.4	5.1	6.3	9.4	11.2	3.4	4.0	10.2

Table 33 Proportion of promising families with multiple characters in different treatments in M_2 generation

Treatment	Total families studied	Promising families		Families with various combinations of characters						Families with multiple characters	
		No.	%	1	2	3	4	5	6	No.	%
Gamma rays											
5 kR	187	33	17.6	14	7	6	4	2	-	19	57.6
10 kR	272	53	19.5	19	13	10	8	2	1	34	64.2
20 kR	283	63	22.3	22	15	11	8	5	2	41	65.1
Overall	742	149	20.1	55	35	27	20	9	3	94	63.1
EI											
0.005%	212	41	19.3	15	11	8	5	1	1	26	63.4
0.01%	238	64	26.9	23	17	12	7	4	1	41	64.1
0.02%	238	56	23.4	16	12	14	9	3	2	40	71.4
Overall	688	161	23.3	54	40	34	21	8	4	107	66.5
NEU											
0.005%	193	39	20.2	14	6	8	5	4	2	25	64.1
0.01%	245	71	30.0	25	20	9	9	6	2	46	64.8
0.02%	309	76	24.6	22	14	14	14	7	5	54	71.1
Overall	747	186	24.9	61	40	31	28	17	9	125	67.2

Table 34 Frequency of promising families with multiple characters in different groups of mutagenic damage pooled over all treatments in M_2 generation

Group	Total families studied	Promising families		Families with various combinations of characters						Families with multiple characters	
		No.	%	1	2	3	4	5	6	No.	%
LL	591	72	12.2	30	21	13	7	1	-	42	58.3
LH	543	105	19.3	38	29	17	14	6	1	67	63.8
HL	506	137	27.1	46	29	28	17	12	5	91	66.4
HH	537	182	33.9	56	36	34	31	15	10	126	69.2
Overall	2177	496	22.8	170	115	92	69	34	16	326	65.7

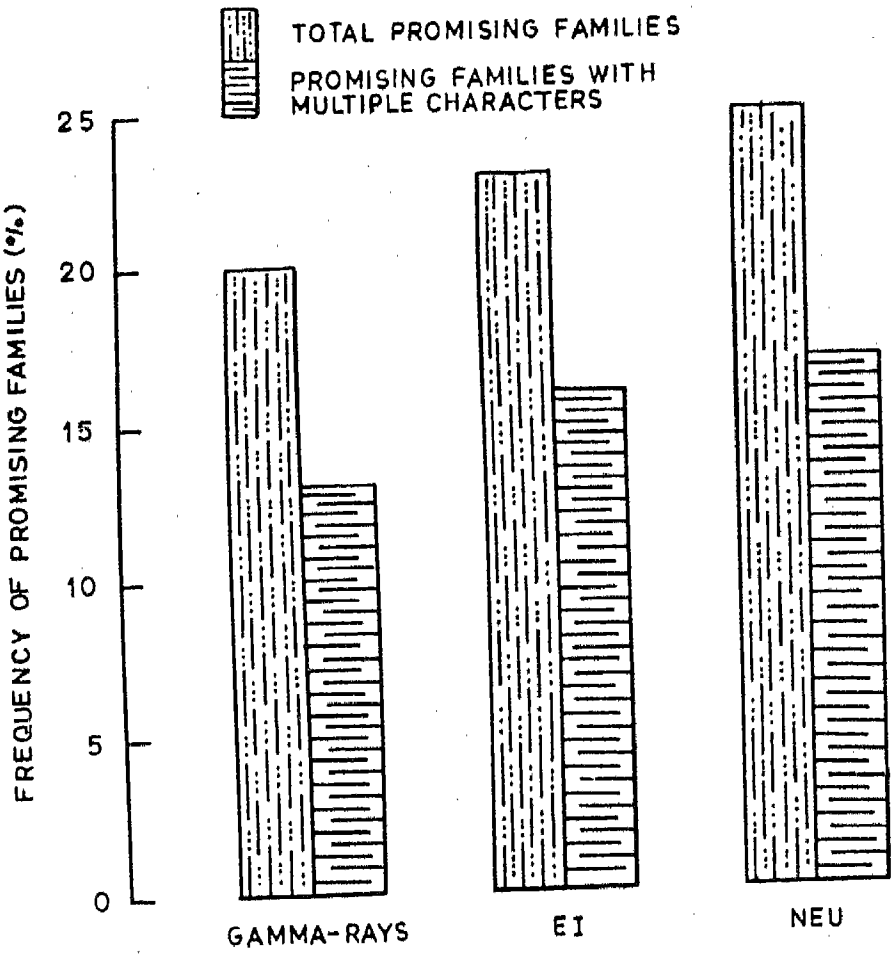


Fig.6. FREQUENCY OF PROMISING FAMILIES WITH DIFFERENT MUTAGENS IN M_2 GENERATION

(0.02% EI) of the total promising families in various treatments. The proportion of promising families (with single + multiple characters) was highest (24.9%) in the NEU-treated population (Fig.6). Next in order were EI (23.3%) and gamma-rays (20.1%). The same trend was observed when promising families with multiple characters (2-6) were considered: the proportion of mutated families with multiple promising characters out of the total promising families was in the order of NEU (67.2%) $>$ EI (66.5%) $>$ gamma-rays (63.1%). As regards the proportion of promising families and those with multiple characters in different mutagenic damage groups, the trend was : HH $>$ HL $>$ LH $>$ LL (Table 34).

After identification of the promising families, intrafamily selection was carried out and three best plants from each promising family were advanced to the M_3 generation.

3. Observations in M_3 generation

The main purpose of raising M_3 generation was to confirm and study in detail the magnitude and direction of induced polygenic variability for the characters under study. Attempts were also made to compare the parameters of variability in M_2 and M_3 generations. The M_3 families were raised from the seeds of individual M_2 plants in augmented design with 79 blocks and three controls (PS, L4076 and S74-3). The observations were recorded on five random plants in each M_3 progeny. The data on eight characters were analysed as augmented design as a whole, and also as completely randomized design for each population separately. The induced variability in M_3 generation was analysed and presented in the same manner as for the M_2 generation. The entire M_3 material was divided into three

separate populations: (i) progenies of three normal looking plants from each M_2 progeny carrying a macromutation, which did not segregate for such mutations in M_3, (ii) progenies of three best plants in the M_2 families identified as promising on the basis of character mean and CV in the two extreme groups of mutagenic damage, i.e. LL and HH; and (iii) progenies of three random plants from each M_2 family not included in the above two populations. These three M_3 populations were called macromutational (I), selected (II), and unselected (III). In M_3 also, observations were recorded on the same eight quantitative traits as in M_2.

3.1 The results on polygenic mutations are presented character wise.

3.1.1 **Days to maturity**

Table 35 shows that the range for days to maturity increased in both directions in all the treated populations in relation to control (110-118 days). However, the extent of increase in the range varied in different populations. Maximum increase in range was observed in the macromutational M_3 populations, where the maturity time varied from 106 to 135 days. The selection practised for early maturity in M_2 lowered the range to 106-125 days as compared to 107-131 days in the unselected populations. This trend was maintained in all the mutagenized populations irrespective of mutagens and groups of mutagenic damage. Among the mutagens used, NEU showed widest range (106-135 days) for days to maturity in macromutational and unselected populations, and in the two groups of mutagenic damage, followed by EI (107-135 days) and gamma-rays (107-133 days). In case of selected populations, EI showed the widest range (106-125 days), followed by NEU (106-124 days) and gamma-rays (106-122 days). Among the two groups of mutagenic damage compared in M_3, HH always showed a slightly wider

Table 35 : Range, mean, variance, CV, SE, analysis of varaince, components of variation, heritability and genetic advance for days to maturity in M_3 generation

Treatment		Range	Mean	Vari-ance	CV	SE	Variance		GCV (%)	PCV (%)	Herita-bility (%)	GA % of mean
							Inter-family	Intra-family				
Control	: PS	110.0-118.0	113.9	8.0	2.5	0.2	12.4	6.9	0.9	2.5	13.8	0.7
	L 4076	124.0-137.0	127.4	12.0	2.7	0.2	22.0	9.5	2.4	2.7	20.8	1.2
	S74-3	123.0-138.0	126.0	14.0	3.0	0.2	23.2	11.7	1.2	3.0	16.4	1.0
				Macromutational population								
Gamma rays	:LL	108.0-128.0	114.8	41.9	5.6	0.5	116.3**	23.3	3.8	5.6	44.4	5.2
	HH	107.0-133.0	114.0	48.7	6.1	0.3	171.1**	18.1	4.9	6.1	62.8	7.9
	Overall	107.0-133.0	114.2	43.9	5.8	0.3	137.1**	20.6	4.2	5.8	53.1	6.3
EI	: LL	108.0-130.0	115.6	47.4	6.0	0.5	147.5**	22.6	4.3	6.0	52.6	6.5
	HH	107.0-135.0	114.3	50.5	6.2	0.3	186.7**	17.3	5.1	6.2	66.2	8.5
	Overall	107.0-135.0	114.8	49.0	6.1	0.3	168.2**	19.2	4.7	6.1	60.8	7.6
NEU	: LL	107.0-132.0	113.8	44.8	5.9	0.4	146.4**	19.4	4.4	5.9	56.7	6.9
	HH	106.0-135.0	113.6	59.3	6.8	0.3	227.7**	17.2	5.7	6.8	71.0	9.9
	Overall	106.0-135.0	113.7	52.0	6.3	0.2	188.0**	18.0	5.1	6.3	65.4	8.5
				Selected population								
Gamma rays:	LL	107.0-120.0	112.1	26.5	4.6	0.3	68.1**	16.1	2.9	4.6	39.2	3.7
	HH	106.0-122.0	110.9	32.6	5.1	0.2	87.0**	19.0	3.3	5.1	41.7	4.4
	Overall	106.0-122.0	111.5	29.5	4.9	0.2	77.5**	17.5	3.1	4.9	40.7	4.1
EI	: LL	106.0-123.0	110.8	31.3	5.0	0.3	80.9**	18.9	3.2	5.0	39.6	4.1
	HH	106.0-125.0	109.7	36.0	5.5	0.2	99.6**	20.1	3.6	5.5	44.2	5.0
	Overall	106.0-125.0	110.2	33.7	5.3	0.2	90.9**	19.4	3.4	5.3	42.4	4.6
NEU	: LL	107.0-123.0	111.6	29.9	4.9	0.2	78.3**	17.8	3.1	4.9	40.5	4.1
	HH	106.0-124.0	110.2	34.5	5.3	0.2	90.9**	20.4	3.4	5.3	40.9	4.5
	Overall	106.0-124.0	110.9	32.2	5.1	0.1	85.0**	19.0	3.3	5.1	41.0	4.3
				Unselected population								
Gamma rays	: LL	110.0-125.0	114.6	35.6	5.2	0.1	95.6**	20.6	3.4	5.2	42.1	4.5
	HH	109.0-127.0	114.1	41.0	5.6	0.2	133.4**	17.9	4.2	5.6	56.3	6.5
	Overall	109.0-127.0	114.4	38.8	5.4	0.1	117.6**	19.1	3.9	5.4	50.8	5.7
EI	: LL	108.0-128.0	116.2	40.3	5.5	0.1	116.3**	21.3	3.8	5.5	47.1	5.3
	HH	107.0-129.0	115.4	46.5	5.9	0.2	165.1**	16.9	4.7	5.9	63.6	7.8
	Overall	107.0-129.0	115.7	43.0	5.7	0.1	139.0**	19.0	4.2	5.7	55.8	6.5
NEU	: LL	109.0-129.0	115.3	43.2	5.7	0.2	135.5**	20.2	4.2	5.7	53.3	6.3
	HH	108.0-131.0	114.7	45.5	5.9	0.2	156.3**	18.2	4.6	5.9	60.3	7.3
	Overall	108.0-131.0	115.1	44.3	5.8	0.1	144.7**	19.2	4.3	5.8	56.7	6.8

** = Significant at 1% level.

range (106-135 days) against LL (107-132 days).

The mean duration of maturity shifted towards lateness (115.1 days) as compared to control (113.9 days) in the absence of selection in M_2 generation, and towards earliness (110.9 days) as a result of selection. Different mutagens and groups of damage had no significant effect on mean number of days to maturity.

The induced variability in M_3 generation was measured through estimates of variance, CV and SE. All the mutagenic treatments increased variance (26.5-59.3) and, consequently, CV (4.6-6.8%) as compared to control (variance 8.0; CV 2.5%). However, the increase in variability was not similar in all the populations or mutagens and groups of mutagenic damage compared. The variance and CV decreased considerably as a result of M_2 selection. On the other hand, variance significantly increased in the macromutational population than in the selected and unselected ones. Though variance increased in all the treatments, there were significant differences among the mutagens. The variance in the NEU-treated macromutational and unselected populations was higher (43.2-59.3) than in analogous populations of the EI (40.3-50.5) and gamma-ray (35.6-48.7) treatments, whereas variance of the selected populations, was higher in EI treatments (31.3-36.0), followed by NEU (29.9-34.5) and gamma-rays (26.5-32.6). The range of CV in the treated populations was 4.6-6.8% as compared to 2.5% in control. The pattern was the same as for variance in different treated populations and mutagens. The HH group always showed higher variance and CV than LL group in all the treated populations.

The analysis of variance showed that all the populations had significant differences among the families as against non-significant difference

(12.4) in the control. The macromutational populations had maximum interfamily variance, followed by the unselected and selected populations. Among the mutagens used , NEU induced higher interfamily variance (135.5-227.7) in the macromutational and unselected populations than EI (116.3-186.7) and gamma-rays (95.6-171.1), whereas EI had maximum interfamily variance in case of selected populations, followed by NEU and gamma-rays. The damage group HH had higher interfamily variance (87.0-227.7) than group LL (68.1-147.5).

With regard to different genetic parameters, all the populations had significant differences among the families, which were non-significant in the control. The phenotypic coefficient of variability (PCV) increased to (4.6-6.8%) in the mutagenized populations from 2.5% in the control. The increase in genotypic coefficient of variability (GCV) in the treated populations was even more (2.9-5.7% as against 0.9% in the control). Both PCV and GCV showed similar trend in differnt populations, mutagens and damage groups as observed for variance and CV. On the basis of increasing variation, various populations were arranged as : macromutational $>$ unselected $>$ selected populations; mutagen: NEU $>$ EI $>$ gamma-rays; and damage groups: HH $>$ LL. The relatively greater increase in GCV and PCV was also reflected in the higher magnitude of heritability for days to maturity in the treated populations. The heritability estimates were much higher in the treated populations (39.2-71.0%) as compared to control (13.8%). The estimates of heritability were also higher in M_3 (51.9%, pooled over treatments) than those obtained in M_2 (43.7%). The heritability was higher in the macromutational populations (44.4-71.0%) than in the unselected (42.1-63.6%) and selected (39.2-44.2%) ones.

Similarly, the genetic advance (GA) was higher (3.7-9.9% of mean) in the treated populations than in the control (0.7%). The estimates of GA were also higher in M_3 (6.0% of mean, pooled over treatments) than those obtained in M_2 (2.1%). The GA was higher in the macromutational populations (5.2-9.9%) than in the unselected (4.5-7.8%) and selected (3.7-5.0%) populations.

3.1.2 Plant height

Table 36 shows that the range for plant height increased in the treated populations (13.2-35.0 cm) in relation to control (19.8-27.0 cm). The plant height varied depending on the type of population, mutagen and group of mutagenic damage. Maximum increase in range was observed in the macromutational M_3 popualtions (13.2-32.8 cm) as compared with the unselected populations (13.5-30.8 cm). Selection in M_2 narrowed the range to 19.8-35.0 cm. Among the mutagens used, NEU resulted in the widest range (13.2-35.0 cm), followed by EI (15.6-33.6 cm) and gamma-rays (15.0 - 32.8 cm). The mutagenic damage group HH showed wider range (13.5-35.0 cm) than LL group (13.2-33.0 cm) in all the three populations and with all the mutagens.

In general, the mutagenic treatments shifted the population mean (Table 36) in positive direction (taller plants) in all the three populations, except HH group of NEU in the unselected population where it decreased marginally. The mutagenic treatments only slightly altered mean plant height in the unselected and macromutational populations. However, selection applied in M_2 generation increased the mean height in M_3 generation (23.5-26.9 cm) in comparison to the control (21.2 cm). In general, no significant differences were noted among the mutagens tested with regard to

Table 36 : Range, mean, variance, CV, SE, analysis of variance, components of variation, heritability and genetic advance for plant height in M_3 generation

Treatment		Range	Mean	Variance	CV	SE	Variance		GCV (%)	PCV (%)	Heritability (%)	GA % of mean
							inter-family	Intra-family				
Control :	LL	19.8-27.0	21.2	4.5	10.0	0.12	8.5	3.5	4.7	10.0	22.2	4.6
	L 4076	30.4-36.2	32.1	5.3	7.2	0.13	8.9	4.4	3.0	7.2	17.0	2.5
	S74-3	29.8-35.0	31.1	5.1	7.3	0.12	9.9	3.9	3.9	7.3	23.5	3.5
					Macromutational population							
Gamma rays:	LL	15.2-30.2	24.2	17.9	17.5	0.3	43.5**	11.5	10.4	17.5	35.6	12.8
	HH	15.0-31.4	22.9	29.2	23.6	0.3	80.4**	16.4	15.7	23.6	44.0	21.4
	Overall	15.0-31.4	23.6	23.6	20.6	0.2	61.2**	14.2	13.0	20.6	39.8	16.9
EI :	LL	16.8-30.9	23.7	21.1	19.4	0.3	53.1**	13.1	11.9	19.4	37.8	15.1
	HH	15.6-31.2	22.3	30.6	24.8	0.2	87.8**	16.3	17.0	24.8	46.7	23.9
	Overall	15.6-31.2	23.0	25.8	22.1	0.2	69.4**	14.9	14.4	22.1	42.3	19.2
NEU :	LL	13.2-31.0	23.0	22.9	20.8	0.3	60.1**	13.6	13.2	20.8	40.4	17.3
	HH	14.0-32.8	21.5	31.2	26.0	0.2	91.6**	16.1	18.1	26.0	48.5	26.0
	Overall	13.2-32.8	22.3	27.1	23.3	0.2	75.5**	15.0	15.6	23.3	44.5	21.4
					Selected population							
Gamma rays :	LL	20.8-30.2	25.6	10.3	12.5	0.2	22.7**	7.2	6.8	12.5	29.8	7.7
	HH	21.4-32.8	23.5	16.8	17.4	0.1	42.0**	10.5	10.7	17.4	37.4	13.4
	Overall	20.8-32.8	24.6	13.6	15.0	0.1	32.0**	9.0	8.7	15.0	33.6	10.4
EI :	LL	20.2-33.0	26.3	12.0	13.2	0.2	27.2**	8.2	7.4	13.2	31.6	8.6
	HH	22.2-33.6	24.0	17.9	17.6	0.1	46.3**	10.8	11.1	17.6	39.5	14.3
	Overall	20.2-33.6	25.2	15.0	15.3	0.1	36.2**	9.7	9.2	15.3	35.6	11.3
NEU :	LL	19.8-32.2	26.9	13.2	13.5	0.2	30.4**	8.9	7.7	13.5	32.4	9.0
	HH	21.4-35.0	24.7	20.0	18.1	0.1	53.2**	11.7	11.6	18.1	41.3	15.4
	Overall	19.8-35.0	25.8	16.6	15.8	0.1	41.0**	10.5	9.6	15.8	36.9	12.0
					Unselected population							
Gamma rays :	LL	16.0-29.2	23.0	13.0	15.7	0.07	30.2**	8.7	9.0	15.7	33.2	10.7
	HH	16.8-30.0	22.0	19.4	20.0	0.13	51.4**	11.4	12.9	20.0	41.4	17.1
	Overall	16.0-30.0	22.5	16.2	17.9	0.07	40.2**	10.2	10.9	17.9	37.3	13.7
EI :	LL	17.0-28.0	22.4	14.5	17.0	0.08	34.9**	9.4	10.1	17.0	35.5	12.4
	HH	16.0-30.8	21.3	20.4	21.2	0.13	56.0**	11.5	14.0	21.2	43.7	19.1
	Overall	16.0-30.8	21.9	17.5	19.1	0.07	45.1**	10.6	12.0	19.1	39.6	15.6
NEU :	LL	14.6-29.2	21.8	14.7	17.6	0.09	36.3**	9.3	10.7	17.6	36.8	13.3
	HH	13.5-30.2	20.9	23.9	23.4	0.17	67.5**	13.0	15.8	23.4	45.6	22.0
	Overall	13.5-30.2	21.4	19.2	20.5	0.08	50.8**	11.3	13.1	20.5	41.2	17.4

**= Significant at 1% level.

mean plant height. However, LL group of mutagenic damage showed higher plant height (21.8-26.9 cm) than HH group (20.9-24.7 cm) in all the popualtions and mutagens studied.

The analysis of induced variability for plant height (Table 36) revealed that mutagenic treatments increased variance significantly. The patterns were identical with respect to variance as well as CV. The CV ranged in the mutagenized populations from 12.5 to 26.0% as against 10.0% in the control. Maximum increase was observed in the macromutational populations (17.5-26.0%). Selection in M_2 significantly reduced variability (CV 12.5-18.1 cm). In general, variability (CV) in the NEU-treated populations was significantly higher (13.5-26.0%) than in the EI (13.2-24.8%) and gamma-ray (12.5-23.6%) treated popualtions. Among the two groups of mutagenic damage, HH showed significantly higher variance (16.8-31.2) and CV (17.4-26.0%) than LL group (variance 10.3-22.9, CV 12.5-20.8%).

All the treated populations showed significant differences for interfamily variance, which ranged from 22.7-91.6 as compared to 8.5 in the control. The populations were arranged in the order of macromutational $>$ unselected $>$ selected. As is evident from these results, the interfamily variance for plant height decreased drastically as a result of selection applied in M_2 generation. Among the mutagens compared, NEU induced maximum interfamily variance (41.0-75.5) followed by EI (36.2-69.4) and gamma-rays (32.0-61.2). The mutagenic damage group HH (42.0-91.6) had an edge over LL group (22.7-60.1).

Both PCV and GCV increased in the mutagenised populations over the control. The patterns were identical for both. The range of PCV was 12.5-26.0% in the treated popualtion as against 10.0% in the control, and GCV ranged between 6.8 and 18.1% as against 4.7% in the control popultion.

Among the three types of M_3 populations, the macromutational populations had higher GCV and PCV than the unselected and selected populations. Both GCV and PCV decreased drastically as a result of M_2 selection. The fact that these two components of variation increased in M_3 generation over M_2 is evident from the increase of heritability in M_3. The order of mutagens for GCV as well as PCV was NEU $>$ EI $>$ gamma-rays. The GCV and PCV were also higher in the mutagenic damage group HH than LL. The high magnitude of GCV in M_2 and M_3 indicates that the variability generated in M_2 was transmitted to M_3 generation.

The estimates of heritability (Table 36) were higher in all the treated populations (29.8-48.5%) as compared to control (22.2%). The heritability estimate increased from28.7% in M_2 to 39.0% in M_3. Consequently the expected GA also increased in all the treated populations. The GA for plant height ranged between 7.7 and 26.0% (of mean) as compared to 4.6% in the control. The GA was higher in M_3 (15.3%) than in M_2 (9.7%).

3.1.3 **Number of branches per plant**

The mutagenic treatments increased branching (2.6-22.6 branches/ plant as compared to 6.2-13.0 in the control; Table 37). The range was much wider (2.6-19.4 branches/plant) in the macromutational populations than in the selected (6.8-22.6 branches/plant) and unselected (3.0-15.8) populations. The chemical mutagen NEU increased the range to the maximum extent (2.6-19.4 branches/plant), followed by EI (2.8-18.2) and gamma-rays (3.6-17.2). Among the groups of mutagenic damage, the range was wider in HH (2.6-22.6) than in LL (3.0-21.0) group.

The overall population mean for number of branches per plant in the treated populations increased from 7.5 to 9.0 (Table 37). Selection in M_2 generation increased the mean considerably in M_3 (11.0 branches per plant) in comparison with other populations (8.2 branches/plant in macromutational and 7.8 in unselected). The HH group of mutagenic damage had higher mean value (9.7 branches/plant) than the LL group (8.3 branches/plant).

The magnitude of variability recorded in terms of variance, CV and SE (Table 37) increased in all the treated populations (variance 11.2-37.4, CV 36.0-71.4%) over the control (variance 3.9, CV 26.5%). The variance decreased significantly in M_3 due to selection in M_2 (variance 11.2-24.5, CV 36.0-38.4%). The macromutational populations showed maximum variance (21.6-37.4) as compared to both unselected (19.4-32.3) and selected (11.2-24.5) populations. Similar to variance, the increase in CV was also maximum in the macromutational populations (59.6-71.4%), followed by unselected (62.9-68.5%) and selected (36.0-38.4%) populations. The mutagens showed significant differences among themselves with regard to induced variability. The trend was NEU $>$ EI $>$ gamma-rays in all the populations. Out of the two mutagenic damage groups, HH had higher variability for branching (variance 16.4-37.4, CV 37.5-71.4%) than LL (variance 11.2-28.2, CV 36.0-64.0%).

The interfamily variances (Table 37) were highly significant in the treated populations (21.8-84.0) and non-significant in the control (6.2). The macromutational populations showed maximum interfamily variance (36.6-84.0), followed by the unselected(31.2-64.5) and selected (21.8-64.0) populations. Thus, interfamily variance decreased in M_3 when selection was applied in M_2 generation for branches per plant. Based on

Table 37 : Range, mean, variance, CV, SE, analysis of variance, components of variation, heritability and genetic advance for total fruiting branches/plant in M_3 generation

Treatment		Range	Mean	Variance	CV	SE	Variance		GCV (%)	PCV (%)	Heritability (%)	GA % of mean
							Inter family	Intra-family				
Control :	PS	6.2-13.0	7.5	3.9	26.3	0.11	6.2	3.3	10.2	26.3	14.9	8.2
	L4076	10.6-18.4	14.4	6.1	17.2	0.14	10.9	4.9	7.6	17.2	19.7	7.0
	S74-3	12.0-18.2	13.8	5.4	16.9	0.13	10.2	4.2	8.0	16.9	22.2	7.7
							Macromutational population					
Gamma rays:	LL	3.6-14.4	7.4	21.6	62.8	0.4	36.6**	17.9	26.1	62.8	17.3	22.4
	HH	4.0-17.2	8.5	32.4	67.0	0.3	63.5**	24.7	32.8	67.0	24.0	33.1
	Overall	3.6-17.2	7.9	26.5	65.2	0.2	51.7**	20.2	31.8	65.2	23.8	31.9
EI :	LL	3.2-14.8	8.1	23.3	59.6	0.3	44.0**	18.2	28.0	59.6	22.1	27.1
	HH	2.8-18.2	8.5	36.8	71.4	0.3	82.0**	25.6	39.5	71.4	30.6	45.0
	Overall	2.8-18.2	8.3	30.0	66.0	0.2	65.3	21.4	35.7	66.0	29.1	39.7
NEU :	LL	3.0-16.0	8.3	28.2	64.0	0.3	58.5**	20.7	33.1	64.0	26.8	35.4
	HH	2.6-19.4	8.6	37.4	71.1	0.3	84.0**	25.8	39.7	71.1	31.1	45.6
	Overall	2.6-19.4	8.5	32.8	67.4	0.2	71.7**	23.1	36.7	67.4	29.6	41.1
							Selected population					
Gamma rays :	LL	6.8-18.4	9.3	11.2	36.0	0.2	21.8**	8.6	17.5	36.0	23.5	17.5
	HH	7.4-20.0	10.8	16.4	37.5	0.1	37.0**	11.4	21.0	37.5	31.0	24.0
	Overall	6.8-20.0	10.1	13.9	36.9	0.1	28.9**	10.2	19.1	36.9	26.8	20.4
EI :	LL	7.0-19.0	9.7	12.4	36.3	0.2	27.1**	8.8	19.7	36.3	29.4	22.0
	HH	8.2-22.2	12.0	21.0	38.2	0.2	52.0**	13.5	23.1	38.2	36.3	28.7
	Overall	7.0-22.2	11.0	16.8	37.3	0.1	40.2**	11.1	21.9	37.3	34.4	26.5
NEU :	LL	7.4-21.0	10.1	14.2	37.3	0.2	35.0**	9.1	22.5	37.3	36.3	28.0
	HH	9.0-22.6	12.9	24.5	38.4	0.2	64.0**	14.7	24.3	38.4	40.1	31.7
	Overall	7.4-22.6	11.8	19.6	37.5	0.1	50.6**	11.9	23.6	37.5	39.4	30.5
							Unselected population					
Gamma rays :	LL	4.0-13.2	7.0	19.4	62.9	0.09	31.2**	16.5	24.5	62.9	15.1	19.6
	HH	4.6-14.4	8.2	28.8	65.4	0.16	53.0**	23,1	29.8	65.4	20.6	27.9
	Overall	4.0-14.4	7.5	23.2	64.2	0.08	40.0**	19.0	27.3	64.2	18.1	23.9
EI :	LL	3.5-14.0	7.1	20.5	63.8	0.10	34.7**	17.0	26.5	63.8	17.2	22.6
	HH	4.2-15.6	8.3	31.2	67.3	0.16	59.6**	24.2	32.1	67.3	22.7	31.5
	Overall	3.5-15.6	7.9	26.0	64.5	0.09	49.1**	20.3	30.4	64.5	22.1	29.4
NEU :	LL	4.2-14.8	7.5	23.6	64.8	0.11	47.8**	17.6	32.8	64.8	25.5	34.1
	HH	3.0-15.8	8.3	32.3	68.5	0.20	64.5**	24.3	34.2	68.5	24.9	35.1
	Overall	3.0-15.8	8.0	27.4	65.4	0.10	55.7**	20.4	33.2	65.4	25.7	34.7

**= Significant at 1% level.

the magnitude of interfamily variance, the mutagens were arranged in order of NEU $>$ EI $>$ gamma-rays. The HH group of mutagenic damage had greater interfamily variance (37.0-84.0) than LL group (21.8-58.5).

The study of components of variation (Table 37) showed that both GCV (17.5-39.7%) and PCV (36.0-71.4%) increased in the treated populations over the control (GCV 10.2%, PCV 26.3%). Out of the three populations studied, macromutational populations showed higher GCV (26.1-39.7%) and PCV (59.6-71.4%) than the unselected (GCV 24.5-34.2%, PCV 62.9-68.5%) and selected (GCV 17.5-24.3%, PCV 36.0-38.4%) populations. A marked decline in GCV and PCV was recorded due to selection applied in M_2 generation. Among the groups of mutagenic damage, HH showed higher GCV (21.0-39.7%) and PCV (37.5-71.4%) than LL group (GCV 17.5-33.1%, PCV 36.0-64.0).

The heritability estimates increased considerably (15.1-40.1%) in the treated populations as compared to control (14.9%). Further, the heritability in M_3 (27.7%) increased over the M_2 level (22.1%). Similarly, GA increased in all the mutagenized populations (17.5-45.6% of mean) as compared to control (8.2%). Higher GA was recorded in the macromutational populations (22.4-45.6% of mean), followed by unselected (19.6-35.1%) and selected (17.5-31.7%) populations.

3.1.4 Number of fruiting clusters per plant

The data presented in Table 38 show that the range for effective pod clusters per plant increased in both directions in all the treated populations (5.0-48.5 clusters/plant) in relation to the control population (12.2-23.2 clusters/plant). However, the extent of increase in range varied

in different populations. The range was much wider (5.0-47.8 clusters/ plant) in the macromutational populations than in the unselected (5.9-41.4) and selected (12.0-46.5) populations. As can be seen, selection in M_2 narrowed the range for pod clusters per plant in M_3 generation in comparison with other populations. The chemical mutagen NEU increased the range to the maximum extent (5.0-46.5 clusters/plant), followed by EI (6.0-47.5) and gamma-rays (5.6-41.2). Among the groups of mutagenic damage, the range of pod clusters per plant was wider in HH (5.0-47.5) than in LL (5.4-40.8) group.

In general, mutagenic treatments shifted the population mean in positive direction in all the three populations. But the mutagenic treatments had little effect on mean number of clusters per plant in the unselected (13.8-17.1 clusters/plant) and macromutational (13.5-18.7 clusters/plant) populations in the absence of selection. However, selection applied in M_2 generation increased the mean in different treatments (19.2-28.1 clusters/plant) in comparison to the control (13.7 clusters/plant). In general, no significant differences were noted among the mutagens tested with regard to mean number of clusters per plant. However, the HH group of mutagenic damage had higher mean number of pod clusters per plant in the various treatments (14.5-28.1) than LL group (13.5-23.4).

The magnitude of variability recorded in terms of variance, CV and SE (Table 38) increased in all the treated populations (variance 71.4-204.8, CV 37.9-82.9%) over the control (variance 11.2, CV 24.4%). The variation decreased significantly in M_3 due to selection in M_2 generation (variance 71.4-115.8, CV 37.9-44.0%). The macromutational populations showed maximum variance (118.2-204.8) as compared to both

Table 38 : Range, mean, variance, CV, SE, analysis of variance, components of variation, heritability and genetic advance for effective clusters per plant in M_3 generation

Treatment		Range	Mean	Variance	CV	SE	Variance: Inter-family	Variance: Intra-family	GCV (%)	PCV (%)	Heritability	GA % of mean
Control :	PS	12.2-23.2	13.7	11.2	24.4	0.2	21.6	8.6	11.8	24.4	23.2	11.7
	L4076	36.6-53.4	44.0	18.5	9.8	0.2	34.9	14.4	4.6	9.8	22.2	4.5
	S 74-3	38.0-57.8	43.2	26.4	11.9	0.3	48.0	21.0	5.4	11.9	20.5	5.0
Macromutational population												
Gamma rays:	LL	5.6-34.0	15.0	118.2	72.5	0.8	241.2**	87.6	36.9	72.5	26.0	38.8
	HH	5.8-39.0	15.5	132.0	74.1	0.6	318.1**	85.6	44.0	74.1	35.2	53.7
	Overall	5.6-39.0	15.2	125.8	73.8	0.5	282.9**	86.5	41.2	73.8	31.2	47.4
EI :	LL	6.0-34.8	14.5	118.9	75.2	0.8	274.8**	80.0	43.0	75.2	32.8	50.7
	HH	7.2-47.5	18.7	183.0	72.3	0.6	606.0**	77.0	55.0	72.3	57.9	86.2
	Overall	6.0-47.5	16.3	149.4	75.0	0.5	427.1**	80.0	51.1	75.0	46.4	71.7
NEU :	LL	5.4-35.2	13.5	125.2	82.9	0.7	290.0**	84.5	47.5	82.9	32.7	55.9
	HH	5.0-46.4	18.7	204.8	76.5	0.6	586.6**	109.8	52.2	76.5	46.5	73.4
	Overall	5.0-46.4	16.5	164.4	77.7	0.5	437.1**	96.4	50.0	77.7	41.4	66.3
Selected population												
Gamma rays:	LL	12.0-37.0	19.2	71.4	44.0	0.5	157.0**	50.0	24.1	44.0	30.0	27.2
	HH	13.4-41.2	22.6	87.0	41.3	0.3	218.2**	54.2	25.3	41.3	37.7	32.1
	Overall	12.0-41.2	21.0	80.0	42.6	0.3	190.8**	52.3	25.1	42.6	34.6	30.4
EI :	LL	13.2-39.6	22.5	77.4	39.1	0.5	206.6**	45.1	25.3	39.1	41.7	33.6
	HH	14.8-45.4	27.0	104.7	37.9	0.3	329.9**	48.4	27.8	37.9	53.8	42.0
	Overall	13.2-45.4	24.9	92.2	38.6	0.3	276.2**	46.2	27.2	38.6	49.9	39.6
NEU :	LL	15.0-40.8	23.4	83.5	39.1	0.4	231.5**	46.5	26.0	39.1	44.3	35.6
	HH	13.6-46.5	28.1	115.8	38.3	0.3	401.8**	44.8	30.1	38.3	61.7	48.7
	Overall	13.6-46.5	26.0	101.6	38.8	0.3	324.8**	45.8	28.7	38.8	54.9	43.8
Unselected population												
Gamma rays:	LL	6.5-30.0	13.8	98.5	71.9	0.2	186.5**	76.5	34.0	71.9	22.3	33.0
	HH	5.9-32.6	14.5	118.3	75.0	0.3	270.3**	80.3	42.5	75.0	32.1	49.6
	Overall	5.9-32.6	14.2	104.8	72.1	0.2	223.2**	75.2	38.3	72.1	28.2	41.9
EI :	LL	8.2-30.8	14.1	105.7	72.9	0.2	228.5**	75.0	39.2	72.9	29.0	43.6
	HH	6.0-39.4	16.2	158.9	77.8	0.4	446.1**	87.1	52.3	77.8	45.2	72.5
	Overall	6.0-39.4	15.2	125.6	73.7	0.2	321.2**	76.9	46.0	73.8	38.9	59.1
NEU:	LL	7.8-35.0	14.6	114.8	73.4	0.2	253.6**	80.1	40.3	73.4	30.2	45.7
	HH	6.6-41.4	17.1	185.3	79.6	0.4	514.5**	103.0	53.0	79.6	44.4	72.8
	Overall	6.6-41.4	16.0	141.4	74.3	0.2	368.3**	85.0	46.9	74.3	40.0	61.2

**= Significant at 1% level.

unselected (98.5-185.3) and selected (71.4-115.8) populations. Likewise, the increase in CV was also much higher (72.3-82.9%) in the macromutational populations than in the unselected (71.9-79.6%) and selected (37.9-44.0%) populations. The mutagens showed significant differences among themselves with regard to variability. The trend, as before, was NEU $>$ EI $>$ gamma-rays in all the populations, except in the selected populations where CV decreased in EI and NEU treated populations as compared to gamma-ray treatments. Out of the two mutagenic damage groups, HH had higher variance for clusters per plant (87.0-204.8) than LL (71.4-125.2). The CV was also higher in unselected population in the HH group compared to LL group of mutagenic damage, but higher CV was observed in the LL group compared to HH group in selected population with all the mutagens and also in macromutational population except with gamma-rays.

The interfamily variances (Table 38) were highly significant in the treated populations (157.0-606.0), and non-significant in the control (21.6). The macromutational populations showed maximum interfamily variance (241.2-606.0), followed by unselected (186.5-514.5) and selected (157.0-401.8) populations. Thus, interfamily variance reduced drastically in M_3 when selection was applied in M_2 generation for pod clusters. Based on the magnitude of interfamily variance, the mutagens were arranged in the order of NEU $>$ EI $>$ gamma-rays. The HH group of mutagenic damage had higher magnitude of interfamily variance (218.2-606.0) than LL group (157.0-290.0).

The study of components of variation showed that a major part

of phenotypic variance was due to the genetic reasons (relatively higher GCV). Both GCV (24.1-55.0%) and PCV (37.9-82.9%) increased over the control (GCV 11.8%, PCV 24.4%) as a result of mutagenic treatments. Out of the three populations studied, macromutational populations showed higher GCV (36.9-55.0%) and PCV (72.3-82.9%) than the unselected (GCV 34.0-53.0%, PCV 71.9-79.6%) and selected (GCV 24.1-30.1, PCV 37.9-44.0%) populations. The GCV and PCV decreased noticeably as a consequence of M_2 selection. Among the groups of mutagenic damage, GCV was higher in HH (25.3-55.0%) than LL group (GCV 24.1-47.5%). The pattern of PCV was also the same as in the case of CV for this character.

The heritability estimates increased considerably (22.3-61.7%) in the treated populations as compared to the control (23.2%). The heritability increased further in M_3 (40.6%) over M_2 level (24.1%). Similarly, GA also increased in all the mutagenized populations (27.2-86.2% of mean) as compared to the control (11.7%). The GA was maximum in the macromutational populations (38.8-86.2% of mean). The unselected (33.0-72.8%) and selected (27.2-48.7%) populations were next in order. Based on the magnitude of GA (% of mean), the mutagens were arranged in the familiar pattern of NEU $\succ$ EI $\succ$ gamma-rays in the selected and unselected populations, but in case of macromutational populations, the order of the mutagens was EI $\succ$ NEU $\succ$ gamma-rays. The HH group of mutagenic damage showed higher GA than LL group in all mutagens and populations.

3.1.5 Number of pods per plant

A comparison of pods/plant in the treated and control populations

(Table 39) shows that the range for this character increased in the treated populations (7.5-80.0 pods/plant) much beyond the limits of the control (16.8-31.8 pods/plant). The span of range varied depending on population, mutagen and group of mutagenic damage. The maximum increase in the range of pods/plant was recorded in the macromutational M_3 populations (7.5-73.4 pods/plant) as compared with the unselected materials (8.3-69.8 pods/plant). Selection in M_2 shifted the range to 15.5-80.0 pods per plant. Among the mutagens used, NEU caused the widest range (7.5-80.0 pods/plant), followed by EI (8.2-76.8) and gamma-rays (8.0-73.0). The mutagenic damage group HH showed a wider range of pods/plant (7.5-80.0) than LL group (8.6-74.4) in all the three populations with all the mutagens.

In general, mutagenic treatments shifted the population mean in positive direction (higher pod number) in all the three populations. The mutagenic tretments had little difference in their effect on podding intensity in the unselected and macromutational populations. However, selection applied in M_2 generation increased the mean in different treatments (28.3-40.2 pods/plant) in comparison with the control (19.4 pods/plant). With the only exception of selected population, no significant differences were noted among the mutagens tested with regard to mean podding intensity. However the HH group of mutagenic damage showed higher number of pods per plant (22.3-40.2) than LL group (19.3-32.6).

The analysis of variability induced for pods per plant by mutagenic treatments (Table 39) revealed that the mutagenic treatments increased variance significantly. The patterns were almost identical for variance as well as CV. The CV ranged in the mutagenized populations from 43.0 to

Table 39 : Range, mean, variance, CV, SE, analysis of variance, components of variation, heritability and genetic advance for effective pods per plant in M_3 generation

Treatment		Range	Mean	Vari-ance	CV	SE	Variance		GCV (%)	PCV (%)	Herita-bility (%)	GA % of mean
							Inter-family	Intra-family				
Control :	PS	16.8-31.8	19.4	34.5	30.3	0.3	56.1	29.1	12.0	30.3	15.6	9.7
	L 4076	62.2-79.6	67.4	40.4	9.4	0.4	66.0	34.0	3.8	9.4	15.8	3.1
	S 74-3	58.4-80.2	64.2	49.6	11.0	0.4	82.8	41.3	4.5	11.0	16.7	3.8
				Macromutational population								
Gamma rays :	LL	8.6-53.8	20.4	216.3	72.1	1.1	416.9**	166.2	34.7	72.1	23.2	34.5
	HH	8.0-54.4	24.6	377.7	79.0	0.9	883.7**	251.2	45.7	79.0	33.5	54.5
	Overall	8.0-54.4	22.6	296.6	76.2	0.7	648.0**	208.8	41.5	76.2	29.5	46.5
EI :	LL	9.0-48.6	21.0	235.5	73.1	1.1	476.7**	175.4	37.0	73.1	25.6	38.6
	HH	8.2-62.4	27.5	463.2	78.3	1.0	1125.3**	297.8	46.8	78.3	35.7	57.6
	Overall	8.2-62.4	24.2	351.8	77.5	0.7	814.0**	236.4	44.4	77.5	32.8	52.4
NEU :	LL	8.9-59.6	21.9	259.3	73.5	1.0	552.9**	185.9	39.1	73.5	28.3	42.9
	HH	7.5-73.4	29.5	596.0	82.8	1.0	1523.8**	364.2	51.6	82.8	38.9	66.3
	Overall	7.5-73.4	25.1	401.2	79.8	0.7	932.4**	268.4	45.9	79.8	33.1	54.4
				Selected population								
Gamma rays:	LL	17.2-71.4	28.3	152.4	43.6	0.7	314.0**	112.0	22.4	43.6	26.5	23.8
	HH	18.6-73.0	32.5	246.7	48.3	0.5	595.1**	159.6	28.7	48.3	35.3	35.1
	Overall	17.2-73.0	30.5	201.6	46.6	0.4	451.8**	139.3	25.9	46.6	31.0	29.7
EI:	LL	19.0-72.2	31.4	193.8	44.3	0.8	422.4**	137.4	24.0	44.3	29.3	26.8
	HH	18.2-76.8	37.8	338.9	48.7	0.6	799.1**	224.3	28.4	48.7	33.9	34.0
	Overall	18.2-76.8	34.6	270.4	47.5	0.5	584.0**	192.1	25.6	47.5	29.6	28.4
NEU :	LL	16.9-74.4	32.6	212.5	44.7	0.7	446.7**	154.2	23.5	44.7	32.2	27.5
	HH	15.5-80.0	40.2	398.3	49.6	0.6	989.9**	250.4	32.7	49.6	43.4	44.4
	Overall	15.5-80.0	36.3	299.7	47.7	0.5	737.8**	190.4	28.8	47.7	36.5	35.9
				Unselected population								
Gamma rays:	LL	9.0-48.4	19.3	185.6	70.6	0.3	351.0**	144.5	33.2	70.6	22.3	32.4
	HH	8.4-51.6	22.2	286.2	76.2	0.5	612.6**	204.9	40.7	76.2	28.5	44.8
	Overall	8.4-51.6	20.5	230.8	74.1	0.2	462.4**	173.1	37.1	74.1	25.1	38.3
EI:	LL	9.2-44.8	20.0	219.9	74.1	0.3	428.7**	168.0	36.0	74.1	23.7	36.2
	HH	10.4-57.5	24.6	357.9	76.9	0.6	814.1**	244.1	43.4	76.9	31.8	50.4
	Overall	9.2-57.5	22.4	285.3	75.4	0.3	601.0**	206.8	39.6	75.4	27.6	42.9
NEU:	LL	11.4-55.6	21.0	245.4	74.6	0.4	504.6**	180.6	38.3	74.6	26.4	40.6
	HH	8.3-69.8	27.3	474.6	79.8	0.8	1152.3**	305.6	47.7	79.8	35.5	58.5
	Overall	8.3-69.8	24.0	341.5	77.0	0.4	754.9**	238.4	42.4	77.0	30.2	47.9

**= Significant at 1% level.

82.8%, as against 30.3% in the control. Though variance increased in all the populations, the increase was maximum in the macromutational populations (CV 72.1-82.8%) as compared to the unselected populations (70.6-79.8%). Selection in M_2 conspicuously reduced variability (CV 43.6-49.6%). In general, variability (CV) in the NEU-treated populations was markedly higher (44.7-82.8%) than in the EI (44.3-78.3%) and gamma-ray (43.6-79.0%) treated populations. Among the two groups of mutagenic damage, HH showed significantly higher variance (246.7-596.0) and CV (48.3-82.8%) than the LL group(variance 152.4-259.3, CV 43.6-74.6%).

As can be seen from Table 39, all the treated populations showed significant differences for interfamily variance, which ranged from 314.0 to 1523.8 as compared to 56.1 in the control. With regard to interfamily variances, the populations were arranged in the order of macromutational $>$ unselected $>$ selected. Thus, interfamily variance for pods per plant decreased as a result of selection applied in M_2 generation. Among the mutagens used, NEU induced maximum interfamily variance (446.7-1523.8), followed by EI (422.4-1125.3) and gamma-rays (3140.0-883.7). The mutagenic damage group HH (595.1 -1523.8) had significant edge over LL group (314.0 - 552.9).

Both PCV and GCV (Table 39) increased in the mutagenized populations over the control. The range of PCV was 43.6 - 82.8% in the treated populations as against 30.3% in the control, and GCV ranged from 22.4 to 51.6% as against 12.0% in the control population. Among the three types of M_3 populations, the macromutational populations had higher GCV and PCV than the unselected and selected populations. Both GCV and PCV decreased drastically as a result of selection in M_2 generation. The fact

that these two components of variation increased in M_3 generation over M_2 is evident from the increased values of heritability in M_3. The order of mutagens for GCV as well as PCV was NEU > EI > Gamma-rays. The GCV and PCV were also higher in the mutagenic damage group HH than LL. The high magnitude of GCV in M_2 and M_3 indicates that a large part of variability generated in M_2 was transmitted to M_3 generation.

The estimates of heritability were higher in all the treated populations (22.3-43.4%) as compared to the control (15.6%). The pattern observed with regard to different mutagens was NEU > EI > gamma-rays. The heritability estimate was higher in M_3 (average of treatments 30.6%) than in M_2 (25.8%). Similarly, the GA increased in all the treated populations (23.8 -66.3% of mean) as against 9.7% in the control population. The GA was higher in M_3 (41.8% over all the treatments) than in M_2 (39.8%).

3.1.6 Number of seeds per pod

As a result of mutagenic treatments, the range of seeds per pod almost doubled to 1.0 - 2.1 from 1.1 - 1.6 seeds/pod in the control (Table 40). The range was much wider in the macromutational (1.0-1.9 seeds/pod) and selected (1.2-2.1 seeds/pod) populations than in the unselected (1.0-1.8 seeds/pod) populations. The chemical mutagen NEU caused maximum increase in the range (1.0-2.1 seeds/pod), followed by EI (1.0-2.0) and gamma-rays (1.0-1.8). Among the groups of mutagenic damage, the range of seeds per pod was wider in HH (1.0-2.1) than in LL (1.0-1.9) group. The overall population mean for seeds/pod in the treated populations increased to 1.33 from 1.2 in the control (Table 40). Selection in M_2 generation increased mean in M_3 (1.38 seeds/pod) in comparison with other

treated populations (1.34 in macromutational and 1.27 seeds/pod in unselected. The HH group of mutagenic damage had higher mean value (1.35 seeds/pod) against 1.31 seeds/pod in the LL group. NEU was the most effective mutagen in increasing the number of seeds per pod, followed by EI and gamma-rays.

The magnitude of variability recorded in terms of variance, CV and SE (Table 40) increased in all the treated populations (variance 0.03 - 0.1, CV 13.9-23.1%) over the control (variance 0.02, CV 12.5%). The patterns were almost identical for variance as well as CV. Though CV increased in all the populations, the increase was maximum (19.8 - 23.1%) in the macromutational populations. Selection in M_2 reduced variability (13.9 - 18.5%) significantly. In general, variability (CV) in the NEU-treated populations was marginally higher (16.3-23.1%) than in the EI (15.2-22.5%) and gamma-ray (13.9-22.1%) treated popultions. Among the two groups of mutagenic damage, HH showed significantly higher variance (0.05-0.1) and CV (17.1-23.1%) than LL group (variance 0.03-0.07, CV 13.9-20.2%).

The interfamily variances (Table 40) increased from 0.04 in the control to 0.05 - 0.21 in the treated populations. Among the different types of populations, the macronutational populations showed maximum interfamily variance (0.12 - 0.21), followed by unselected (0.10 -0.17) and selected (0.05 - 0.13) populations. Thus, the interfamily variance decreased drastically in M_3 due to M_2 selection for seeds per pod. Based on the magnitude of interfamily variance the mutagens followed the already known pattern: NEU $>$ EI $>$ gamma-rays. The HH group of mutagenic damage displayed more interfamily variance (0.09-0.21) than LL group

Table 40 : Range, mean, variance, CV, SE, analysis of variance, components of variation, heritaility and genetic advance for seeds per pod in M_3 generation

Treatment		Range	Mean	Vari-ance	CV	SE	Variance		GCV (%)	PCV (%)	Heritabi-lity (%)	GA % of mean
							Inter-family	Intra-family				
Control :	PS	1.1-1.6	1.2	0.02	12.5	0.01	0.04	0.02	5.2	12.5	16.7	4.4
	L 4076	1.2-1.8	1.5	0.03	11.9	0.01	0.05	0.02	5.3	11.9	20.0	4.9
	S 74-3	1.1-1.7	1.5	0.03	12.0	0.09	0.05	0.03	4.4	12.0	13.3	3.3
					Macromutational population							
Gamma rays:	LL	1.1-1.6	1.31	0.07	19.8	0.02	0.12**	0.06	8.4	19.8	17.6	7.0
	HH	1.0-1.7	1.33	0.09	22.1	0.01	0.16**	0.07	10.1	22.1	20.7	9.2
	Overall	1.0-1.7	1.32	0.07	20.3	0.01	0.13**	0.06	9.0	20.3	18.4	7.8
EI:	LL	1.1-1.7	1.32	0.07	20.0	0.02	0.13**	0.06	9.0	20.0	18.2	7.6
	HH	1.0-1.8	1.35	0.09	22.5	0.01	0.18**	0.07	10.7	22.5	22.3	10.4
	Overall	1.0-1.8	1.34	0.08	20.8	0.01	0.15**	0.06	9.7	20.8	20.4	8.8
NEU:	LL	1.1-1.8	1.35	0.07	20.2	0.02	0.14**	0.06	9.4	20.2	19.7	8.2
	HH	1.0-1.9	1.37	0.10	23.1	0.01	0.21**	0.07	11.5	23.1	26.2	12.5
	Overall	1.0-1.9	1.36	0.09	21.4	0.01	0.17**	0.07	10.7	21.4	23.5	10.4
					Selected population							
Gamma rays:	LL	1.2-1.7	1.33	0.03	13.9	0.01	0.05**	0.03	5.2	13.9	13.8	3.9
	HH	1.2-1.8	1.35	0.05	17.1	0.01	0.09**	0.04	7.0	17.1	17.0	6.0
	Overall	1.2-1.8	1.34	0.04	15.6	0.01	0.07**	0.04	6.2	15.6	15.9	4.9
EI:	LL	1.2-1.9	1.35	0.04	15.2	0.01	0.07**	0.04	5.7	15.2	14.3	4.5
	HH	1.2-2.0	1.40	0.06	17.9	0.01	0.11**	0.05	7.8	17.9	19.0	7.0
	Overall	1.2-2.0	1.37	0.05	16.8	0.01	0.09**	0.04	6.9	16.8	17.0	5.9
NEU:	LL	1.2-1.9	1.37	0.05	16.3	0.01	0.08**	0.04	6.5	16.3	16.0	5.4
	HH	1.3-2.1	1.46	0.07	18.5	0.01	0.13**	0.06	8.4	18.5	20.5	7.8
	Overall	1.2-2.1	1.42	0.06	17.5	0.01	0.11**	0.05	7.7	17.5	19.3	7.0
					Unselected population							
Gamma rays:	LL	1.1-1.5	1.26	0.06	19.4	0.005	0.10**	0.05	7.9	19.4	16.2	6.5
	HH	1.0-1.6	1.29	0.08	21.6	0.008	0.14**	0.06	9.8	21.6	18.8	8.4
	Overall	1.0-1.6	1.27	0.07	20.1	0.004	0.11**	0.05	8.3	20.1	17.6	7.3
EI:	LL	1.0-1.6	1.27	0.06	19.8	0.005	0.11**	0.05	8.2	19.8	17.5	7.1
	HH	1.1-1.7	1.30	0.08	21.9	0.008	0.15**	0.07	10.0	21.9	20.4	9.2
	Overall	1.0-1.7	1.29	0.07	20.5	0.005	0.12**	0.06	8.8	20.5	19.1	8.1
NEU:	LL	1.1-1.7	1.25	0.06	20.2	0.006	0.11**	0.05	8.8	20.2	18.6	7.8
	HH	1.0-1.8	1.28	0.08	22.6	0.010	0.17**	0.06	11.3	22.6	24.5	11.4
	Overall	1.0-1.8	1.26	0.07	21.0	0.050	0.13**	0.06	9.7	21.0	22.2	9.6

**= Significant at 1% level.

(0.05-0.14).

The study of the components of variation showed that both GCV (5.2-11.5%) and PCV (13.9-23.1%) increased in the treated populations over the control levels (GCV 5.2%, PCV 12.5%). Out of the three populations studied, macromutational populations showed higher GCV (8.4-11.5%) and PCV (19.8-23.1%) than the unselected (GCV 7.9-11.3%, PCV 19.4-22.6%) and selected (GCV 5.2-8.4%, PCV 13.9-18.5%) populations. A marked decline in GCV and PCV was noted when selection was applied in M_2 generation. Based on GCV and PCV, the mutagens were arranged in the order of NEU $>$ EI $>$ gamma-rays. Among the groups of mutagenic damage, HH showed higher GCV (7.0-11.5%) and PCV (17.1-23.1%) than LL group (GCV 5.2-9.4%, PCV 13.9-20.2%).

The heritability estimates increased from 16.7% in the control to 13.8-26.2% in the treated populations. Heritability further increased in M_3 to 19.3% from the M_2 level of 14.2%. Consequently, GA increased in all the mutagenized populations (4.5-12.5% of mean) except LL group of gamma-rays in selected populations where it was 3.9% as compared to 4.4% of the control. The maximum GA was recorded in the macromutational populations (7.0-12.5%), followed by unselected (6.5-11.4%) and selected (3.9-7.8%) populations.

3.1.7 100-seed weight (seed size)

A comparison of seed size in the treated and untreated populations (Table 41)showed that the range for this character increased in all the treated populations over the control. The 100-seed weight ranged between 0.8 and 4.8g in the treated populations as compared to 1.7-3.8g in the control . Selection for seed size in M_2 narrowed the range to 1.3-4.8g. The range in

M_3 was widest (0.8-4.8g) in the macromutational populations, followed by unselected (1.0-4.5g) and selected (1.3-4.8g) populations. The maximum expansion of range was caused by NEU (1.0-4.8g), followed by EI (1.1-4.8g) and gamma-rays (0.8-4.2g). Among the groups of mutagenic damage, HH showed a wider range (0.8-4.8g) than LL group (1.1-4.6g).

The population mean for seed size shifted in positive direction (higher seed weight) in all but two mutagenized populations (2.0-3.1g) where it was at par with that of the control (2.0g). As expected, the seed size increased maximum in the selected M_3 populations (2.3-3.1g). All three mutagens affected seed size differently, however, without significant differences among themselves. The mutagenic damage group HH had generally lower seed weight (2.0-2.6g) than the LL group (2.2-3.1g).

The variability in terms of variance, CV and SE (Table 41) increased in the treated populations, except in the selected populations where CV decreased drastically. The damage group LL of gamma-rays in selected population showed lower variance (0.26) than in the control (0.30). The estimates of variance ranged between 0.26-0.64 in different mutagenized populations, against 0.30 in the control. The increase in variance was greater in the macromutational populations (0.38-0.64) than in the unselected (0.32-0.38) and selected (0.26-0.35) populations. With the exception of LL group of mutagenic damage of gamma-rays (CV 26.2%), all macromutational populations showed higher CV (27.3-35.4%) than control (27.0%). The selected populations had lower CV (17.7-24.2%) than control, and so was the case with LL groups of mutagenic damage in unselected populations of all the three mutagens. In the macromutational and unselected populations, NEU was the most effective mutagen in increasing

Table 41 : Range, mean, variance, CV, SE, analysis of variance, components of variation, heritability and genetic advance for 100-seed weight in M_3 generation

Treatment		Range	Mean	Variance	CV	SE	Variance		GCV (%)	PCV (%)	Heritability (%)	GA % of mean
							Inter-family	Intra-family				
Control :	PS	1.7-3.8	2.0	0.3	27.0	0.03	0.5	0.3	10.2	27.0	14.3	8.0
	L 4076	1.6-3.7	2.1	0.3	26.6	0.03	0.5	0.2	11.9	26.6	20.0	11.0
	S 74-3	1.7-3.8	2.2	0.4	29.0	0.03	0.7	0.3	13.0	29.0	20.0	12.0
					Macromutational population							
Gamma rays:	LL	1.1-3.9	2.4	0.38	26.2	0.05	0.75**	0.29	12.9	26.2	24.1	13.1
	HH	0.8-4.0	2.3	0.52	31.6	0.03	1.14**	0.37	17.2	31.6	29.4	19.2
	Overall	0.8-4.0	2.3	0.47	29.8	0.03	0.96**	0.35	15.2	29.8	26.0	16.0
EI:	LL	1.4-4.4	2.7	0.54	27.3	0.05	1.07**	0.41	13.5	27.3	24.4	13.8
	HH	1.2-4.8	2.3	0.64	34.3	0.04	1.45**	0.44	19.3	34.3	31.5	22.3
	Overall	1.2-4.8	2.5	0.59	31.2	0.03	1.26**	0.42	16.6	31.2	28.3	18.2
NEU:	LL	1.2-4.6	2.3	0.44	28.5	0.04	0.87**	0.33	14.0	28.5	24.3	14.3
	HH	1.4-4.8	2.2	0.62	35.4	0.03	1.36**	0.44	19.3	35.4	29.7	21.7
	Overall	1.2-4.8	2.2	0.53	32.5	0.03	1.10**	0.39	16.9	32.5	26.8	17.9
					Selected population							
Gamma rays:	LL	1.7-4.2	2.5	0.26	20.1	0.03	0.47**	0.21	9.0	20.1	19.8	8.3
	HH	1.6-4.0	2.3	0.32	24.2	0.02	0.61**	0.25	11.5	24.2	22.4	11.2
	Overall	1.6-4.2	2.4	0.30	22.6	0.02	0.55**	0.24	10.3	22.6	20.5	9.6
EI:	LL	1.8-4.2	3.1	0.30	17.7	0.03	0.55**	0.24	8.0	17.7	20.7	7.5
	HH	1.5-4.8	2.5	0.34	23.3	0.02	0.68**	0.26	11.7	23.3	24.9	12.0
	Overall	1.5-4.8	2.8	0.32	20.2	0.02	0.61**	0.25	9.6	20.2	22.6	9.4
NEU:	LL	1.6-4.5	2.6	0.32	21.8	0.03	0.57**	0.26	9.6	21.8	19.3	8.7
	HH	1.3-4.8	2.6	0.35	22.8	0.02	0.69**	0.27	11.1	22.8	23.8	11.2
	Overall	1.3-4.8	2.6	0.33	22.2	0.02	0.62**	0.26	10.3	22.2	21.4	9.8
					Unselected population							
Gamma rays:	LL	1.1-3.8	2.3	0.32	24.6	0.01	0.61**	0.25	11.7	24.6	22.4	11.4
	HH	1.0-3.9	2.1	0.33	27.5	0.02	0.67**	0.25	13.9	27.5	25.3	14.4
	Overall	1.0-3.9	2.2	0.33	26.1	0.01	0.64**	0.25	12.6	26.1	23.4	12.6
EI :	LL	1.3-4.2	2.3	0.33	25.0	0.01	0.63**	0.26	12.0	25.0	23.0	11.8
	HH	1.1-4.4	2.0	0.36	30.0	0.02	0.73**	0.27	15.1	30.0	25.2	15.6
	Overall	1.1-4.4	2.1	0.34	27.8	0.01	0.68**	0.26	13.9	27.8	25.0	14.3
NEU:	LL	1.2-4.0	2.2	0.35	26.9	0.01	0.64**	0.28	12.2	26.9	20.7	11.5
	HH	1.0-4.5	2.0	0.38	30.8	0.02	0.75**	0.29	15.2	30.8	24.1	15.3
	Overall	1.0-4.5	2.1	0.36	28.6	0.01	0.68**	0.28	13.6	28.6	22.5	13.3

**= Significant at 1% level.

CV, followed by EI and gamma-rays, but in case of selected populations, the trend observed was gamma-rays $>$ NEU $>$ EI. The comparison of variance and CV in different populations showed that the mutagenic damage group HH (variance 0.32-0.64, CV 22.8-35.4%) was superior to LL (variance 0.26-0.54, CV 17.7-28.5%) in terms of magnitude of variability.

The analysis of variance for seed size (Table 41) showed that all the treated populations (except LL group of gamma-rays in selected populations) had significantly higher interfamily variance than the control. The range of interfamily variance in the treated populations was from 0.47-1.45 in comparison with 0.50 in the control. The magnitude of interfamily variance differed depending on the nature of population, mutagen used and groups of mutagenic damage. Among the populations compared, the macromutational populations showed maximum interfamily variance (0.75-1.45), followed by unselected (0.61 -0.75) and selected (0.47 0 0.69) populations. Based on the magnitude of interfamily variance induced in selected and unselected populations, the mutagens were arranged in the order of NEU $>$ EI $>$ gamma-rays, however in macromutational populations, the order was EI $>$ NEU $>$ gamma-rays. Among the two groups of mutagenic damage, HH showed higher magnitude of interfamily variance (0.61-1.45) for seed size than the LL group (0.47-1.07).

Among the components of variation, GCV was higher in all the macromutational populations (12.9-19.3%), followed by all the unselected (11.7-15.2%) populations, whereas in selected populations only the mutagenic damage group HH of all the mutagens showed higher GCV (11.1-11.7%) than control (10.2%). As a result of selection in M_2 generation, GCV decreased in M_3 (8.0-11.7%). The PCV also followed almost a similar pattern for different mutagenic populations. Although both GCV and

PCV were higher in the damage group HH than LL, they did not follow a definite trend with regard to the mutagens. The order of mutagens differed in different populations.

The heritability estimates were higher in various mutagenized populations (19.3-31.5%) than in the control (14.3%) population. The estimates of heritability were also higher in M_3 (24.1%) than in M_2 (20.9%) generation. The GA also increased (8.3-22.3% of mean) over control (8.0%), the only exception being LL group in selected populations of EI, where GA decreased to 7.5%. The GA was higher in the macromutational populations (13.1-22.3%) than in the unselected (11.4-15.6%) and selected (7.5-12.0%) populations. The order of mutagens differed in the various populations with regard to GA.

3.1.8 Seed yield per plant

The range for yield per plant (Table 42) increased in the mutagenized populations (0.1-3.0g) over the control (0.4-1.6g). The range for yield per plant narrowed to 0.3-3.0g as a result of selection applied in M_2 generation. Maximum increase in range was noticed in the macromutational population (0.1-3.0g), followed by unselected (0.2-3.0g) population. The order of mutagens with regard to range for yield per plant was NEU (0.2-3.0g) $>$ EI (0.1-2.9g) $>$ gamma-rays (0.2-2.6g). Among the groups of mutagenic damage, HH had a wider range than LL for grain yield/ plant (0.1-3.0 and 0.2-2.7g, respectively).

The mean yield per plant increased with all the mutagens. The increase in mean yield per plant was more pronounced (1.0-1.5g) when selection was practised in M_2 generation. Among the mutagens, NEU caused greater increase in mean yield in its treatments (range 0.8-1.5g)

than EI (0.7-1.4g) and gamma-rays (0.6-1.4g). The mutagenic damage group HH showed higher mean yield per plant (range 0.8- 1.5g) than LL group (0.6-1.3g).

The mutagenic treatments increased variance for plant productivity significantly in all the cases. The magnitude of increase was variable in various populations and mutagens. In the treated populations, estimates of variance ranged between 0.12-1.16 in comparison with 0.09 of control. The CV varied from 79.5 to 90.1% in the macromutational and unselected populations as compared to 48.4% in the control. The CV reduced drastically in M_3 (33.3-47.6%) as a result of selection in M_2 generation. The variance was maximum in the macromutational M_3 populations (0.34-1.16), followed by unselected (0.24-0.96) and selected (0.12-0.51) populations. The mutagens differed significantly in respect of induced variance, which were arranged in the following order on the basis of efficiency: NEU $>$ EI $>$ gamma-rays. The above order of mutagens also repeated for CV in the selected and unselected populations, but the order in the macromutational populations was EI $>$ NEU $>$ gamma-rays. Among the groups of mutagenic damage, HH showed greater variance (0.26-1.16) and higher CV (36.4-90.1%) than LL (variance 0.12-0.56, CV 33.3-83.3%).

Table 42 also shows the analysis of variance, components of variation and genetic parameters for seed yield/plant in M_3 generation. The interfamily difference for plant productivity was significant in each treatment. The interfamily variance varied from 0.21 to 2.79 in different mutagenized populations, as compared to 0.2 in the control. The inferfamily variance decreased drastically when selection for yield was applied in M_2 generation. The range of variance in these materials narrowed to 0.21-1.06.

Table 42: Range, mean, variance, CV, SE, analysis of variance, components of variation, heritability and genetic advance for yield per plant in M_3 generation

Treatment		Range	Mean	Variance	CV	SE	Variance		GCV (%)	PCV (%)	Heritability (%)	GA % of mean
							Inter-family	Intra-family				
Control:	PS	0.4-1.6	0.6	0.09	48.4	0.02	0.2	0.07	22.8	48.4	22.2	22.1
	L 4076	1.4-3.5	2.1	0.20	21.3	0.02	0.4	0.14	10.9	21.3	26.3	11.5
	S 74-3	1.6-3.0	2.1	0.10	16.3	0.02	0.2	0.10	8.2	16.3	25.0	8.4
					Macromutational population							
Gamma rays:	LL	0.2-1.8	0.7	0.34	83.3	0.04	0.66**	0.26	40.4	83.3	23.5	40.3
	HH	0.2-2.0	0.9	0.63	88.2	0.04	1.36**	0.45	47.4	88.2	28.8	52.4
	Overall	0.2-2.0	0.8	0.45	86.0	0.03	0.91**	0.34	43.5	86.0	25.5	45.2
EI:	LL	0.2-2.1	0.8	0.42	81.0	0.05	0.86**	0.31	41.3	81.0	25.9	43.3
	HH	0.1-2.4	0.9	0.67	89.9	0.04	1.54**	0.45	51.2	89.9	32.4	60.1
	Overall	0.1-2.4	0.8	0.54	87.5	0.03	1.17**	0.38	47.2	87.5	29.1	52.5
NEU:	LL	0.3-2.6	0.9	0.56	83.1	0.05	1.15**	0.41	42.6	83.1	26.2	44.9
	HH	0.2-3.0	1.2	1.16	89.8	0.04	2.79**	0.76	53.2	89.8	35.0	64.8
	Overall	0.2-3.0	1.0	0.76	86.6	0.03	1.71**	0.53	48.7	86.6	31.0	55.8
					Selected population							
Gamma rays :	LL	0.6-2.4	1.0	0.12	33.3	0.02	0.21**	0.10	14.3	33.3	17.9	12.5
	HH	0.6-2.6	1.4	0.26	36.4	0.02	0.51**	0.20	17.8	36.4	24.0	18.0
	Overall	0.5-2.6	1.2	0.17	34.4	0.01	0.31**	0.14	15.6	34.4	20.5	14.5
EI:	LL	0.6-2.3	1.1	0.16	36.4	0.02	0.29**	0.13	16.4	36.4	20.2	15.2
	HH	0.4-2.9	1.4	0.34	41.6	0.02	0.68**	0.26	20.9	41.6	25.1	21.5
	Overall	0.4-2.9	1.2	0.22	39.1	0.01	0.42**	0.17	18.4	39.1	22.0	17.7
NEU:	LL	0.4-2.7	1.3	0.30	42.1	0.03	0.56**	0.24	19.6	42.1	21.5	18.7
	HH	0.3-3.0	1.5	0.51	47.6	0.02	1.06**	0.37	24.7	47.6	26.8	26.3
	Overall	0.3-3.0	1.4	0.39	44.6	0.02	0.77**	0.30	21.9	44.6	24.0	22.1
					Unselected population							
Gamma rays:	LL	0.3-1.8	0.6	0.24	81.6	0.01	0.44**	0.19	38.0	81.6	21.5	36.3
	HH	0.3-1.9	0.8	0.48	86.6	0.02	1.00**	0.36	44.9	86.6	26.7	47.8
	Overall	0.3-1.9	0.7	0.35	84.5	0.01	0.69**	0.27	40.3	84.5	23.9	40.5
EI:	LL	0.3-2.0	0.7	0.31	79.5	0.01	0.61**	0.24	39.1	79.5	24.1	39.6
	HH	0.2-2.2	0.8	0.52	90.1	0.02	1.19**	0.37	50.8	90.1	31.1	58.3
	Overall	0.2-2.2	0.8	0.49	86.4	0.01	1.03**	0.36	45.2	86.4	27.2	48.6
NEU :	LL	0.4-2.3	0.8	0.44	82.9	0.02	0.92**	0.33	42.9	82.9	26.1	45.1
	HH	0.3-3.0	1.1	0.96	89.1	0.03	2.24**	0.65	51.2	89.1	32.7	60.3
	Overall	0.3-3.0	0.9	0.68	87.7	0.02	1.50**	0.48	48.0	87.7	29.8	54.0

**= Significant at 1% level.

The macromutational populations showed greater interfamily variance (0.66-2.79), followed by unselected (0.44-2.24) and selected (0.21-1.06) populations. The mutagens differed significantly with regard to the magnitude of interfamily variance. On the basis of efficiency of induced interfamily variance the mutagens were arranged in the following order: NEU $\succ$ EI $\succ$ gamma-rays. Higher interfamily variance was recorded in the mutagenic damage group HH (0.51-2.79) than LL (0.21-1.15).

Both the components of variation (GCV and PCV) were higher in the treated populations (macromutational and unselected) than in the control. Both GCV and PCV were higher in the macromutational populations (GCV 40.4-53.2%, PCV 81.0-89.9%) followed by unselected populations (GCV 38.0-51.2%, PCV 79.5-90.1%). Both GCV and PCV decreased drastically as a result of M_2 selection. The GCV ranged from 14.3 to 24.7% and PCV from 33.3 to 47.6% as against 22.8% GCV and 48.4% PCV in the control. On the basis of efficiency of GCV induced, the mutagens were arranged in the order of NEU $\succ$ EI $\succ$ gamma-rays. The GCV and PCV were also higher in the HH group of mutagenic damage (GCV 17.8-53.2%, PCV 36.4-90.1%) than in LL group (GCV 14.3-42.9%, 33.3-83.3%).

The estimates of heritability as well as GA increased in the macromutational as well as unselected populations compared with the control. Heritability and GA in selected populations in M_3 generation decreased drastically due to selection in M_2 generation. The heritability of plant productivity was highest in the macromutational populations (23.5-35.0%), followed by unselected (21.5-32.7%) and selected (17.9-26.8%) populations, as against 22.2% in the control. The magnitude of heritability in M_3 (25.9%) was higher than that in M_2 generation (20.8%). The GA for

yield per plant was highest in the macromutational populations (40.3-64.8% of mean), followed by unselected (36.3-60.3%) and selected population (12.5-26.3%). The heritability and GA were higher in HH group of mutagenic damage (heritability 24.0-35.0%, GA 18.0-64.8% of mean) than in LL group (heritability 17.9-26.2%, GA 12.5-45.1%).

3.2 Selection of promising families in M_3

The family mean was used as a criterion to identify promising progenies in M_3 generation, since intrafamily variance is expected to decline in M_3. The families were identified as promising for various characters by comparing their means with the highest character mean of the control. Therefore, in order to identify the families with significantly higher mean than the highest value of control at 1 or 5% level, the entire material was grown in augmented block design with three controls (untreated variety Precoz Selection (PS), L 4076 and S74-3). The analysis of variance in augmented block design for eight characters (Table 43) showed that the entries (M_3 families) differed signficantly among themselves in respect of mean for all the eight characters. The estimates of block effects and different SE and CD for these eight characters are presented in Appendices XXXIII and XXXIV. Tables 44 and 45 show the proportion(%) of promising families identified on the basis of superiority of their means for various characters. It can be seen that the maximum proportion of families (17.6%) over the entire experiment was identified as promising for pods/plant, followed by yield/plant (13.9%), pod clusters/plant (12.0%), branches/plant (8.6%), plant height (4.9%), days to maturity (3.9%), 100-seed weight (2.9%) and seeds per pod (2.7%). Thus, pods per plant showed maximum improvement among the eight characters studied, followed

Table 43 Analysis of variance in augmented block design for various characters in M_3 generation

Sum of Squares	DF	Mean sum of squares							
		Days to maturity	Plant height	Fruiting branches/ plant	Effective peduncles/ plant	Effective pods/plant	Seeds/ pod	100-seed weight	Yield / plant
Blocks	78	393.28	126.61	77.64	822.83	1948.41	0.13	6.02	4.05
Entries (Check+new entries)	3156	29.31**	16.52**	10.89**	107.08**	234.26**	0.02*	0.44**	0.37**
Check varieties	2	4564.38**	2736.12**	1339.37**	28584.06**	67103.34**	1.00**	0.94*	70.65**
New entries and check vs. new entries	3154	26.44**	14.79**	10.04**	89.01**	191.84**	0.02*	0.44**	0.32**
Intrablock error	156	11.60	6.90	7.3	66.14	140.50	0.01	0.20	0.23
	3390								

* Significant at 5% level

** Significant at 1% level

Table 44 Percentage of promising families for different characters in various treatments in M_3 generation

Treatment		Total families studied	Days to maturity	Plant height	Fruiting branches/ plant	Fruiting/ clusters/ plant	Pods/ plant	Seeds/ pod	100-seed weight	Yield/ plant	Families with multiple characters
Gamma rays											
	LL	600	1.2	1.0	2.5	5.2	7.3	0.3	0.3	5.7	7.5
	HH	483	6.0	6.8	11.4	16.4	24.6	3.9	4.6	20.3	28.6
	Overall	1083	3.3	3.6	6.5	10.2	15.1	1.9	2.2	12.2	16.9
EI											
	LL	552	1.4	2.2	4.2	5.8	9.2	1.1	1.1	6.7	10.1
	HH	514	5.2	7.8	12.8	17.5	26.1	4.3	4.5	20.4	30.7
	Overall	1066	3.3	4.9	8.3	11.4	17.4	2.6	2.7	13.3	20.1
NEU											
	LL	529	2.6	2.6	6.8	9.1	12.1	1.7	1.9	9.6	14.7
	HH	476	7.8	10.3	16.0	21.0	30.0	5.7	5.9	23.7	36.8
	Overall	1005	5.1	6.3	11.1	14.7	20.6	3.6	3.8	16.3	25.2
Total of the experiment		3154	3.9	4.9	8.6	12.0	17.6	2.7	2.9	13.9	20.6

Table 45 Percentage of promising families for different characters in various M_3 populations

Population	Total families studied	Days to maturity	Plant height	Fruiting branches/ plant	Fruiting clusters/ plant	Pods/ plant	Seeds/ pod	100-seed weight	Yield/ plant	Families with multiple characters
Macromutational	424	2.4	2.1	4.0	6.8	11.6	2.1	1.2	8.5	11.3
Selected	762	12.9	16.3	29.5	39.6	56.2	8.4	10.0	45.4	69.0
Unselected	1968	0.7	1.1	1.5	2.5	4.0	0.6	0.5	2.8	3.9
Total of the experiment	3154	3.9	4.9	8.6	12.0	17.6	2.7	2.9	13.9	20.6

by seed yield per plant. The remaining characters showed medium to low response to selection (Fig.7). The chemical mutagen NEU generated promising families with multiple characters with the highest frequency (25.2% of all M_3 families), followed by EI (20.1%) and gamma-rays (16.9%) (Fig.8). Different promising families with multiple characters were isolated involving combination of two or more than two different characters.

Among the three populations compared in M_3 (Table 45 and 47, Fig.9), the population subjected to selection in M_2 generation showed maximum frequency of promising families for the various characters (8.4% for seeds/pod to 56.2% for pods/plant) as well as promising families with multiple characters (69.0% of the selected families). Next in order were the macromutational populations (11.3% promising families with multiple characters) and unselected populations (3.9%). Out of the two groups of mutagenic damage compared (Fig. 10) HH had much higher frequency of promising families (28.6-36.8%) with multiple characters, than LL group (7.5-14.7%).

The analysis of the proportion of promising families with various combination of characters (Tables 46 and 47) shows that the proportion of promising families with multiple characters among the total promising families was highest in the NEU-treated populations (80.8%), followed by EI (79.0%) and gamma-rays (76.9%). Out of the two groups of mutagenic damage (Table 46), HH had much higher proportion (79.8-84.1%) of promising families with multiple characters than LL group (69.2-74.3%). The proportion of promising families with multiple characters to the total promising families was highest in the selected popualtion (85.4%), followed by macromutational (65.8%) and unselected (57.1%)

Table 46 Proportion of promising families for multiple characters in M_3 generation

Treatment		Total families studied	Total promising families		Families with various combinations of characters						Families with multiple characters	
			No.	%	1	2	3	4	5	6	No.	%
Gamma rays												
	LL	600	65	10.8	20	20	19	6	-	-	45	69.2
	HH	483	173	35.8	35	58	40	23	12	5	138	79.8
	Overall	1083	238	22.0	55	79	59	29	12	5	183	76.9
EI												
	LL	552	77	13.9	21	27	16	12	1	-	56	72.7
	HH	514	194	37.7	36	70	45	25	11	7	158	81.4
	Overall	1066	271	25.4	57	97	61	37	12	7	214	79.0
NEU												
	LL	529	105	19.8	27	36	24	15	3	-	78	74.3
	HH	476	208	43.7	33	73	52	23	16	11	175	84.1
	Overall	1005	313	31.1	60	109	76	38	19	11	253	80.8
Total of the experiment		3154	882	26.1	172	285	196	104	43	23	650	79.1

Table 47 Proportion of promising families for multiple characters in different M_3 populations

Population	Total families studied	Total promising families		Families with various combinations of characters						Families with multiple characters	
		No.	%	1	2	3	4	5	6	No.	%
Macromutational	424	73	17.2	25	19	16	11	2	–	48	65.8
Selected	762	616	80.8	90	228	158	80	37	23	526	85.4
Unselected	1968	133	6.8	57	37	22	13	4	–	76	57.1
Total of the experiment	3154	822	26.1	172	284	196	104	43	23	650	79.1

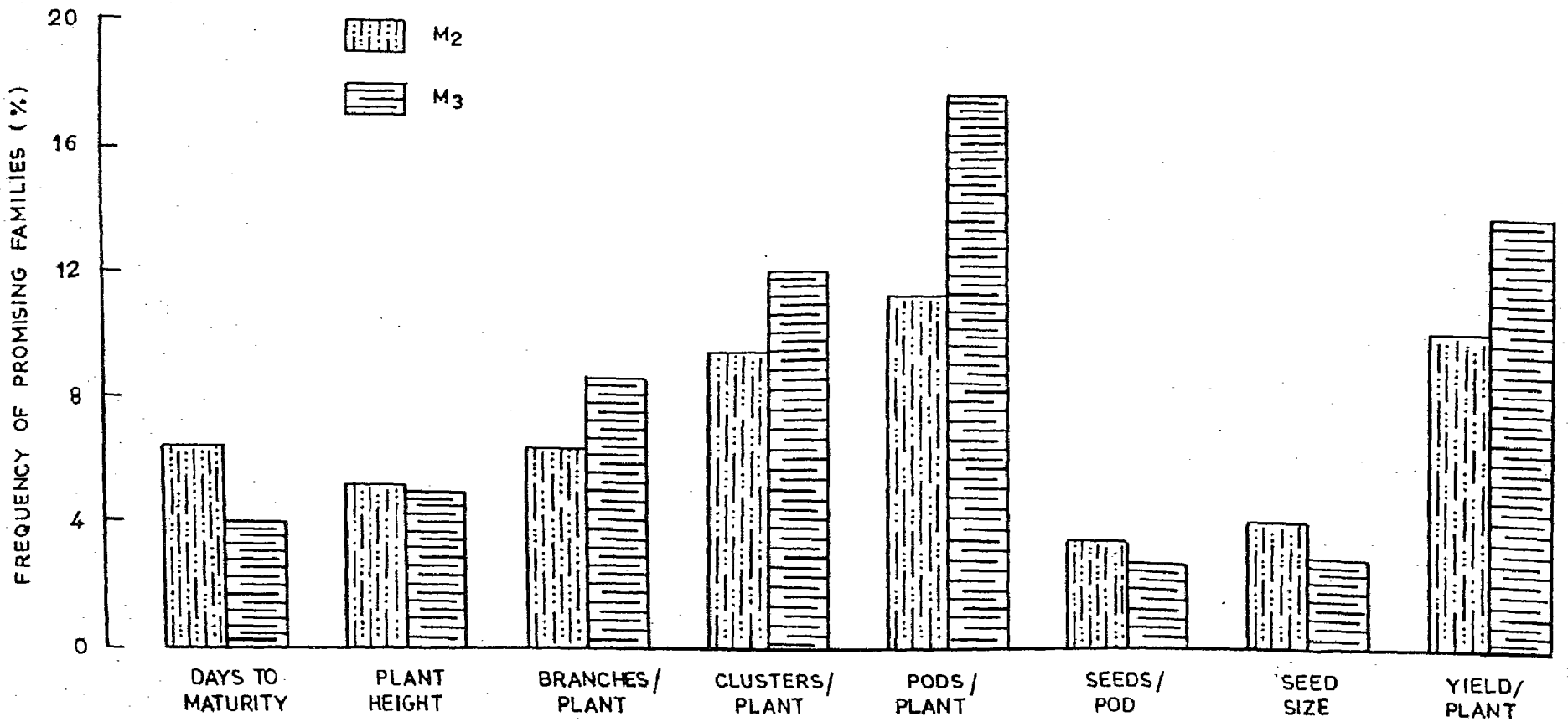


Fig.7. FREQUENCY OF PROMISING FAMILIES FOR DIFFERENT CHARACTERS IN M_2 AND M_3 GENERATIONS

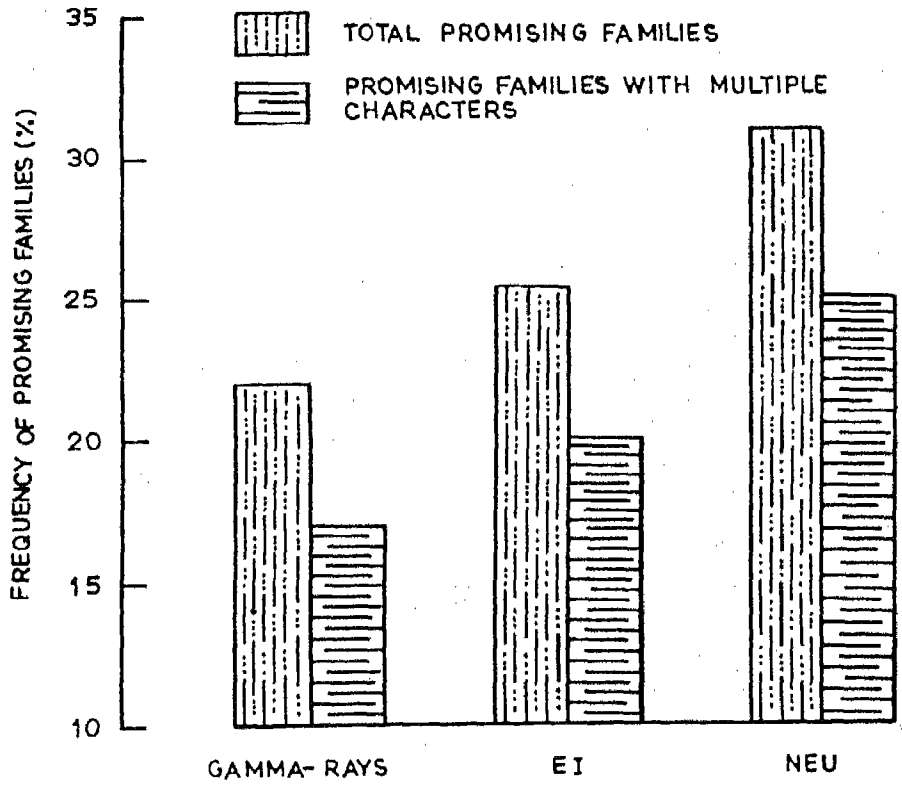


Fig.8. FREQUENCY OF PROMISING FAMILIES WITH DIFFERENT MUTAGENS IN M_3 GENERATION

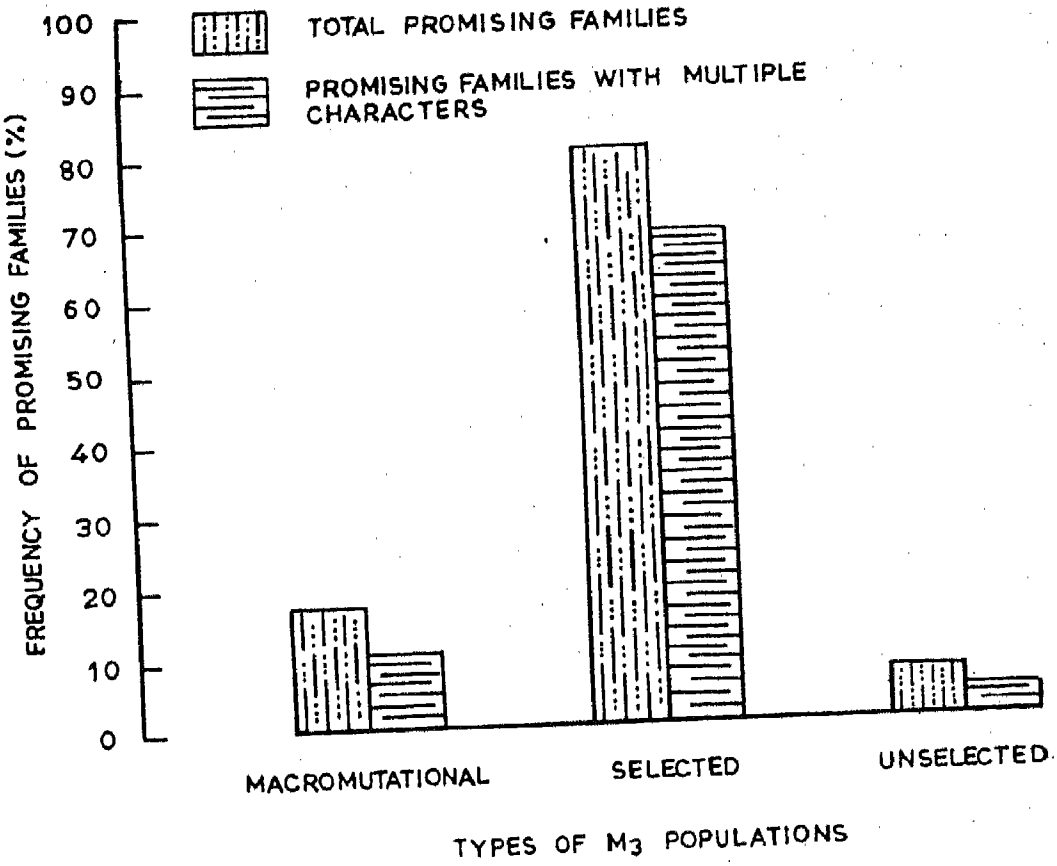


Fig. 9. FREQUENCY OF PROMISING FAMILIES IN DIFFERENT M_3 POPULATIONS

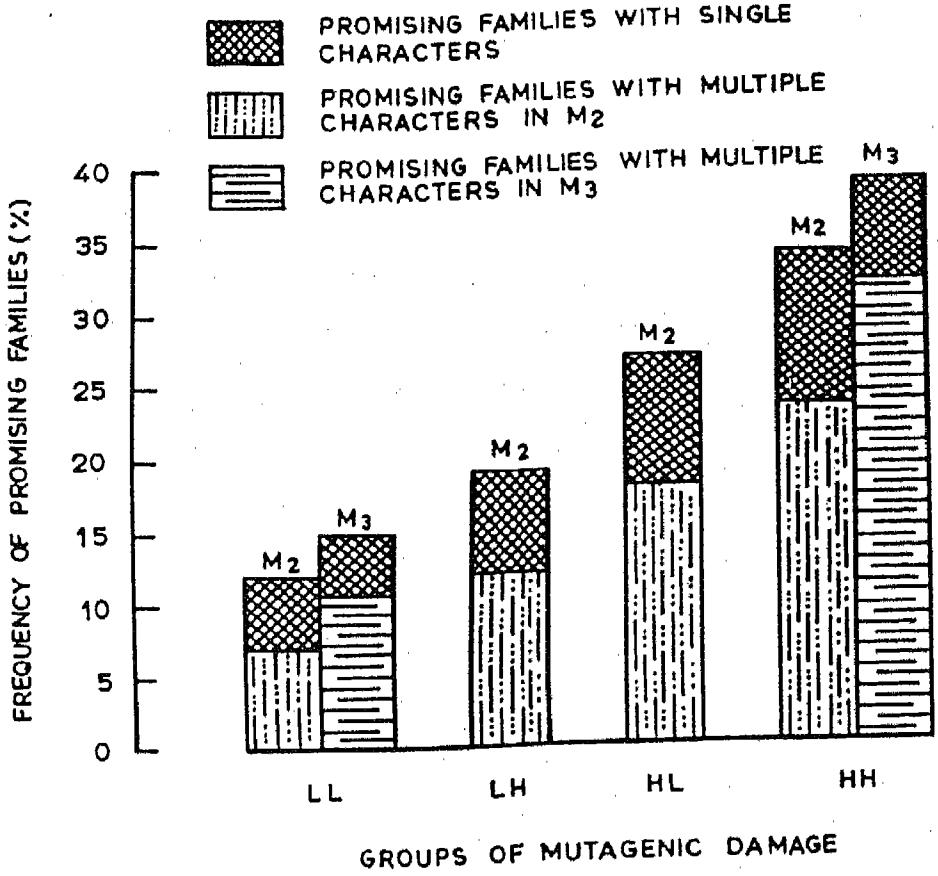


Fig. 10. FREQUENCY OF PROMISING FAMILIES WITH DIFFERENT GROUPS OF MUTAGENIC DAMAGE IN M_2 AND M_3 GENERATIONS

populations (Table 47).

A comparison of the selection efficiency for promising families in M_2 and M_3 generations (Table 48) shows that a very large proportion of plants selected in M_2 as promising were confirmed as promising families in M_3 also (from 73.7% in LL group of gamma-rays to 83.3% in HH group of NEU). The contribution of M_3 generation to the total number of promising families was smaller in the macromutational (14.3-20.0%) and unselected (3.5-12.5%) groups of mutagenized materials. Thus, selection for quantitative characters can be effectively practised in M_2 generation itself, although selection in M_2 did not exhaust the entire variability generated through mutagenic treatments, as 24.0 per cent of the total promising families were added in M_3 generation.

Similarly Table 49 shows a comparison of selection efficiency for promising families with multiple characters in M_2 and M_3 generations. It can be seen that a very large proportion of plants selected in M_2 as promising for multiple characters were confirmed as promising families with the same multiple characters in M_3 also (from 57.9% in LL group of gamma-rays to 75.3% in HH group of NEU). The M_3 generation added a smaller proportion to the total number of promising families for multiple characters in M_3: 8.6 - 12.7% in the macromutational and 1.8-7.3% in unselected populations. Thus, selection even for multiple quantitative characters can be practised in M_2 generation itself with reasonably high degree of reliability, although selection in M_2 did not exhaust the entire variability generated through mutagenic treatments, as 19.1% of the total promising families with multiple characters were added by M_3 screening (Table 50). NEU contributed maximum number of promising families with

Table 48 Selection efficiency for promising families in different populations in M_3 generation

Treatment	Macromutational population			Selected population			Unselected population		
	Total M_3 families	Promising M_3 families	% of families promising in M_3	Total M_3 families	Promising M_3 families	% of families promising in M_3	Total M_3 families	Promising M_3 families	% of families promising in M_3
Gamma rays									
LL	35	5	14.3	57	42	73.7	508	18	3.5
HH	85	14	16.5	168	135	80.4	230	24	10.4
Overall	120	19	15.8	225	177	78.7	738	42	5.7
EI									
LL	41	6	14.6	66	51	77.3	445	20	4.5
HH	102	18	17.6	180	149	82.8	232	27	11.6
Overall	143	24	16.8	246	200	81.3	677	47	6.9
NEU									
LL	51	8	15.7	93	74	79.6	385	23	6.0
HH	110	22	20.0	198	165	83.3	168	21	12.5
Overall	161	30	18.6	291	239	82.1	553	44	8.0

Table 49 Selection efficiency for promising families with multiple characters in M_3 generation

Treatment		Macromutational population			Selected population			Unselected population		
		Total M_3 families	Promising M_3 families	% of families promising in M_3	Total M_3 families	Promising M_3 families	% of families promising in M_3	Total M_3 families	Promising M_3 families	% of families promising in M_3
Gamma rays	LL	35	3	8.6	57	33	57.9	508	9	1.8
	HH	85	9	10.6	168	113	67.3	230	16	7.0
	Overall	120	12	10.0	225	146	64.9	738	25	3.4
EI										
	LL	41	4	9.8	66	42	63.6	445	10	2.3
	HH	102	12	11.8	180	129	71.7	232	17	7.3
	Overall	143	16	11.2	246	171	69.5	677	27	4.0
NEU										
	LL	51	6	11.8	93	60	64.5	385	12	3.1
	HH	110	14	12.7	198	149	75.3	168	12	7.1
	Overall	161	20	12.4	291	209	71.8	553	24	4.3
Total of the experiment		424	48	11.3	762	526	69.0	1968	76	3.9

Table 50. Contribution of M_2 and M_3 generations to the total promising M_3 selections for multiple characters

Treatment		Promising families in M_3 generation						
		Total	Macromutational		Non-macromutational			
					Selected		Unselected	
			No.	%	No.	%	No.	%
Gamma rays								
	LL	45	3	6.7	33	73.3	9	20.0
	HH	138	9	6.5	113	81.9	16	11.6
	Overall	183	12	6.6	146	79.8	25	13.7
EI								
	LL	56	4	7.1	42	75.0	10	17.9
	HH	158	12	7.6	129	81.6	17	10.8
	Overall	214	16	7.5	171	79.9	27	12.6
NEU								
	LL	78	6	7.7	60	76.9	12	15.4
	HH	175	14	8.0	149	85.1	12	6.9
	Overall	253	20	7.9	209	82.6	24	9.5
Total of the experiment		650	48	7.4	526	80.9	76	11.7

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higher magnitude of heritability than M_2 for all the eight characters. The estimates of genetic advance either increased or remained unchanged in M_3 over M_2 depending on the nature of a character, population, mutagen and group of mutagenic damage. The GA was expected to be higher in the macromutational populations than in the unselected and selected populations. The groups of mutagenic damage were in the order of HH $>$ LL with regard to the magnitude of GA. The above trends for the mutagens, groups of mutagenic damage, various type of populations and characters were confirmed by the proportion of promising families isolated in M_2 and M_3 generations.

many factors, internal as well as external, that influence the frequency of induced mutations. All these factors interact in determining the efficiency of a particular treatment in induced mutagenesis. The results obtained in Pisum (Blixt et al., 1963) indicate that the initial mutation rate is perhaps not appreciably altered. The main impact of the modifying factors, genetic as well as environmental, is through the various stages between the initial mutational event and the realization of the mutation in the next generation. Therefore, the number of mutations recovered in M_2 is often as (or even more) closely related to the factors like M_1 lethality and sterility as to the dose administered. Reproducible results with respect to the mutation rate in M_1 are, therefore, often easier to obtain using the total M_1 damage as an integrated system of biological effect. In a series of experiments, similar M_1 effects resulted in similar mutation rates in M_2, although the dose applied to induce a particular M_1 effect and M_2 mutation rate varied in wide limits. The same is true for chemical treatments. The variation here tends to be even greater for different mutagens (Blixt, 1972).

The early record of the phenomenon of leaf-aberrations, subsequently called a-sectors, can be found in the paper of Arntzen and Krebs (1925). The phenomenon was confirmed in leguminous crops by Burn (1954) and Kaplan (1954). It was demonstrated to be dose-dependent and directly related with chromosomal aberrations. The phenomenon has attracted special attention since it makes possible the estimation of mutagenic effects that may be more closely related to gene mutations than determination of growth reduction or plant lethality (Burns, 1954; Kaplan, 1954; Blixt et al., 1960, 1964, 1965; Zachrias and Ehrenberg, 1962). The importance of leaf-aberrations

in experimental mutagenesis increased since a close relationship between leaf spotting in M_1 and chlorophyll mutations in M_2 was demonstrated by Blixt et al. (1964) and Singh (1988). Some chlorophyll mutations scored in M_2 could be caused by a mechanism similar to the cause of leaf spots and streaks appearing in M_1 generation (Moutschen-Dahmen et al., 1959). Therefore, keeping in view the importance of leaf-aberration as a criterion for concentrating mutations in the mutagenized population, the M_1 material was classified into categories of high damage and low damage. Blixt (1972) also indicated that selection of M_1 plants in legumes, in general, and in peas in particular,with appropriate degree of leaf-aberrations makes it possible to maintain a high mutation rate which can be regulated almost at will for a potent agent like ethyl methane sulphonate (EMS). The efficiency of mutagenic agents can be manipulated not only by changing the conditions before, during, or after treatment, but also by identifying the M_1 plants most likely to carry mutations.

Different systems can be evolved for measuring these immediate M_1 effects on the basis of various characters used as indicators of mutagenic damage. Since these effects are utilized to determine the mutagenic effect of an agent as an indication of mutation frequency, i.e. the initial effect on DNA, the various M_1 parameters differ in their informational value. Leaf and chromosomal abberrations and sterility parameters are probably most accurate in this respect, whilst the characters reflecting general metabolic disturbances due to the treatment, such as, germination and growth inhibition are least important (Blixt, 1972). Therefore, plant sterility (seed setting) was used as the other criterion for grouping M_1

material. Singh (1988) also used sterility as a parameter for grouping M_1 material in peas; the other parameter taken for this purpose was leaf-aberrations (a-sectors) on seedlings, and classified the M_1 material in four groups of mutagenic damage, viz., LL, LH, HL and HH. The effect on M_1 fertility was studied following treatment with x-rays and neutrons (Heringa, 1964), gamma-rays (Heringa, 1964) and EMS (Heringa, 1964; Speckman, 1964; Wellensiek, 1965). In case of chemicals, sterility has been found to be caused by factors other than chromosomal aberrations also (Wildervanck, 1964). Positive correlations between sterility and mutation rate have been reported from several studies (Kivi, 1965; Ehrenberg, et al., 1961; Walther, 1970; Singh et al., 1972).

In the present study, the highest frequency of chlrophyll and morphological mutations has been recorded in the HH group (14.3 and 1.37% mutated M_2 progenies and plants, respectively) and lowest in LL group (6.0 and 0.58%) with all the mutagens and doses (Table 13, Appendix X, Fig. 3). Among the remaining two intermediate groups, the HL group (11.4 and 1.07%) was superior to LH group (8.7 and 0.83%) with regard to the induction of total mutations. Similar results were obtained by Singh (1988) in peas, where the order of groups with regard to the induction of macromutations in M_2 generation was HH $>$ HL $>$ LH $>$ LL. This indicates that seedling damage (leaf aberrations) is a better measure of the genetic change induced by mutagenic treatments than seed fertility. Likewise, Blixt (1972) found leaf-aberrations to be the most dependable index among all the M_1 parameters. As in the present investigation , Blixt et al.(1964) and Singh (1988) also found positive correlation between

the degree of leaf-aberrations in M_1 and chlorophyll mutation rate in M_2 generation. With regard to the sterility in M_1 also, several reports can be cited in support of the results of the present study (Kivi, 1965; Ehrenberg, et al., 1961; Walther, 1970; Singh et al., 1972; Singh, 1988). These studies showed positive correlation between sterility level in M_1 and frequency of chlorophyll and morphological mutations in M_2 generations. The highest chlorophyll and morphological mutation frequency was recorded in the fertility range of 30-70% which is in close agreement with the results of the present investigation. From the results of the present investigation, it can be concluded that higher the damage caused to M_1 plants in the form of leaf-aberrations and seed sterility by particular doses of different mutagens (in this case, e.g. 20 kR of gamma-rays and 0.1% of both the chemical mutagens, EI and NEU), the higher the frequency of mutations obtained in M_2 generation. As discussed below, the same groups of mutagenic damage also carry higher frequency of micromutations for different characters in succeeding generations.

In general, the mutation spectrum was not influenced by the groups of M_1 damage, except that some of the mutation types occurred more frequently than others in certain groups (quantitative differences only). This may be due to a relatively high frequency of mutation induction in that particular group. The independence of chlorophyll mutation spectrum from the degree of sterility in M_1 generation has been reported earlier (Gaul, 1958; 1965b; Singh, 1988). Similarly, the degree of leaf aberrations and mutation spectrum were also found to be independent of each other in peas (Singh, 1988).

2.1.4 Mutagenic effectiveness and efficiency

In general, both mutagenic effectiveness and efficiency decreased with increasing doses of mutagens, however, the highest dose of gamma-rays and medium doses of chemicals were found to be most efficient for inducing mutations (Fig.5). This obviously shows that the increase in mutation rate was not proportional to the increase in the doses of various chemical mutagens. The higher mutagenic effectiveness does not reflect per se mutation frequency and hence cannot be used as an index for maximization of mutation rates (Sharma, 1977; Singh, 1988). There are several biological, environmental and chemical factors which modify and influence the response of cells in higher plants to physical and chemical mutagens, consequently, mutagenic effectiveness and efficiency also change (Blixt, 1972). The exact nature and mechanism of the factors influencing mutation frequency vis-a-vis the biological damage caused by a given radiation or chemical mutagen are not known.

The mutagenic effectiveness and efficiency have been discussed separately as follows.

2.1.4.1 Mutagenic effectiveness

Effectiveness pertains to the rate of mutation induction in relation to mutagenic dose. Extensive studies on mutagenic effectiveness and efficiency of various mutagens were carried out by Konzak et al. (1965). In the present investigation, effectiveness of mutagens differed considerably (Table 15). Among the mutagens used, NEU was the most effecitve mutagen, followed by EI and gamma-rays. Thus, NEU was 1.2 and 241 times more effective than EI and gamma-rays, respectively. The

order of effectiveness of mutagens was NEU > EI > gamma-rays. Higher mutagenic effectiveness of NEU and NMU (both nitroso compounds) over other chemical mutagens and ionizing radiations has been demonstrated earlier in lentil (Sharma, 1977; Sarker, 1985), rice (Siddiq, 1967), wheat (Desai and Bhatia, 1975), greengram (Prasad, 1972), Lathyrus (Nerkar, 1977) and peas (Monti, 1968; Mohan, 1983; Singh, 1988).

2.1.4.2 **Mutagenic efficiency**

Mutagenic efficiency is referred to as the mutation rate in relation to M_1 damage. Effectiveness and efficiency are two different properties of mutagens. A highly effective mutagen may not necessarily show high efficiency and vice versa. The results presented in Table 15 indicate that mutagenic efficiency is not as variable as mutagenic effectiveness among the mutagens used. This is an interesting observation. It would be desirable to compare these two parameters whenever recorded in other experiments. The mutagenic effectiveness being more variable could be a direct reflection of differential mutagenicity per unit dose of various mutagens. The low variability for efficiency can be interpreted by assuming that the extent of damage in M_1 determines the mutability of genes, irrespective of the mutagen. In other words, with equal degree of damage, all mutagens and their doses will yield more or less comparable amount of mutation. However, the trend was similar among the mutagens. Similar to mutagenic effectiveness, NEU showed the highest efficiency (0.38), followed by EI (0.33) and gamma-rays (0.31). Thus, NEU was 1.2 and 1.1 times as much efficient as gamma-rays and EI, respectively. Higher efficiency of nitroso-compounds than other mutagens has been reported

in wheat (Desai and Bhatia, 1975), lentil (Sharma and Sharma, 1979b; Sarker, 1985; Dixit and Dubey, 1986; Sarker and Sharma, 1989) and peas (Mohan, 1983; Singh, 1988). However, Nerkar (1977) reported contradictory results. In his study, the order of mutagens based on their efficiency was gamma-rays $>$ EMS $>$ NMU. The higher efficiency of a mutagen indicates relatively less biological damage (seedling injury, lethality or sterility, etc.) leading to more mutations. In this study, higher efficiency of NEU indicates relatively more mutations induced even with less biological damage (sterility), whereas the reverse was true for gamma-rays. The low efficiency of gamma-rays may be attributed to the use of low doses corresponding to their mutation induction (Sarker 1985), whereas in case of NEU the choice of doses used was more appropriate (Singh, 1988).

2.2 Micromutations

The best example of breeding for micromutations is the extensive and detailed work of Gregory (1956, 1961,1967) in groundnut and Gaul et al. (1969) in barley. They demonstrated substantial improvement in yield following selection in irradiated populations.

In view of the importance of induced micromutations in improving the polygenically controlled characters of economic importance, an attempt was made to explore the possibility of increasing the efficiency of induction of micromutations of breeding value. The results related to different aspects of induced polygenic variability are discussed generation wise for various characters.

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in the mutagenized populations in M_3 generation as compared with M_2 generation (18.4-27.8% heritability and 20.8-36.8% of mean GA). A higher GA in M_3 over M_2 was also reported by Sharma (1977) and Sarker (1985) in lentil, and Goud (1967) in wheat. Similar trend has been observed in the present study. Genotypic variance, heritability and GA were reported to increase as a result of mutagenic treatment in rice (Jana and Roy. 1973), Brassica Juncea (Verma, 1973; Mahla, 1988), groundnut (Sarma, 1975), ragi (Raveendran et al., 1982), mungbean (Khan, 1984) and lentil (Sarker, 1985). The substantial increase in the estimates of heritability and GA in M_3 over M_2 as a result of release of additional variability in M_3 generation suggests that although selection in M_3 could be more advantageous than in M_2 generation, it could also be practised effectively in M_2 generation with reasonable success. This is evident from the proportion of promising families obtained for this character increasing from 6.8% in M_2 to 8.6% in M_3 generation.

2.2.1.4 **Number of clusters per plant**

The number of clusters per plant increased slightly in the treated populations over control in both M_2 and M_3 generations (Table 22 and 38, Appendix XVI). The increase in mean number of clusters per plant in the treated populations has been repeatedly reported by various workers (Krishnaswamy et al., 1977; Sharma and Haque, 1983; Verma and Singh, 1984; Bhadra, 1982) and can be explained on the basis of induction of more positive mutations. Sarker (1985) reported increase in mean in two of the treatments in lentil. However, contrary to these findings, lower or unaltered means in the treated populations were also reported by several

workers (Gaul, 1965; Goud,1967; Mandal, 1974; Gill et al, 1974; Sarker, 1985). This is attributed to the induction of lower or equal number of mutations that increase the number of clusters.

The range for clusters per plant increased in the treated populations over control in M_2, which further increased slightly in M_3 generation. The increase in variance and CV was also significant in the treated populations over control in both M_2 and M_3 generations. However, the magnitude of increase was slightly higher in M_3 than in M_2 generation. Thus, additional variability was released in M_3 generation for this character. These results are in agreement with the findings of several previous workers (Bhadra, 1982; Sharma and Haque, 1983; Verma and Singh, 1984).

Both components of variation, viz., PCV and GCV increased in the treated populations than in the control in M_2 as well as M_3 generations (Tables 23 and 38). A relatively higher correspondence between GCV and PCV resulted in higher heritability for this character. Thus, a considerable proportion of the induced variability is genetic which also enhanced genetic advance over the control in both M_2 and M_3 generations. The considerable increase in heritability and GA indicates that there is a tremendous scope for improvement of clusters per plant. The increase in genotypic variability, heritability and GA for clusters per plant as a result of induced mutations has been reported in many crops (Bhadra, 1982; Sharma and Haque, 1983; Verma and Singh, 1984). Higher GA in M_3 over M_2 suggests that selection for clusters per plant in M_3 is expected to give better dividends than in M_2. However, selection in M_2 can also be affected with almost equal success as large amount of variability (CV) is expressed in M_2 itself, 73.4% as against 73.9% in M_3. The proportion of promising families in

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with a reasonable success. Although the success in terms of isolation of promising families through selection in M_2 generation (11.4%) is reasonably good, it can be enhanced to almost 1.5 times for this character (to 17.6% promising families) if extensive selection is carried out a generation later (in M_3).

2.2.1.6 **Number of seeds per pod**

The range as well as population mean for seeds/pod increased in M_2 and M_3 generations compared to the controls (Tables 26 and 40, Appendix XVIII). Increase in mean seed setting in the treated populations has been reported from studies in various crop plants (Shakoor and Haq, 1980; Mohan, 1983; Sarker, 1985; Singh, 1988; Sarker and Sharma, 1989). The increase in seed settings in the mutagenized populations again, can be explained on the basis of induction of more positive mutations, as was the case with number of pods per plant. However, contrary to these findings, lower or unaltered means in the treated populations were reported by Pathirana (1982) in groundnut; Rajput and Siddiqui (1983) in soybean, and Verma and Singh (1984) in mungbean. The reduction in average seed number could be only due to induction of mutations causing sterility more frequently in the treated populations.

The estimates of induced variability, calculated as variance and CV, were higher in both M_2 and M_3 generations as compared to controls. The comparison of variability (CV) for different characters revealed that seed no./pod had relatively lower variability (19.9% CV in M_2 and 20.5% CV in M_3) than most other characters except days to maturity where CV observed was the lowest, 2.4% in M_2 and 5.6% in M_3 (Table 52).

The GCV and PCV also increased in the treated populations over control in both M_2 (6.3-8.5% GCV, 18.5-20.6% PCV) and M_3 (5.2-11.5% GCV) generations. This resulted in higher heritability and GA in the mutagenized populations. It can be seen that a considerable proportion of induced variability was genetic in nature, which increased heritability and genetic advance over control in both generations. Similar observations were reported earlier (Mandal, 1974; Tickoo and Jain, 1980; Pathirana, 1982; Ravi et al., 1980; Mohan, 1983; Sarker, 1985; Singh, 1988; Sarker and Sharma, 1989). However, Verma and Singh (1984) noticed lower variance for this character. It is difficult to explain why mutagenic treatments should reduce the variance. The estimates of both components of variation, GCV and PCV, were relatively higher in M_3 than in M_2 generation, indicating release of small amount of additional variability in M_3 generation. The values of heritability (13.8-26.2%) as well as GA (3.9-12.5% of mean) were little higher in M_3 than M_2 generation (10.5-17.7% heritability and 4.4-7.4% of mean GA). The release of additional variability in M_3 was most probably responsible for greater heritability and GA over M_2 generation. The magnitude of induced variability (CV) in M_3 generation (20.5%) was a little higher than in M_2 generation (19.9%). Simultaneously, the proportion of promising families isolated dropped from 3.6% in M_2 to 2.7% in M_3. Therefore, it is reasonable to suggest that selection for seeds/pod should be preferably excercised only in M_2, advancing the material to one more generation (M_3) will not result in any substantial advantage through selection.

2.2.2 Specificity of parameters

In the present investigation, certain specific patterns were observed which were constantly maintained throughout the experiment. The specificity of such patterns is discussed.

2.2.2.1 Mutagen specificity

An attempt has been made to know the relative effect of different mutagens on mean and magnitude of induced variability for polygenic characters. In general, it was found that all the mutagens are not equally effective in inducing variability for polygenic traits. Among the mutagens used, the chemicals induced more variability than radiations for all the eight quantitative characters in the order: seed yield per plant $>$ pods per plant $>$ clusters per plant $>$ branches per plant $>$ 100-seed weight (seed size) $>$ seeds per pod $>$ plant height $>$ days to maturity (Table 51). However, differences among the mutagens were more pronounced for seed yield per plant. Superiority of alkylating agents over radiations, in general, in inducing mutations in all kinds of genes is now an established fact. This is also true for polygenic variability in higher plants (Mohan, 1983; Sarker, 1985; Singh, 1988; Sarker and Sharma, 1989). Thus, the present study has yielded expected results, as both the chemical mutagens (NEU and EI) belong to the highly effective group of alkylating compounds and are known to induce point mutations in the biological systems with very high frequency. On the other hand, ionizing radiations (gamma-rays) act primarily through induction of chromosomal aberrations, therefore, induce point mutations with lower frequency than chemicals.

In general, the character means shifted in desirable directions with

all the three mutagens. However, the mutagens showed differences among themselves with regard to shift in character means. The mean values in the NEU-treated material were higher than in the EI and gamma-ray treatments. This indicates that NEU induces higher frequency of mutations with positive effects than EI and gamma-rays. The increase in progeny mean for a number of characters following mutagenic treatments have been reported in lentil (Sharma, 1977), rice (Matsuo and Onozawa, 1961) and peas (Mohan, 1983; Singh, 1988) . Rajput (1974) recorded shift in mean towards positive direction in all the characters (except pod length) in mungbeans. Sidorova (1971) reported higher proportion of economically important mutants following EMS treatments than NEU in peas, and also found that early mutants appeared more frequenctly after gamma-ray treatment and mutants with higher pod number after EMS treatment. Similar to the results of the present study, Akhund-Zade (1979) and Singh (1988) reported superiority of nitroso compounds with respect to shift in mean and enhancement of induced variation for all the quantitative characters studied. The order of mutagens with regard to shift in mean and enhancement of induced variability for all the eight characters, in both M_2 and M_3 generations was NEU $>$ EI $>$ gamma-rays (Table 51, Fig. 6 and 8).

2.2.2.2. **Dose dependence**

Another distinct feature of this investigation was the dose-dependent increase in the magnitude of polygenic variability. The dosage effects within a mutagen were conspicuous with respect to mean and coefficient of variability. As discussed earlier, the highest dose of gamma-

rays (20 kR) and the medium dose of chemicals (0.01%) induced maximum variability for almost all the eight polygenic traits in M_2 generation. The lowest dose of gamma-rays (5 kR) generated smallest amount of variability than the medium dose (10 kR). In the case of chemicals, the highest dose (0.02%) induced higher or almost the same magnitude of variability as the lowest dose (0.005%) but it was always less than their medium doses. Interestingly, the highest dose of gamma-rays and medium doses of both chemicals, which induced maximum variability, are biologically comparable (Table 7). Thus, these doses of various mutagens can be treated as most optimum for induction of polygenic mutations in lentil. This conclusion is also supported by the frequency of macromutations in M_2 generation. As can be seen from Table 12, the highest frequency of macromutations (chlorophyll and morphological) was induced at the highest dose (20 kR) of gamma-rays (9.6 and 0.88% M_2 mutated progenies and plants, respectively) and medium doses (0.01%) of the chemical mutagens, NEU (13.3% and 1.54%) and EI (11.6% and 1.11%). This differential dose response of different mutagens for frequency of mutations is understandable, as radiations predominantly act through induction of chromosomal aberrations. The variation in dose-dependent increase in mutations induced by mutagens of both categories can also be explained by assuming that the gamma-ray doses in the present study are not strong enough to reach a saturation point beyond which mutation rate begins to decline. It appears that the stronger mutagens, EI and NEU in this study, reached their saturation point at their medium dose and further increase in dose did not enhance the mutation frequency.

It was also observed that the medium dose of strong mutagens (0.01% EI and NEU) and higher dose of the relatively weaker mutagen (20 kR gamma-rays) are comparable in their effectiveness. Srivastava et al (1973), Hussein et al. (1974) and Singh (1988) also demonstrated that higher doses of the strong mutagens are more toxic than the higher dose of relatively weaker mutagens. According to Vo Hung (1974), the highest dose is not always the most effective one.

It is thus clear that high doses cannot always be used for maximization of mutation rates. The response of plant cells to physical and chemical mutagens is influenced by several biological, environmental and chemical factors. These factors ultimately determine the effectiveness (mutations per unit dose) and efficiency (ratio of mutations to damage) of mutagens. The exact nature and mechanism of the factors influencing mutation frequency vis-a-vis biological damage caused by a given radiation or chemical mutagen are not known.

Scossiroli (1977) found, as noticed in the present investigation, that polygenic variability increases with radiation dose but the relationship between variance and dose is not linear. It has been generally observed that when a wide range of doses is used, the intermediate dose causes maximum variation and there is a marked decline in mutation rate with further increase in dose. The linear relationship may be disturbed by elimination of mutations through gametic or zygotic selections, thereby reducing the potential genetic variability initially induced. In rice, Oka et al. (1958) assuming a proportional increase of variance with radiation dose, estimated on increase of 0.0153 units of genetic variance per 1000 R

generated by the mutagenic treatment starts manifesting in M_2 itself, which is the first segregating generation. Further segregation for the polygenic systems in M_3 is expressed as "release of additional variability". This being the mechanism of induction and inheritance of micromutations, selection in M_2 can certainly help in identifying progenies that are likely to show more variability and better response to selection, and simultaneously reduce the volume of unwanted material by rejecting " roughage" (an expression used by Sharma, 1986).

2.2.2.5 **Difference in character response**

All the eight polygenic characters studied in the present investigation did not respond in identical manner to mutagenic treatments (Table 51, Fig. 7). Among the characters studied, seed yield showed maximum induced variation (CV 83.8-86.1% in M_2 and 84.5-87.7% in M_3), followed by pods per plant (CV 73.6-76.1% in M_2 and 74.1-77.0% in M_3), clusters per plant (CV 72.1-74.7% in M_2 and 72.6-75.3% in M_3) and branches per plant (CV 55.7-63.3% in M_2 and 64.2-65.4% in M_3). The remaining four characters showed less mutability. Therefore, the four major traits of economic importance , viz., pods, yield, clusters and branches are highly amenable to mutagenic manipulation. Interestingly, these four traits showed induced variability to be more in positive direction, as can be seen from the shift of population means. These results are in agreement with those reported from many earlier studies (Mandal, 1974; Rao, 1974; Rajput, 1974; NaLampang and Janon, 1982; Bhadra, 1982; Mohan, 1983; Singh, 1988). It is interesting to note that the economically most important characters gave maximum response to mutagenic treatments. They are

not only highly mutable but also showed increased variability in positive directions, which can be exploited through effective selection.

The other interesting feature of this investigation was that, despite similar pattern of variability in M_2 and M_3 for all the eight traits, they were not identical in the expression of change (Table 51 and 53). The increase in variability (CV) due to generation advancement was very small in case of fruiting clusters (73.4% in M_2 and 73.9% in M_3), seed yield per plant (84.6% and 86.2%), pods per plant (74.8% and 75.4%) and seeds per pod (19.9% and 20.5%). However, it was significantly higher for the remaining four characters viz., days to maturity (CV 2.4% in M_2 and 5.6% in M_3), plant height (16.4% and 19.2%), seed size (24.7% and 27.5%) and branches per plant (59.8% and 64.7%). In contrast, Singh (1988) reported negligible increase in variance due to generation advancement in case of days to flowering and seed size in peas. The paucity of reports indicates that such differential behaviour of different characters has not been exploited/reported earlier. It remains to be decided whether character-to-character differences can be attributed to the intra-populational structure or previous selection history of different varieties (Sharma, 1986). Such a possibility, however, cannot explain the present situation because the untreated material of the same variety did not show a regular increase in variance with advancing generation.

Even though it cannot be readily explained why some characters should reveal greater variability in latter generations than others, these results clearly demonstrate that some characters have a tendency to stabilize sooner than others. This may be partly related with the number of polygenes controlling them. From the present discussion, it can be agreed

that selection for some characters (fruiting clusters and pods per plant, seeds per pod and seed yield per plant) could be confined to M_2 alone, as much advantage is not expected by further selection in latter generations. There is not much increase in GA in M_3 than M_2 generation for these characters, viz. pods per plant (23.8-66.3% of mean in M_3 and 29.4-50.0% of mean in M_2), clusters per plant (27.2-86.2% and 28.0-44.8%), seeds per pod (3.9%-12.5% and 4.4-7.4%) and seed yield per plant (12.8-64.8% and 30.2-46.6%). Although these characters, as is believed, are governed by a large number of genes, their stabilization in early generations seems difficult, yet due to accumulation and fixation of more favourable genes (positive mutations) in the population, it may become easier. Shakoor and Haq (1980) also selected mutants in M_2 generation for grains per pod and pods and yield per plant which were true breeding in M_3 generation, suggesting that such polygenic characters can be stabilized in early generations. At least for these characters both time and labour can be saved and only the M_2 selections can be advanced to M_3 for confirmation, further selection, preliminary testing and multiplication.

The same rule can also be applied for other characters as well, even though their variance increased in M_3 over M_2 appreciably. The M_2 progenies can be classified as promising on the basis of their higher CV and desired shift in mean than the highest value of control, and only these progenies should be advanced for second cycle of intensive selection.

Therefore, irrespective of whether a character shows increase in variance with the advancing generations or not, preliminary screening in early generations should be of great help in reducing the volume of work and saving time. The reduced volume of material with a definite indication

of induction of change as a result of mutagenic treatments can be identified early and evaluated thoroughly in the subsequent generations.

Only one genotype (Precoz Selection) was used for mutagenic treatments in this study. The possibility of genotypic differences cannot be ruled out as different experiments carried out in the past showed divergent results. The dependence of the direction and magnitude of induced polygenic variability on the genotypic background of the material has been reported earlier (Gregory, 1956; Mohan, 1983).

2.2.3 Screening technique for micromutations

One of the main methodological problems associated with mutation breeding is nonavailability of suitable screening techniques. Most of the mutation breeding experiments failed to give desired results because it was not possible to identify the mutated families which are always in much smaller number than the nonmutated ones.

Different selection techniques have been employed to detect and measure the induced polygenic variability in many studies. Some of these were described in " Review of Literature". An important difference between the earlier and the present study relates to the procedure of handling the material carrying induced variability to identify promising families which offer maximum opportunity to detect polygenic mutations at the earliest possible time. Singh (1988) also followed the same procedure of handling the material carrying induced variability to identify promising families in pea and obtained favourable results. A common practice in the earlier studies was to select the normal looking plants in M_2 generation at random to raise M_3 families, where selection is to be

applied for the first time. The procedure of random selection is highly uncertain and also involves continuation of voluminous unwanted material, therefore, the outcome in M_3 is unpredictable. In contrast to this, the main emphasis in the present study is laid on selection in M_2 generation itself.

Selection in M_2 generation was also practised by many earlier workers (Brock and Latter, 1961; Brock and Andrew, 1965; Bhatia and Van der Veen, 1965; Bansal, 1969). However, their selection was based on mean values without any consideration for variation, although the main objective of induced mutagenesis is to induce variability. Further, they studied characters having high heritability, mostly under controlled conditions. Moreover, the selection techniques followed by some earlier workers were not based on rigorous interfamily and intrafamily selections using progeny mean and CV as the criterion for selection. In the present study, all these parameters were taken care of. Gupta and Swaminathan (1967) and Rao (1974) suggested that different M_2 families should be selected on the basis of desired shift in mean and higher variance than the highest values recorded in the control. However, Jana and Roy (1973) used only family mean as a criterion for selecting promising families in M_2 generation. Bhadra (1982) practised interfamily and intrafamily selection in M_2 on the basis of higher CV and mean than in the control and identified many promising families which were confirmed in M_3 on the basis of higher mean than the control. Similarly, Singh (1988) also practised interfamily and intrafamily selection in M_2 on the basis of higher CV than the highest recorded in the control and higher mean than that

of control population, and identified many promising families which were confirmed in M_3 on the basis of higher mean than the highest recorded in the control. The CV was not used as criterion for selection in M_3 because intrafamily variance is expected to decrease in M_3 generation. Kharkwal (1983) also emphasized the effectiveness of early generation selection for identifying superior progenies for quantitative traits.

2.2.4 Selection efficiency in M_2 and M_3 generations

Comparative studies of selection in M_2 and M_3 generations revealed in many cases that the two populations may not differ in selection response (Scossiroli, 1968; Sharma, 1977). Tickoo and Jain (1980), Bhadra (1982), Kharkwal (1983), Sarker (1985) and Singh (1988) concluded that promising families can be selected with high degree of confidence in M_2 based on the progeny means and variance. On the other hand, some experiments demonstrated that selection in M_3 is more effective than in M_2 (Palenzona, 1966; Jana and Roy, 1973; Kalia and Gupta, 1989). This was, most probably, because the material already selected in M_2 was confirmed with higher probability in subsequent generations (Ravi et al., 1980). Even if the material selected in M_3 or latter generations has higher probability of getting fixed as promising strains, there is no evidence to suggest that the frequency of promising mutations per se is higher in M_3 than in M_2. Because, after all, the variability manifested in M_3 generation could not have arisen afresh without causing any impact on the M_2 population. Therefore, the question arises, why not start selection a generation earlier and reject most of the unmutated "roughage" in M_2 itself, concentrate on the drastically reduced

Table 54 Nature of M_2 selections with multiple characters and their contribution to total micromutations (pooled over eight traits)

Mutagen	Total promising selections in M_3	M_2 selections confirmed in M_3, %	Proportion of total selections, %	
			M_2 selections	M_3 selections (expected)
Gamma rays	183	64.9	79.8	20.2
EI	214	69.5	79.9	20.1
NEU	253	71.8	82.6	17.4

quantity of material selected in this preliminary screening, and save one generation in the breeding procedure?

A perusal of Tables 54 and 55 reveals many interesting features of the present investigation. As can be seen from Table 54, 64.9 to

Table 55 Selection efficiency for micromutations in M_2 and M_3 generations (Pooled over eight traits)

Mutagen	M_2 generation		M_3 generation	
	Total progenies	Promising selections (%)	Total progenies	Promising selections (%)
Gamma rays	742	20.1	1083	22.0
EI	688	23.3	1066	25.4
NEU	747	24.9	1005	31.1
Total of the experiment	2177	22.8	3154	26.1

71.8% M_2 selections were confirmed as promising in M_3 generation. This suggests that selection in M_2 was very effective and dependable. Although , the characters showed increase in variance with the advancing generation (M_3), which is confirmed by the fact that 17.4 to 20.2% promising progenies were added in M_3 to the total number of promising selections, nevertheless, early generation selection is of great help in reducing the volume of work and saving time. As can be seen from Table 54, the contribution of M_2 and M_3 generations to the total selections was 79.8 to 82.6% and 17.4 to 20.2%, respectively. This suggests that although new mutated progenies (about one-fifth of the total) were added (which were not identified in M_2) in M_3 to those already selected in M_2, the quantum of material nearly trebled. Selection efficiency for micromutations in M_2 and M_3 generations pooled over eight traits (Table 55), also supports the above view. The above observations are similar to those of Singh (1988) in peas.

The overall analysis of the results obtained in this investigation reveals that there is tremendous possibility to improve polygenic characters through induced mutagenesis coupled with efficient selection techique. The basic philosophy behind the selection procedure adopted here is to reject at the first available opportunity the nonmutated or poorly mutated bulk and advance only the reduced amount of material which is likely to yield higher variability. Efficiency of mutation breeding for polygenic traits can be increased further immensely by selecting the M_1 plants with maximum primary damage, the normal looking M_2 plants from the macromutational families as well as nonsegregating families with high

variance and maximum desired shift in mean, followed by confirmation of the mutational change and assessment of the potential of these selections in M_3.

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APPENDIX - I

Population size for macromutations in M_2 generation

Treatment		Gamma rays		EI		NEU	
		progenies	plants	progenies	plants	progenies	plants
Control		174	3132				
5 kR/0.005%							
	LL	56	805	72	1080	63	819
	LH	61	854	74	1036	57	790
	HL	56	763	74	1126	66	908
	HH	60	796	70	1033	64	872
	Overall	233	3218	290	4275	250	3389
10 kR/0.01%							
	LL	87	1218	84	1196	85	1095
	LH	88	1144	88	1232	85	1115
	HL	80	1113	87	1218	93	1296
	HH	82	1142	86	1118	77	1024
	Overall	337	4617	345	4764	340	4530
20 kR/0.02%							
	LL	94	1405	94	1316	86	1290
	LH	98	1366	95	1425	88	1408
	HL	83	1154	93	1302	105	1680
	HH	86	1118	92	1375	104	1560
	Overall	361	5043	374	5418	383	5938

APPENDIX - II

Comparative mutation frequency in M_2 generation

Mutation	M_2 progenies basis		M_2 population basis	
	chlorophyll (%)	morphological (%)	chlorophyll (%)	morphological (%)
Control	0.0	0.0	0.0	0.0
Gamma-rays	4.7	3.9	0.40	0.37
EI	5.4	4.3	0.48	0.42
NEU	6.3	5.5	0.65	0.56
Overall experiment	5.5	4.6	0.51	0.45

APPENDIX - III

Frequency of chlorophyll mutations in M_2 generation

Treatment		Gamma rays % Mutated		EI % Mutated		NEU % Mutated	
		progenies	plants	progenies	plants	progenies	plants
5 kR/0.005%							
	LL	1.8	0.12	2.8	0.28	4.8	0.37
	LH	3.3	0.23	4.1	0.29	5.3	0.51
	HL	5.4	0.39	5.4	0.44	6.3	0.55
	HH	6.7	0.63	7.1	0.58	6.1	0.69
	Overall	4.3	0.34	4.8	0.40	5.6	0.53
10 kR/0.01%							
	LL	3.5	0.25	3.6	0.33	4.7	0.73
	LH	3.4	0.35	5.7	0.57	5.9	0.81
	HL	5.0	0.36	6.9	0.66	8.6	0.85
	HH	7.3	0.61	8.1	0.81	10.4	1.20
	Overall	4.7	0.39	6.1	0.59	7.4	0.88
20 kR/0.02%							
	LL	3.2	0.28	2.1	0.23	3.5	0.31
	LH	5.1	0.37	4.2	0.35	5.7	0.50
	HL	6.0	0.52	6.5	0.54	6.7	0.60
	HH	7.0	0.72	8.7	0.73	7.8	0.71
	Overall	5.2	0.46	5.4	0.46	6.0	0.54

APPENDIX - IV

Spectrum of chlorophyll mutations in M_2 generation

Treatment		Distribution of different chlorophyll mutations (%)				Total mutations	
		Albina	Chlorina	Xantha	Viridis	No.	%
Control		-	-	-	-	-	-
Gamma rays							
	5 kR	9.1	27.3	54.5	9.1	11	21.2
	10 kR	5.5	22.2	55.6	16.7	18	34.6
	20 kR	13.1	17.4	39.1	30.4	23	44.2
	Overall	9.6	21.1	48.1	21.2	52	24.5
EI							
	0.005%	5.9	11.8	35.3	47.0	17	24.3
	0.01%	10.7	10.7	28.6	50.0	28	40.0
	0.02%	4.0	24.0	28.0	44.0	25	35.7
	Overall	7.1	15.7	30.0	47.2	70	33.0
NEU							
	0.005%	5.6	22.2	38.9	33.3	18	20.0
	0.01%	7.5	25.0	30.0	37.5	40	44.4
	0.02%	6.3	28.1	28.1	37.5	32	35.6
	Overall	6.7	25.6	31.1	36.6	90	42.5
Total mutations		16 (7.6)	45 21.2)	74 (34.9)	77 (36.3)	212	100.0

Appendix V : Spectrum of chlorophyll mutations in M_2 generation

Treatment		Distribution of different chlorophyll mutations (No. of mutants)				Total
		Albina	Chlorina	Xantha	Viridis	
Control		-	-	-	-	-
Gamma rays:						
5 kR :	LL	-	-	1	-	1
	LH	-	1	1	-	2
	HL	-	1	2	-	3
	HH	1	1	2	1	5
	Overall	1	3	6	1	11
10 kR:	LL	-	-	2	1	3
	LH	-	1	2	1	4
	HL	-	1	3	-	4
	HH	1	2	3	1	7
	Overall	1	4	10	3	18
20 KR:	LL	1	-	2	1	4
	LH	-	1	2	2	5
	HL	1	1	2	2	6
	HH	1	2	3	2	8
	Overall	3	4	9	7	23
EI :						
0.005% :	LL	-	-	1	2	3
	LH	-	-	1	2	3
	HL	-	1	2	2	5
	HH	1	1	2	2	6
	Overall	1	2	6	8	17
0.01% :	LL	-	-	1	3	4
	LH	-	1	3	3	7
	HL	1	1	2	4	8
	HH	2	1	2	4	9
	Overall	3	3	8	14	28
0.02% :	LL	-	-	1	2	3
	LH	-	2	1	2	5
	HL	-	2	2	3	7
	HH	1	2	3	4	10
	Overall	1	6	7	11	25
NEU :						
0.005%	LL	-	1	1	1	3
	LH	-	1	2	1	4
	HL	-	1	2	2	5
	HH	1	1	2	2	6
	Overall	1	4	7	6	18
0.01%	LL	-	3	2	3	8
	LH	1	3	2	3	9
	HL	1	2	4	4	11
	HH	1	2	4	5	12
	Overall	3	10	12	15	40
0.02%:	LL	-	1	1	2	4
	LH	-	2	2	3	7
	HL	1	3	3	3	10
	HH	1	3	3	4	11
	Overall	2	9	9	12	32

APPENDIX- VI

Frequency of morphological mutations in M_2 generation

Treatment		Gamma rays % Mutated		EI % Mutated		NEU % Mutated	
		progenies	plants	progenies	plants	progenies	plants
5 kR/0.005%							
	LL	1.8	0.12	1.4	0.19	3.2	0.24
	LH	3.3	0.23	2.7	0.29	3.5	0.38
	HL	3.6	0.39	4.1	0.44	6.1	0.55
	HH	5.0	0.50	5.7	0.48	7.8	0.69
	Overall	3.4	0.31	3.5	0.35	5.2	0.47
10 kR/0.01%							
	LL	2.3	0.16	3.6	0.33	3.5	0.46
	LH	3.4	0.36	4.5	0.41	5.9	0.54
	HL	3.8	0.45	5.7	0.57	6.5	0.69
	HH	6.1	0.53	8.1	0.81	7.8	0.98
	Overall	3.9	0.37	5.5	0.52	5.9	0.66
20 kR/0.02%							
	LL	2.1	0.21	3.2	0.23	3.5	0.39
	LH	3.1	0.37	3.2	0.35	5.7	0.50
	HL	6.0	0.52	4.3	0.46	5.7	0.60
	HH	7.0	0.63	5.4	0.51	6.7	0.64
	Overall	4.4	0.42	4.0	0.39	5.5	0.54

APPENDIX - VII

Spectrum of morphological mutations induced by different mutagens

Kind of mutation	Control	Gamma rays	EI	NEU	Total mutations No.	Total mutations %
Compact	-	8.3	6.6	6.4	13	7.0
Bushy	-	6.3	9.8	11.5	18	9.6
Prostrate	-	10.4	6.6	7.7	15	8.0
Narrow leaf	-	14.6	8.2	11.6	21	11.2
Broad leaf	-	8.3	4.9	7.7	13	7.0
Rogue	-	6.3	6.6	6.4	12	6.4
Curly leaf	-	6.3	8.2	7.7	14	7.5
Laciniata	-	-	4.9	6.4	8	4.3
Tendrillar	-	6.3	4.9	6.4	11	5.9
Tall	-	6.2	9.8	5.1	13	7.0
Dwarf	-	6.2	11.5	7.7	16	8.6
Early	-	10.4	11.5	7.7	18	9.6
Late	-	8.3	3.3	5.1	10	5.3
Sterile	-	2.1	3.3	2.7	5	2.7
Total mutations	-	48 (25.7)	61 (32.6)	78 (41.7)	187	100.0

APPENDIX - VIII

Spectrum of morphological mutations (%) induced by different mutagens

Kind of mutation	Control	Gamma rays			EI			NEU			Total mutations	
		5 kR	10 kR	20 kR	0.005%	0.01%	0.02%	0.005%	0.01%	0.02%	No.	%
Compact	-	10.0	5.9	9.5	6.7	8.0	4.8	6.2	6.7	6.2	13	7.0
Bushy	-	10.0	11.8	-	13.3	12.0	4.8	12.5	13.3	9.4	18	9.6
Prostrate	-	20.0	11.8	4.8	6.7	8.0	4.8	6.2	10.0	6.2	15	8.0
Narrow leaf	-	20.0	11.8	14.3	13.3	8.0	4.8	6.3	13.3	12.5	21	11.2
Broad leaf	-	20.0	5.9	4.8	6.7	4.0	4.8	6.3	6.7	9.4	13	7.0
Rogue	-	-	5.9	9.5	6.7	8.0	4.8	6.3	6.7	6.3	12	6.4
Curly leaf	-	10.0	5.9	4.8	6.7	12.0	4.8	12.5	10.0	3.1	14	7.5
Laciniata	-	-	-	-	-	4.0	9.5	6.3	3.3	9.4	8	4.3
Tendrillar	-	-	5.9	9.5	6.7	4.0	4.8	6.3	6.7	6.3	11	5.9
Tall	-	-	5.9	9.5	6.7	8.0	14.3	6.2	3.3	6.2	13	7.0
Dwarf	-	-	5.9	9.5	13.3	8.0	14.3	6.2	6.7	9.4	16	8.6
Early	-	10.0	11.8	9.5	13.3	8.0	14.3	12.5	6.7	6.3	18	9.6
Late	-	-	11.8	9.5	-	4.0	4.8	6.2	3.3	6.2	10	5.3
Sterile	-	-	-	4.8	-	4.0	4.8	-	3.3	3.1	5	2.7
Total mutations	-	10 (20.8)	17 (35.4)	21 (43.8)	15 (24.6)	25 (41.0)	21 (34.4)	16 (20.5)	30 (38.5)	32 (41.0)	187	100.0

Appendix IX Spectrum of morphological mutations induced by different mutagens affecting different plant parts in M_2 generation

(No. of mutations)

Treatment		Growth habit			Foliage						Plant height		Maturity			Total
		compact (1)	bushy (2)	prostrate (3)	narrow (4)	broad (5)	rogue (6)	curly (7)	laciniata (8)	tendrillar (9)	tall (10)	dwarf (11)	early (12)	late (13)	sterile (14)	(15)
Control		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Gamma rays																
5 kR	LL	1	-	-	-	-	-	-	-	-	-	-	-	-	-	1
	LH	-	-	-	1	1	-	-	-	-	-	-	-	-	-	2
	HL	-	-	1	-	1	-	1	-	-	-	-	-	-	-	3
	HH	-	1	1	1	-	-	-	-	-	-	-	1	-	-	4
	Overall	1	1	2	2	2	-	1	-	-	-	-	1	-	-	10
10 kR	LL	-	-	1	-	-	-	-	-	-	1	-	-	-	-	2
	LH	1	-	1	-	1	-	1	-	-	-	-	-	-	-	4
	HL	-	1	-	1	-	-	-	-	1	-	-	1	1	-	5
	HH	-	1	-	1	-	1	-	-	-	-	1	1	1	-	6
	Overall	1	2	2	2	1	1	1	-	1	1	1	2	2	-	17
20 kR	LL	1	-	-	-	1	-	-	-	-	1	-	-	-	-	3
	LH	1	-	1	1	-	-	-	-	-	1	-	1	-	-	5
	HL	-	-	-	1	-	-	1	-	1	-	1	-	1	1	6
	HH	-	-	-	1	-	2	-	-	1	-	1	1	1	-	7
	Overall	2	-	1	3	1	2	1	-	2	2	2	2	2	1	21
EI																
0.005%	LL	1	-	-	-	-	-	-	-	-	1	-	-	-	-	2
	LH	-	1	1	-	1	-	-	-	-	-	-	-	-	-	3
	HL	-	1	-	1	-	-	1	-	-	-	1	1	-	-	5
	HH	-	-	-	1	-	1	-	-	1	-	1	1	-	-	5
	Overall	1	2	1	2	1	1	1	-	1	1	2	2	-	-	51
0.01%	LL	1	1	-	-	-	-	-	1	-	1	-	-	-	-	4
	LH	1	-	-	-	1	-	1	-	-	1	-	1	-	-	5
	HL	-	1	1	1	-	1	1	-	-	-	1	-	-	1	7
	HH	-	1	1	1	-	1	1	-	1	-	1	1	1	-	9
	Overall	2	3	2	2	1	2	3	1	1	2	2	2	1	1	25
0.02%	LL	1	-	-	-	-	-	-	-	-	1	-	1	-	-	3
	LH	-	-	-	-	1	-	-	2	-	1	1	-	-	-	5
	HL	-	-	-	1	-	1	1	-	-	1	1	1	-	-	6
	HH	-	1	1	-	-	-	-	-	1	-	1	1	1	1	7
	Overall	1	1	1	1	1	1	1	2	1	3	3	3	1	1	21
NEU																
0.005%	LL	1	-	-	-	-	-	-	-	-	1	-	-	-	-	2
	LH	-	1	1	-	-	-	-	1	-	-	-	-	-	-	3
	HL	-	1	-	1	-	-	1	-	-	-	-	1	1	-	5
	HH	-	-	-	-	1	1	1	-	1	-	1	1	-	-	6
	Overall	1	2	1	1	1	1	2	1	1	1	1	2	1	-	16
0.01%	LL	2	1	1	-	-	-	-	-	-	1	-	-	-	-	5
	LH	-	1	1	1	1	-	1	-	-	-	-	1	-	-	6
	HL	-	1	1	1	1	1	1	-	1	-	1	1	-	-	9
	HH	-	1	-	2	-	1	1	1	1	-	1	-	1	1	10
	Overall	2	4	3	4	2	2	3	1	2	1	2	2	1	1	30
0.02%	LL	1	1	-	1	-	-	-	-	-	1	-	1	-	-	5
	LH	1	1	-	1	1	-	-	1	-	1	1	-	-	-	7
	HL	-	1	1	1	1	1	1	1	-	1	-	-	1	1	10
	HH	-	-	1	1	1	1	1	1	1	-	1	1	1	-	10
	Overall	2	3	2	4	3	2	2	3	1	3	2	2	2	1	32

Appendix X. Frequency of macromutations in different treatments in M_2 generation

Treatment	Gamma-rays		EI		NEU	
	Percentage of mutated		Percentage of mutated		Percentage of mutated	
	progenies	plants	progenies	plants	progenies	plants
5 kR/0.005%						
LL	3.6	0.24	4.2	0.47	8.0	0.61
LH	6.6	0.46	6.8	0.58	8.8	0.89
HL	9.0	0.78	9.5	0.88	12.4	1.10
HH	11.7	1.13	12.8	1.06	13.9	1.38
Overall	7.7	0.65	8.3	0.75	10.8	1.00
10 kR/0.01%						
LL	5.8	0.41	7.2	0.66	8.2	1.19
LH	6.8	0.71	10.2	0.98	11.8	1.35
HL	8.8	0.81	12.6	1.23	15.1	1.54
HH	13.4	1.14	16.2	1.62	18.2	2.18
Overall	8.6	0.76	11.6	1.11	13.3	1.54
20 kR/0.02%						
LL	5.3	0.49	5.3	0.46	7.0	0.70
LH	8.2	0.74	7.4	0.70	11.4	1.00
HL	12.0	1.04	10.8	1.00	12.4	1.20
HH	14.0	1.35	14.1	1.24	14.5	1.35
Overall	9.6	0.88	9.4	0.85	11.5	1.08

Appendix XI. Spectrum of macromutations (%) induced by different mutagens

Mutation type	Control	Gamma rays			EI			NEU			Total mutations	
		5 kR	10 kR	20 kR	0.005%	0.01%	0.02%	0.005%	0.01%	0.02%	No.	%
Albina	-	4.8	2.9	6.8	3.1	5.7	2.2	2.9	4.3	3.1	16	4.0
Chlorina	-	14.3	11.4	9.1	6.3	5.7	13.0	11.8	14.3	14.1	45	11.3
Xantha	-	28.6	28.6	20.4	18.8	15.1	15.2	20.6	17.1	14.1	74	18.5
Viridis	-	4.8	8.6	15.9	25.0	26.4	23.9	17.6	21.4	18.8	77	19.3
Compact	-	4.8	2.3	4.5	3.1	3.8	2.2	2.9	2.9	3.1	13	3.3
Bushy	-	4.8	5.7	-	6.3	5.7	2.2	5.9	5.7	4.7	18	4.5
Prostrate	-	9.5	5.7	2.3	3.1	3.8	2.2	2.9	4.3	3.1	15	3.8
Narrow leaf	-	9.5	5.7	6.8	6.3	3.8	2.2	2.9	5.7	6.2	21	5.3
Broad leaf	-	9.5	2.9	2.3	3.1	1.9	2.2	2.9	2.9	4.7	13	3.2
Rogue	-	-	2.9	4.5	3.1	3.8	2.2	2.9	2.9	3.1	12	3.0
Curly leaf	-	4.8	2.9	2.3	3.1	5.7	2.2	5.9	4.3	1.6	14	3.5
Laciniata	-	-	-	-	-	1.9	4.3	2.9	1.4	4.7	8	2.0
Tendrillar	-	-	2.9	4.5	3.1	1.9	2.2	2.9	2.9	3.1	11	2.8
Tall	-	-	2.9	4.5	3.1	3.8	6.5	2.9	1.4	3.1	13	3.2
Dwarf	-	-	2.9	4.5	6.3	3.8	6.5	2.9	2.9	4.7	16	4.0
Early	-	4.8	5.7	4.5	6.3	3.8	6.5	5.9	2.9	3.1	18	4.5
Late	-	-	5.7	4.5	-	1.9	2.2	2.9	1.4	3.1	10	2.5
Sterile	-	-	-	2.3	-	1.9	2.2	-	1.4	1.6	5	1.2
Total mutations		21(5.3)	35(8.8)	44(11.0)	32(08.0)	53(13.3)	46(11.5)	34(8.5)	70(17.5)	64(16.0)	399(100.0)	

APPENDIX - XII

Population size for micromutations in M_2 generation

Treatment	Progenies		
	Gamma rays	EI	NEU
5 kR/0.005%			
LL	57	46	46
LH	49	58	55
HL	40	49	52
HH	41	59	40
Overall	187	212	193
10 kR/0.01%			
LL	85	73	56
LH	69	55	56
HL	50	41	76
HH	68	69	57
Overall	272	238	245
20 kR/0.02%			
LL	76	73	79
LH	70	55	76
HL	64	56	78
HH	73	54	76
Overall	283	238	309
Total of the mutagen	742	688	747

APPENDIX- XIII

Range, population mean, variance and CV for days to maturity in M_2 generation

Treatment	Gamma rays				EI				NEU			
	Range	Mean	Variance	CV	Range	Mean	Variance	CV	Range	Mean	Variance	CV
Control	116.4-121.0	118.5	2.2	1.3								
5 kR/0.005%												
Total	114.6-133.3	124.3	4.9	1.8	114.2-135.5	124.8	10.0	2.5	114.5-128.0	119.7	7.8	2.3
LL	115.0-128.8	123.4	1.8	1.1	114.2-131.8	123.6	3.2	1.4	118.0-128.0	119.5	3.0	1.4
LH	114.6-128.3	126.1	2.4	1.2	115.0-133.7	125.2	9.9	2.5	114.6-123.0	121.1	6.7	2.1
HL	115.6-130.3	124.8	4.4	1.7	114.8-134.0	126.2	12.1	2.8	115.0-124.0	119.9	6.1	2.1
HH	114.6-133.1	123.0	7.0	2.1	118.9-135.5	124.9	14.4	3.0	114.5-125.3	118.7	12.4	3.0
10 kR/0.01%												
Total	114.2-132.2	125.5	5.9	1.9	114.3-136.8	123.0	11.3	2.7	114.0-130.0	120.9	14.0	3.1
LL	115.0-129.0	126.9	2.0	1.1	115.0-128.1	124.7	7.5	2.2	119.7-125.0	122.8	2.8	1.4
LH	115.0-129.5	124.7	3.7	1.5	114.7-128.0	122.0	9.0	2.5	117.0-124.7	119.8	8.6	2.4
HL	115.0-132.0	126.2	6.6	2.0	114.3-129.5	125.5	13.5	2.9	114.0-124.3	117.8	12.7	3.0
HH	114.2-132.2	124.0	6.2	2.0	115.3-136.8	120.8	15.4	3.2	114.6-130.0	122.6	17.8	3.4
20 kR/0.02%												
Total	114.1-134.0	124.4	7.2	2.2	113.0-126.4	120.2	9.3	2.5	114.0-129.0	120.6	8.5	2.4
LL	118.9-126.8	123.4	4.3	1.7	114.8-124.4	119.2	3.8	1.6	114.0-126.0	121.4	5.7	2.0
LH	114.7-128.0	124.8	5.7	1.9	114.4-125.8	119.9	7.7	2.3	116.2-122.0	120.0	5.5	2.0
HL	115.3-130.0	125.7	8.9	2.4	114.2-126.3	121.7	11.8	2.8	116.0-125.3	120.5	8.1	2.3
HH	114.1-134.0	124.5	9.1	2.4	113.0-126.4	120.0	11.0	2.8	118.0-129.0	120.3	13.3	3.0
Mutagen	114.1-134.0	124.8	6.2	2.0	113.0-136.8	122.2	10.2	2.6	114.0-130.0	120.4	10.5	2.7

APPENDIX - XIV

Range, population mean, variance and CV for plant height in M_2 generation

Treatment	Gamma rays				EI				NEU			
	Range	Mean	Variance	CV	Range	Mean	Variance	CV	Range	Mean	Variance	CV
Control	24.4-36.2	30.3	11.6	11.2								
5 kR/0.005%												
Total	22.8-42.1	32.4	20.3	13.9	19.9-43.4	33.2	25.3	15.1	28.0-43.0	31.3	23.4	15.4
LL	25.4-38.3	33.1	14.9	11.7	28.7-43.4	35.7	22.7	13.5	29.2-39.8	32.8	16.8	12.5
LH	24.3-37.3	32.7	19.4	13.5	24.3-40.6	34.4	24.1	14.3	25.2-38.2	31.6	21.2	14.6
HL	26.8-42.1	32.4	22.2	14.5	24.3-41.7	31.8	25.4	15.7	21.8-43.0	31.6	25.8	16.1
HH	22.8-39.5	31.4	22.5	15.1	19.9-38.3	30.8	29.1	17.5	20.8-40.3	29.3	29.6	18.4
10 kR/0.01%												
Total	20.3-43.2	32.0	23.4	15.1	19.8-43.6	31.7	32.1	17.9	18.3-42.9	31.1	36.9	19.5
LL	25.8-43.2	33.6	18.8	12.9	27.8-42.0	35.2	21.7	13.2	26.0-37.7	33.6	19.9	13.4
LH	28.8-41.8	31.7	19.8	14.0	24.0-35.3	31.1	24.7	16.0	24.0-42.9	33.3	28.9	16.2
HL	26.8-39.0	31.4	25.8	16.2	19.8-36.0	29.8	35.5	20.0	18.3-39.7	31.5	43.4	20.9
HH	20.3-38.6	31.3	29.3	17.3	24.3-43.6	29.0	46.6	23.5	18.3-41.8	25.8	55.2	28.7
20 kR/0.02%												
Total	20.2-43.5	32.1	24.1	15.3	19.9-42.0	31.2	23.0	15.4	17.0-42.8	29.5	32.8	19.4
LL	28.8-40.0	34.9	18.9	12.5	26.2-38.6	32.0	16.3	12.6	25.4-43.0	31.4	21.7	14.8
LH	30.0-43.5	31.9	20.2	14.1	26.7-39.0	32.2	18.2	13.2	24.5-38.0	31.8	28.4	16.8
HL	22.3-41.4	31.8	26.6	16.2	19.9-39.3	29.4	27.2	17.7	19.7-42.8	29.8	36.9	20.4
HH	20.2-40.3	29.7	30.5	18.6	21.6-42.0	30.5	30.5	18.1	17.0-42.7	24.9	44.1	26.7
Mutagen	20.2-43.5	32.2	22.6	14.8	19.8-43.6	32.0	26.8	16.2	17.0-43.0	30.6	31.0	18.2

APPENDIX - XV

Range, population mean, variance and CV for total fruiting branches in M_2 generation

Treatment	Gamma rays				EI				NEU			
	Range	Mean	Variance	CV	Range	Mean	Variance	CV	Range	Mean	Variance	CV
Control	9.8-21.8	13.4	32.0	42.2								
5 kR/0.005%												
Total	4.3-35.3	15.5	72.0	54.8	6.8-39.7	16.8	86.4	55.3	7.3-42.0	18.0	98.9	55.2
LL	4.3-26.0	13.7	54.4	53.5	9.0-30.6	15.6	57.8	48.7	8.3-34.6	15.7	63.1	50.6
LH	10.2-32.3	12.8	56.3	58.6	9.2-32.5	18.0	83.2	50.7	7.4-39.8	16.9	82.7	54.0
HL	5.7-32.0	17.4	74.7	49.7	6.8-37.3	17.5	93.1	55.1	7.3-42.0	18.5	107.5	56.0
HH	6.3-35.3	17.1	84.3	53.6	8.2-39.7	16.0	111.3	65.9	7.3-42.0	20.5	142.2	58.2
10 kR/0.01%												
Total	4.0-39.6	13.7	78.6	64.7	4.3-48.3	17.1	103.8	59.8	5.5-55.0	19.4	115.0	55.3
LL	4.0-23.3	10.5	53.8	70.1	7.0-29.2	15.6	7 6.6	56.1	8.3-40.0	17.6	75.6	49.3
LH	4.4-24.8	12.4	54.3	59.4	6.0-35.0	16.9	90.3	56.2	6.6-39.7	18.5	97.1	53.3
HL	9.2-32.8	12.8	55.3	57.9	7.3-39.0	18.8	112.4	56.5	5.5-42.3	19.8	123.7	56.2
HH	5.2-39.6	19.3	114.6	55.6	4.3-48.3	19.3	137.3	60.6	10.0-55.0	21.9	163.6	58.4
20 kR/0.02%												
Total	7.0-50.0	18.4	141.8	64.6	4.8-56.2	16.1	106.8	64.2	4.7-61.0	21.3	143.5	56.2
LL	10.0-31.3	15.7	77.3	55.9	4.8-25.7	13.1	75.4	66.4	7.8-36.0	20.0	108.2	52.0
LH	7.5-43.0	17.8	104.7	57.5	5.4-28.2	15.1	93.6	64.1	5.5-37.0	21.2	140.0	55.8
HL	7.0-43.5	16.7	117.8	65.0	6.0-34.2	17.8	116.1	60.6	7.8-41.3	21.7	151.4	56.7
HH	9.2-50.0	22.3	218.9	66.3	7.0-56.2	18.2	185.5	74.8	4.7-61.0	22.3	174.3	59.2
Mutagen	4.0-50.0	15.8	99.9	63.3	4.3-56.2	16.7	100.3	60.3	4.7-61.0	19.6	119.1	55.7

APPENDIX - XVI

Range,population mean, variance and CV for effective clusters per plant in M_2 generation

Treatment	Gamma rays				EI				NEU			
	Range	Mean	Variance	CV	Range	Mean	Variance	CV	Range	Mean	Variance	CV
Control	14.4-54.6	25.0	127.7	45.2								
5 kR/0.005%												
Total	9.5-76.8	24.3	305.0	71.9	8.4-78.0	27.9	346.3	66.7	7.0-103.0	31.3	509.2	72.1
LL	12.5-56.7	21.0	203.3	67.9	10.3-56.3	23.3	200.0	60.7	11.8-66.7	27.9	277.0	60.0
LH	12.8-64.8	22.7	253.8	70.2	11.4-65.8	25.7	245.7	61.0	7.0-75.7	31.0	410.5	65.4
HL	11.6-70.3	25.7	350.4	72.8	11.7-72.3	30.4	435.7	68.7	7.0-88.8	32.2	603.4	76.3
HH	9.8-76.8	27.7	412.5	73.3	8.4-78.0	32.2	503.8	69.7	10.8-103.0	34.1	745.9	80.1
10 kR/0.01%												
Total	10.8-95.3	29.7	400.8	67.4	8.3-135.3	28.6	508.4	79.1	9.3-152.3	35.5	724.6	75.8
LL	13.0-69.7	25.9	268.4	63.2	8.3-66.7	23.8	292.5	71.9	9.3-72.7	32.2	437.2	64.9
LH	13.2-78.8	27.2	324.5	66.2	9.2-80.6	25.9	395.7	76.8	7.7-91.7	34.9	655.8	73.4
HL	13.7-95.0	31.4	463.5	67.4	8.8-120.3	30.8	592.5	79.0	11.7-126.8	36.3	812.0	78.5
HH	10.8-95.3	33.8	546.8	69.2	11.2-135.3	33.9	752.9	80.9	10.0-152.3	38.6	993.4	81.7
20 kR/0.02%												
Total	8.3-128.7	30.8	566.0	77.4	9.6-107.3	28.5	438.7	73.5	7.4-126.0	31.7	574.7	75.6
LL	8.8-63.3	26.4	360.9	72.0	11.0-58.8	23.3	249.8	67.8	9.8-71.0	29.2	383.6	67.1
LH	10.0-75.0	29.4	453.2	72.4	10.2-68.8	26.2	360.5	72.5	7.5-80.7	30.1	464.3	71.6
HL	12.0-113.3	32.5	654.5	78.7	9.6-101.5	31.0	513.3	73.1	8.6-105.3	33.0	640.3	76.7
HH	8.3-128.7	34.9	795.4	80.8	10.4-107.3	33.5	631.3	75.0	7.4-126.0	34.5	810.6	82.5
Mutagen	8.3-128.7	28.8	431.3	72.1	8.3-135.3	28.5	436.3	73.4	7.0-152.3	33.3	618.2	74.7

APPENDIX - XVII

Range, population mean, variance and CV for pods per plant in M_2 generation

Treatment	Gamma rays				EI				NEU			
	Range	Mean	Variance	CV	Range	Mean	Variance	CV	Range	Mean	Variance	CV
Control	22.4-74.8	45.0	590.5	54.0								
5 kR/0.005%												
Total	14.5-106.0	43.0	987.8	73.2	13.7-142.0	53.3	1271.0	66.9	10.0-166.0	56.4	1790.8	75.0
LL	18.8-76.0	37.1	661.0	69.3	19.0-79.8	45.6	854.4	64.1	14.7-96.7	50.8	989.3	61.9
LH	18.6-99.3	39.6	812.5	71.9	18.4-105.5	48.1	967.5	64.7	10.0-126.7	55.6	1589.2	71.7
HL	17.2-103.0	42.6	965.4	72.9	18.3-120.8	56.0	1374.3	66.2	16.2-135.0	60.4	2129.4	76.4
HH	14.5-106.0	52.7	1568.1	75.1	13.7-142.0	58.9	1625.6	68.5	15.4-166.0	62.5	2436.9	79.0
10 kR/0.01%												
Total	13.8-156.0	54.8	1444.8	69.4	12.8-198.8	54.0	1857.6	79.8	14.5-208.6	62.2	2322.0	77.4
LL	18.0-88.5	49.1	947.9	62.7	18.8-99.8	46.8	1154.4	72.6	20.0-102.5	55.0	1389.5	67.8
LH	18.0-140.7	51.0	1240.7	69.1	18.8-145.5	49.2	1342.5	74.5	18.3-150.4	61.3	1963.7	72.3
HL	17.4-148.3	57.3	1546.1	68.6	17.0-174.3	54.7	1872.1	79.1	20.7-181.8	65.6	2591.4	77.6
HH	13.8-156.0	61.6	1998.6	72.6	12.8-198.8	64.4	2788.4	82.0	14.5-208.6	69.7	3116.1	80.1
20 kR/0.02%												
Total	13.3-182.0	52.6	1664.1	77.5	13.0-184.4	51.2	1557.8	77.1	12.8-192.0	58.3	1886.7	74.5
LL	16.0-91.8	47.9	969.6	65.0	15.4-92.4	46.2	1082.0	7 1.2	19.8-99.5	51.6	1253.0	68.6
LH	15.4-123.0	50.3	1175.0	68.1	15.0-142.3	48.1	1260.1	73.8	15 0 -145.2	56.2	1583.2	70.8
HL	15.0-151.3	58.4	1680.3	70.2	14.4-155.5	53.8	1606.3	74.5	18.2-164.6	61.7	2158.5	75.3
HH	13.3-182.0	62.3	2335. 4	77.6	13.0-184.4	61.5	2386.7	79.4	12.8-192.0	65.9	2656.0	78.2
Mutagen	13.3-182.0	51.2	1419.7	73.6	12.8-198.8	52.8	1556.8	74.8	10.0-208.6	59.1	2020.7	76.1

APPENDIX- XVIII

Range, population mean, variance and CV for seeds per pod in M_2 generation

Treatment	Gamma rays				EI				NEU			
	Range	Mean	Variance	CV	Range	Mean	Variance	CV	Range	Mean	Variance	CV
Control	1.1-1.6	1.3	0.05	17.2								
5 kR/0.005%												
Total	1.0-2.0	1.3	0.07	20.2	1.0-2.2	1.4	0.07	20.1	1.0-2.1	1.4	0.07	19.1
LL	1.2-1.7	1.4	0.07	18.9	1.1-1.7	1.3	0.06	18.8	1.1-1.5	1.4	0.06	18.6
LH	1.1-1.9	1.3	0.06	19.1	1.1-1.2	1.4	0.07	19.4	1.1-1.9	1.3	0.06	18.8
HL	1.1-2.0	1.4	0.07	21.2	1.0-2.1	1.4	0.08	20.2	1.0-2.0	1.4	0.07	18.9
HH	1.0-2.0	1.4	0.08	21.3	1.0-2.2	1.4	0.10	22.6	1.2-2.1	1.5	0.09	20.7
10 kR/0.01%												
Total	1.0-2.1	1.4	0.07	18.5	1.0-2.1	1.4	0.08	20.2	1.1-2.2	1.5	0.09	20.0
LL	1.2-1.9	1.4	0.06	17.6	1.0-1.7	1.4	0.07	17.8	1.2-1.9	1.4	0.07	17.8
LH	1.0-2.0	1.4	0.06	18.3	1.0-1.9	1.4	0.07	18.8	1.1-1.9	1.5	0.07	18.1
HL	1.0-2.1	1.3	0.07	19.0	1.1-2.0	1.4	0.08	20.2	1.2-2.0	1.5	0.08	18.9
HH	1.1-2.1	1.5	0.09	20.3	1.1-2.1	1.5	0.11	22.1	1.1-2.2	1.6	0.12	21.7
20 kR/0.02%												
Total	1.0-2.2	1.4	0.08	20.6	1.0-2.0	1.3	0.07	20.4	1.0-2.1	1.4	0.08	20.5
LL	1.0-1.9	1.4	0.06	17.5	1.1-1.7	1.3	0.06	18.1	1.1-1.8	1.3	0.05	17.5
LH	1.0-2.1	1.4	0.06	17.9	1.1-1.9	1.2	0.05	19.4	1.0-2.0	1.4	0.06	17.4
HL	1.0.2.1	1.4	0.08	20.2	1.1-2.0	1.4	0.08	20.5	1.1-2.1	1.5	0.09	20.0
HH	1.0-2.2	1.5	0.10	21.1	1.0-2.0	1.5	0.10	21.5	1.0-2.1	1.5	0.11	22.1
Mutagen	1.0-2.2	1.4	0.07	19.3	1.0-2.2	1.4	0.08	20.1	1.0-2.2	1.4	0.08	20.2

APPENDIX - XIX

Range, population mean, variance and CV for 100-seed weight in M_2 generation

Treatment	Gamma rays				EI				NEU			
	Range	Mean	Variance	CV	Range	Mean	Variance	CV	Range	Mean	Variance	CV
Control	2.7-3.6	3.1	0.3	17.7								
5 kR/0.005%												
Total	2.0-4.3	3.1	0.5	22.3	1.7-4.4	3.3	0.6	23.0	1.8-4.4	3.2	0.5	22.1
LL	2.2-4.0	3.3	0.4	19.2	2.0-4.1	3.4	0.4	18.6	2.1-4.0	3.4	0.4	18.4
LH	2.1-4.0	3.2	0.5	22.1	2.0-4.2	3.4	0.4	19.5	2.0-4.2	3.3	0.5	21.4
HL	2.0-4.1	3.0	0.5	23.6	1.8-4.3	3.2	0.6	24.2	1.9-4.4	3.1	0.6	24.1
HH	2.0-4.3	3.0	0.6	25.8	1.7-4.4	3.1	0.7	27.0	1.8-4.4	3.1	0.6	25.8
10 kR/0.01%												
Total	1.7-4.4	3.2	0.5	22.5	1.3-4.6	3.2	0.7	26.4	1.8-4.6	3.3	0.6	23.5
LL	2.3-4.0	3.4	0.3	16.1	1.9-4.1	3.3	0.4	19.2	2.0-4.2	3.5	0.5	19.6
LH	2.0-4.3	3.3	0.5	21.4	1.7-4.4	3.2	0.7	26.1	1.9-4.2	3.3	0.5	21.4
HL	1.9-4.4	3.2	0.6	24.6	1.8-4.4	3.1	0.7	27.0	1.8-4.4	3.2	0.6	24.2
HH	1.7-4.4	3.0	0.7	28.4	1.3-4.6	3.0	0.9	31.6	1.8-4.6	3.0	0.7	27.9
20 kR/0.02%												
Total	1.3-4.6	3.4	0.8	26.7	1.3-4.5	3.1	0.7	27.6	1.5-4.5	3.1	0.6	25.0
LL	2.0-4.4	4.0	0.5	18.3	2.0-4.2	3.4	0.5	20.8	1.9-4.2	3.3	0.5	21.2
LH	1.7-4.3	3.6	0.6	22.0	1.8-4.3	3.2	0.7	25.6	1.8-4.4	3.2	0.6	23.6
HL	1.5-4.5	3.1	0.8	28.9	1.4-4.4	3.0	0.7	27.9	1.7-4.4	3.0	0.6	25.8
HH	1.3-4.6	3.0	0.9	31.6	1.3-4.5	2.9	0.8	31.2	1.5-4.5	3.1	0.7	27.0
Mutagen	1.3-4.6	3.3	0.6	24.4	1.3-4.6	3.2	0.7	26.0	1.5-4.6	3.2	0.6	23.6

APPENDIX - XX

Range, population mean, variance and CV for seed yield per plant in M_2 generation

Treatment	Gamma rays				EI				NEU			
	Range	Mean	Variance	CV	Range	Mean	Variance	CV	Range	Mean	Variance	CV
Control	1.0-4.1	2.0	1.9	66.8								
5 kR/0.005%												
Total	0.6-8.2	2.1	3.9	94.0	0.5-8.4	2.3	3.8	85.6	0.4-8.7	2.5	4.3	81.6
LL	0.6-4.2	1.7	2.1	86.3	0.5-4.3	2.0	2.4	79.7	0.8-4.9	2.1	2.5	75.3
LH	0.6-4.6	1.9	2.9	90.0	0.6-5.5	2.2	3.5	84.4	0.4-5.4	2.2	3.5	86.4
HL	1.0-5.5	2.4	4.8	91.3	1.3-7.8	2.3	3.8	84.7	0.7-7.5	2.5	4.6	85.8
HH	0.7-8.2	2.5	5.7	95.6	0.8-8.4	2.6	5.5	91.8	0.4-8.7	3.2	7.3	77.4
10 kR/0.01%												
Total	0.6-8.7	2.4	3.9	83.4	0.7-9.9	2.5	4.8	87.5	0.6-10.2	2.7	5.3	84.6
LL	0.7-4.5	1.9	1.8	70.6	0.8-3.3	2.1	2.6	76.8	0.6-5.3	2.1	2.8	79.7
LH	0.6-4.6	2.3	2.9	73.7	0.9-5.8	2.2	3.4	83.8	0.9-5.7	2.0	2.7	81.6
HL	1.1-7.1	2.8	4.9	79.1	0.7-6.0	2.7	5.5	86.5	1.1-8.2	3.3	7.5	82.9
HH	0.9-8.7	2.9	6.2	85.1	1.4-9.9	3.0	7.4	90.6	1.0-10.2	3.5	8.6	84.0
20 kR/0.02%												
Total	1.0-8.6	2.6	4.1	78.7	0.8-9.6	2.5	4.2	82.3	0.5-9.2	2.6	5.0	85.5
LL	1.0-5.2	2.4	2.7	68.7	0.8-4.2	2.1	2.0	67.3	0.5-6.0	2.3	3.3	78.6
LH	1.0-5.5	2.4	3.5	77.4	0.8-5.6	2.0	2.8	83.7	0.6-6.2	2.4	3.7	80.1
HL	1.1-7.9	2.7	4.8	80.8	1.0-7.9	2.9	5.9	84.0	0.8-7.9	2.8	5.4	83.0
HH	1.1-8.6	3.0	5.9	81.0	1.2-9.6	3.0	7.6	91.9	1.2-9.2	3.7	10.2	86.3
Mutagen	0.6-8.7	2.4	4.0	83.8	0.5-9.9	2.4	4.3	86.1	0.4-10.2	2.6	4.9	83.9

Appendix XXI Classification of families mutated for days to maturity in M_2 generation

Treatment		Total families mutated (%)	Mutated families			
			total (No.)	with lower mean (%)	with unchanged mean (%)	with higher mean (%)
Control						
Gamma rays						
5 kR	LL	7.0	4	0.0	75.0	25.0
	LH	14.3	7	14.3	57.1	28.6
	HL	10.0	8	25.0	50.0	25.0
	HH	34.1	14	35.7	42.9	21.4
	Overall	17.6	33	24.2	51.6	24.2
10 kR	LL	10.6	9	11.1	66.7	22.2
	LH	15.9	11	27.3	45.5	27.3
	HL	28.0	14	28.6	50.0	21.4
	HH	29.4	20	30.0	45.0	25.0
	Overall	19.9	54	25.9	50.0	24.1
20 kR	LL	13.2	10	20.0	50.0	30.0
	LH	18.6	13	30.8	46.2	23.1
	HL	25.0	16	31.3	43.8	25.0
	HH	30.1	22	31.8	36.4	31.8
	Overall	21.6	61	29.5	42.6	27.9
EI						
0.005%	LL	13.0	6	0.0	66.7	33.3
	LH	13.8	8	25.0	50.0	25.0
	HL	20.4	10	30.0	40.0	30.0
	HH	25.4	15	33.3	40.0	26.7
	Overall	18.4	39	25.6	46.2	28.2
0.01%	LL	11.0	8	12.5	62.5	25.0
	LH	18.2	10	30.0	50.0	20.0
	HL	26.8	11	36.4	36.4	27.3
	HH	29.0	20	40.0	35.0	25.0
	Overall	20.6	49	32.7	42.9	24.4
0.02%	LL	12.3	9	22.2	44.4	33.3
	LH	23.6	13	23.1	53.8	23.1
	HL	26.8	15	33.3	40.0	26.7
	HH	33.3	18	38.9	33.3	27.8
	Overall	23.1	55	30.9	41.8	27.3
NEU						
0.005%	LL	15.2	7	14.3	71.4	14.3
	LH	18.2	10	20.0	50.0	30.0
	HL	23.1	12	33.3	41.7	25.0
	HH	30.0	12	41.7	33.3	25.0
	Overall	21.2	41	29.3	46.3	24.4
0.01%	LL	19.6	11	18.2	63.6	18.2
	LH	21.4	12	33.3	50.0	16.7
	HL	22.4	17	35.3	52.9	11.8
	HH	31.6	18	44.4	38.9	16.7
	Overall	23.7	58	34.4	50.0	15.5
0.02%	LL	19.0	15	26.7	53.3	20.0
	LH	22.4	17	29.4	52.9	17.6
	HL	28.2	22	31.8	50.0	18.2
	HH	30.3	23	34.8	47.8	17.4
	Overall	24.9	77	31.2	50.6	18.2

Appendix XXII Classification of families mutated for plant height in M_2 generation

Treatment		Total families mutated (%)	Mutated families			
			total (No.)	with lower mean (%)	with unchanged mean (%)	with higher mean (%)
Control						
Gamma rays						
5 kR	LL	7.0	4	0.0	100.0	0.0
	LH	12.2	6	16.7	66.6	16.7
	HL	20.0	8	25.0	50.0	25.0
	HH	29.3	12	16.7	58.3	25.0
	Overall	16.0	30	16.7	63.3	20.0
10 kR	LL	11.8	10	10.0	80.0	10.0
	LH	15.9	11	9.0	72.7	18.2
	HL	24.0	12	16.7	58.3	25.0
	HH	26.5	18	16.7	55.6	27.8
	Overall	18.8	51	13.7	64.7	21.6
20 kR	LL	14.5	11	9.1	81.8	9.1
	LH	20.0	14	14.3	64.3	21.4
	HL	28.1	18	16.7	55.6	27.8
	HH	32.9	24	16.7	54.2	29.2
	Overall	23.7	67	14.9	61.2	23.9
EI						
0.005%	LL	13.0	6	16.7	66.7	16.7
	LH	13.8	8	12.5	75.0	12.5
	HL	20.4	10	20.0	60.0	20.0
	HH	22.0	13	23.1	46.2	30.8
	Overall	17.5	37	18.9	59.5	21.6
0.01%	LL	11.0	8	12.5	75.0	12.5
	LH	22.2	10	20.0	60.0	20.0
	HL	24.6	12	16.7	50.0	33.3
	HH	29.3	17	17.6	47.1	35.3
	Overall	19.7	47	17.0	55.3	27.7
0.02%	LL	13.7	10	30.0	60.0	10.0
	LH	21.8	12	25.0	50.0	25.0
	HL	25.0	14	21.4	50.0	28.6
	HH	29.6	16	18.8	50.0	31.3
	Overall	21.8	52	23.1	51.9	25.0
NEU						
0.005%	LL	13.0	6	16.7	66.7	16.7
	LH	16.4	9	22.2	55.6	22.2
	HL	19.2	10	20.0	50.0	30.0
	HH	27.5	11	27.3	45.5	27.3
	Overall	18.6	36	22.2	52.8	25.0
0.01%	LL	16.1	9	11.1	77.8	11.1
	LH	17.9	10	20.0	50.0	30.0
	HL	19.7	15	20.0	46.7	33.3
	HH	28.1	16	25.0	37.5	37.5
	Overall	20.4	50	20.0	50.0	30.0
0.02%	LL	17.7	14	14.3	71.4	14.3
	LH	21.1	16	18.8	56.2	25.0
	HL	25.6	20	15.0	60.0	25.0
	HH	27.6	21	19.0	42.9	38.1
	Overall	23.0	71	16.9	56.3	26.8

Appendix XXIII Classification of families mutated for total number of branches per plant in M_2 generation

Treatment		Total families mutated (%)	Mutated families			
			total (No.)	with lower mean (%)	with unchanged mean (%)	with higher mean (%)
Control		-	-	-	-	-
Gamma rays						
5 kR	LL	8.8	5	20.0	80.0	0.0
	LH	14.3	7	28.6	57.1	14.3
	HL	25.0	10	20.0	50.0	30.0
	HH	29.3	12	25.0	41.7	33.3
	Overall	18.2	34	23.5	52.9	23.5
10 kR	LL	11.8	10	20.0	60.0	20.0
	LH	17.4	12	16.7	58.3	25.0
	HL	24.0	12	25.0	50.0	25.0
	HH	27.9	19	21.1	47.4	31.6
	Overall	19.5	53	20.8	52.8	26.4
20 kR	LL	13.2	10	20.0	60.0	20.0
	LH	20.0	14	21.4	50.0	28.6
	HL	26.6	17	17.6	52.9	29.4
	HH	28.8	21	19.0	47.6	33.3
	Overall	21.9	62	19.4	51.6	29.0
EI						
0.005%	LL	13.0	6	16.7	66.7	16.7
	LH	15.5	9	11.1	66.7	22.2
	HL	20.4	10	20.0	60.0	20.0
	HH	27.1	16	18.8	50.0	31.3
	Overall	19.3	41	17.1	58.5	24.4
0.01%	LL	13.7	10	20.0	60.0	20.0
	LH	23.6	13	15.4	61.5	23.1
	HL	26.8	11	27.3	36.4	36.4
	HH	29.0	20	15.0	45.0	40.0
	Overall	22.7	54	18.5	50.0	31.5
0.02%	LL	15.1	11	18.2	63.6	18.2
	LH	23.6	13	23.1	53.8	23.1
	HL	26.8	15	20.0	46.7	33.3
	HH	33.3	18	27.8	33.3	38.9
	Overall	23.9	57	22.8	50.0	29.8
NEU						
0.005%	LL	13.0	6	16.7	66.7	16.7
	LH	18.2	10	20.0	60.0	20.0
	HL	23.1	12	16.7	58.3	25.0
	HH	35.0	14	21.4	35.7	42.9
	Overall	21.8	42	19.0	52.4	28.6
0.01%	LL	19.6	11	18.2	63.6	18.2
	LH	23.2	13	15.4	61.5	23.1
	HL	23.7	18	22.2	38.9	38.9
	HH	26.3	15	26.7	26.7	46.7
	Overall	23.3	57	21.0	45.6	33.3
0.02%	LL	20.3	16	18.8	62.5	18.8
	LH	22.4	17	23.5	52.9	23.5
	HL	26.9	21	19.0	47.6	33.3
	HH	31.6	24	16.7	45.8	37.5
	Overall	25.2	78	19.2	51.3	29.5

Appendix XXIV Classification of families mutated for effective clusters per plant in M_2 generation

Treatment		Total families mutated (%)	Mutated families			
			total (No.)	with lower mean (%)	with unchanged mean (%)	with higher mean (%)
Control		-	-	-	-	-
Gamma rays						
5 kR	LL	14.0	8	12.5	75.0	12.5
	LH	20.4	10	20.0	60.0	20.0
	HL	27.5	11	18.2	45.5	36.4
	HH	31.7	13	15.4	46.2	38.5
	Overall	22.5	42	16.7	54.8	28.6
10 kR	LL	16.5	14	28.6	64.3	21.4
	LH	21.7	15	13.3	60.0	26.7
	HL	30.0	15	20.0	46.7	33.3
	HH	32.4	22	18.2	45.5	36.4
	Overall	24.3	66	16.7	53.0	30.3
20 kR	LL	17.1	13	15.4	61.5	23.1
	LH	24.3	17	17.6	52.9	29.4
	HL	29.7	19	15.8	47.4	36.8
	HH	31.5	23	17.4	43.5	39.1
	Overall	25.4	72	16.7	50.0	33.3
EI						
0.005%	LL	19.6	9	11.1	66.7	22.2
	LH	20.7	12	8.3	66.7	25.0
	HL	26.5	13	23.1	46.2	30.8
	HH	28.8	17	23.5	50.9	41.2
	Overall	24.1	51	17.6	50.9	31.4
0.01%	LL	16.4	12	8.3	66.7	25.0
	LH	27.3	15	13.3	53.3	33.3
	HL	31.7	13	23.1	30.8	46.2
	HH	33.3	23	21.7	30.4	47.8
	Overall	26.5	63	17.5	42.9	39.7
0.02%	LL	19.2	14	14.3	64.3	21.4
	LH	27.3	15	13.3	53.3	33.3
	HL	30.4	17	23.5	41.2	35.3
	HH	38.9	21	28.6	28.6	42.9
	Overall	28.2	67	20.9	44.8	34.3
NEU						
0.005%	LL	19.6	9	0.0	77.8	22.2
	LH	21.8	12	16.7	50.0	33.3
	HL	26.9	14	21.4	35.7	42.9
	HH	35.0	14	21.4	28.6	50.0
	Overall	25.4	49	16.3	44.9	38.8
0.01%	LL	23.2	13	15.4	53.8	30.8
	LH	26.8	15	13.3	46.7	40.0
	HL	27.6	21	19.0	38.1	42.9
	HH	33.3	19	21.0	31.6	47.4
	Overall	27.8	68	17.6	41.2	41.2
0.02%	LL	25.3	20	15.0	50.0	35.0
	LH	27.6	21	14.3	47.6	38.1
	HL	32.1	25	16.0	44.0	40.0
	HH	35.5	27	14.8	40.7	44.4
	Overall	30.1	93	15.1	45.2	39.8

Appendix XXV Classification of families mutated for pods per plant in M_2 generation

Treatment		Total families mutated (%)	Mutated families			
			total (No.)	with lower mean (%)	with unchanged mean (%)	with higher mean (%)
Control		-	-	-	-	-
Gamma rays						
5 kR	LL	17.5	10	10.0	70.0	20.0
	LH	22.4	11	18.2	54.5	27.3
	HL	37.5	15	13.3	53.3	33.3
	HH	41.5	17	17.6	47.1	35.3
	Overall	28.3	53	15.1	54.7	30.2
10 kR	LL	23.5	20	10.0	70.0	20.0
	LH	26.1	18	16.7	55.6	27.8
	HL	36.0	18	16.7	50.0	33.3
	HH	38.2	26	19.2	38.5	42.3
	Overall	30.1	82	15.9	52.4	31.7
20 kR	LL	21.1	16	12.5	56.3	31.3
	LH	30.0	21	14.3	52.4	33.3
	HL	37.5	24	16.7	50.0	33.3
	HH	38.4	28	21.4	42.9	35.7
	Overall	31.4	89	16.9	49.4	33.7
EI						
0.005%	LL	26.1	12	8.3	66.7	25.0
	LH	24.1	14	14.3	57.1	28.6
	HL	30.6	15	20.0	46.7	33.3
	HH	35.6	21	19.0	42.9	38.1
	Overall	29.2	62	16.1	51.6	32.3
0.01%	LL	21.9	16	12.5	56.3	31.3
	LH	34.5	19	10.5	57.9	31.6
	HL	41.5	17	17.6	41.2	41.2
	HH	37.7	26	11.5	46.1	42.3
	Overall	32.8	78	12.8	50.0	37.2
0.02%	LL	24.7	18	11.1	66.7	22.2
	LH	34.5	19	15.8	52.6	31.6
	HL	39.3	22	18.2	40.9	40.9
	HH	44.4	24	16.7	41.7	41.7
	Overall	34.9	83	15.7	49.4	34.9
NEU						
0.005%	LL	23.9	11	9.1	72.7	18.2
	LH	25.5	14	14.3	57.1	28.6
	HL	30.8	16	18.8	43.8	37.5
	HH	45.0	18	16.7	38.9	44.4
	Overall	30.6	59	15.3	50.8	33.9
0.01%						
	LL	30.4	17	11.8	52.9	35.3
	LH	33.9	19	10.5	52.6	36.8
	HL	31.6	24	20.8	41.7	37.5
	HH	38.6	22	18.2	36.4	45.5
	Overall	33.5	82	15.9	45.1	39.0
0.02%	LL	31.6	25	12.0	56.0	32.0
	LH	32.9	25	12.0	52.0	36.0
	HL	38.5	30	16.7	46.7	36.7
	HH	42.1	32	18.8	40.6	40.6
	Overall	36.2	112	15.2	48.2	36.7

Appendix XXVI Classification of families mutated for seeds per pod in M_2 generation

Treatment		Total families mutated (%)	Mutated families			
			total (No.)	with lower mean (%)	with unchanged mean (%)	with higher mean (%)
Control		-	-	-	-	-
Gamma rays						
5 kR	LL	5.3	3	0.0	100.0	0.0
	LH	8.2	4	0.0	100.0	0.0
	HL	12.5	5	20.0	60.0	20.0
	HH	14.6	6	33.3	16.7	50.0
	Overall	9.6	18	16.7	61.1	22.2
10 kR	LL	5.9	5	0.0	100.0	0.0
	LH	10.1	7	14.3	57.1	28.6
	HL	14.0	7	28.6	42.9	28.6
	HH	14.7	10	20.0	50.0	30.0
	Overall	10.7	29	17.2	58.6	24.1
20 kR	LL	6.6	5	0.0	100.0	0.0
	LH	11.4	8	12.5	75.0	12.5
	HL	14.1	9	22.2	44.4	33.3
	HH	16.4	12	25.0	33.3	41.7
	Overall	12.0	34	17.6	55.9	26.5
EI						
0.005%	LL	8.7	4	0.0	100.0	0.0
	LH	8.6	5	20.0	60.0	20.0
	HL	12.2	6	16.7	66.7	16.7
	HH	13.6	8	25.0	37.5	37.5
	Overall	10.8	23	17.4	60.9	21.7
0.01%	LL	6.8	5	20.0	60.0	20.0
	LH	10.9	6	16.7	66.7	16.7
	HL	14.6	6	16.7	50.0	33.3
	HH	17.4	12	16.7	41.7	41.7
	Overall	12.2	29	17.2	51.7	31.0
0.02%	LL	9.6	7	14.3	71.4	14.3
	LH	12.7	7	14.3	71.4	14.3
	HL	16.1	9	22.2	44.4	33.3
	HH	18.5	10	30.0	30.0	40.0
	Overall	13.9	33	21.2	51.5	27.3
NEU						
0.005%	LL	6.5	3	0.0	100.0	0.0
	LH	9.1	5	20.0	60.0	20.0
	HL	11.5	6	16.7	50.0	33.3
	HH	20.0	8	25.0	37.5	37.5
	Overall	11.4	22	18.2	54.5	27.3
0.01%	LL	10.7	6	0.0	83.3	16.7
	LH	12.5	7	14.3	57.1	28.6
	HL	13.2	10	30.0	30.0	40.0
	HH	17.5	10	30.0	30.0	40.0
	Overall	13.5	33	21.2	45.5	33.3
0.02%	LL	11.4	9	22.2	66.7	11.1
	LH	14.5	11	18.2	54.5	27.3
	HL	15.4	12	25.0	41.7	33.3
	HH	17.1	13	30.8	30.8	38.5
	Overall	14.6	45	24.4	46.7	28.9

Appendix XXVII Classification of families mutated for 100-seed weight in M_2 generation

Treatment		Total families mutated (%)	Mutated families			
			total (No.)	with lower mean (%)	with unchanged mean (%)	with higher mean (%)
Control		-	-	-	-	-
Gamma rays						
5 kR	LL	7.0	4	0.0	100.0	0.0
	LH	8.2	4	0.0	100.0	0.0
	HL	12.5	5	20.0	60.0	20.0
	HH	14.6	6	16.7	33.3	50.0
	Overall	10.2	19	10.5	68.4	21.1
10 kR	LL	7.1	6	0.0	100.0	0.0
	LH	11.6	8	12.5	62.5	25.0
	HL	14.0	7	28.6	42.9	28.6
	HH	16.2	11	18.2	45.5	36.4
	Overall	11.8	32	15.6	59.4	25.0
20 kR	LL	9.2	7	14.3	71.4	14.3
	LH	12.9	9	11.1	66.7	22.2
	HL	15.6	10	20.0	50.0	30.0
	HH	16.4	12	25.0	33.3	41.7
	Overall	13.4	38	18.4	52.6	28.9
EI						
0.005%	LL	8.7	4	0.0	100.0	0.0
	LH	8.6	5	20.0	60.0	20.0
	HL	12.2	6	16.6	50.0	33.3
	HH	15.3	9	11.1	55.5	33.3
	Overall	11.3	24	12.5	62.5	25.0
0.01%	LL	9.6	7	0.0	85.7	14.3
	LH	9.1	5	20.0	60.0	20.0
	HL	14.6	6	16.6	50.0	33.3
	HH	17.4	12	16.6	33.3	50.0
	Overall	12.6	30	13.3	53.3	33.3
0.02%	LL	9.6	7	14.3	71.4	14.3
	LH	14.5	8	25.0	50.0	25.0
	HL	17.9	10	20.0	40.0	40.0
	HH	18.5	10	30.0	30.0	40.0
	Overall	14.7	35	22.9	45.7	31.4
NEU						
0.005%	LL	6.5	3	33.3	66.7	0.0
	LH	10.9	6	16.7	66.7	16.7
	HL	15.4	8	12.5	62.5	25.0
	HH	20.0	8	12.5	50.0	37.5
	Overall	13.0	25	16.0	60.0	24.0
0.01%	LL	10.7	6	16.7	66.6	16.7
	LH	14.3	8	12.5	62.5	25.0
	HL	15.8	12	16.7	41.7	41.7
	HH	19.3	11	18.2	36.4	45.5
	Overall	15.1	37	16.2	48.6	35.1
0.02%	LL	12.7	10	10.0	70.0	20.0
	LH	15.8	12	8.3	58.3	33.3
	HL	17.9	14	7.1	57.1	35.7
	HH	19.7	15	20.0	40.0	40.0
	Overall	16.5	51	11.8	54.9	33.3

Appendix XXVIII Classification of families mutated for seed yield per plant in M_2 generation

Treatment		Total families mutated (%)	Mutated families			
			total (No.)	with lower mean (%)	with unchanged mean (%)	with higher mean (%)
Control		-	-	-	-	-
Gamma rays						
5 kR	LL	15.8	9	11.1	77.8	11.1
	LH	20.4	10	20.0	60.0	20.0
	HL	32.5	13	23.1	38.5	38.5
	HH	36.6	15	20.0	40.0	40.0
	Overall	25.1	47	19.1	51.1	29.8
10 kR	LL	20.0	17	11.8	70.6	17.6
	LH	23.2	16	18.8	56.3	25.0
	HL	34.0	17	17.6	47.1	35.3
	HH	35.3	24	20.8	37.5	41.7
	Overall	27.2	74	17.6	51.4	31.1
20 kR	LL	18.4	14	14.3	57.1	28.6
	LH	27.1	19	15.8	52.6	31.6
	HL	34.4	22	18.2	45.5	36.4
	HH	35.6	26	19.2	42.3	38.5
	Overall	28.6	81	17.3	48.1	34.6
EI						
0.005%	LL	21.7	10	10.0	70.0	20.0
	LH	20.7	12	16.7	58.3	25.0
	HL	26.5	13	23.1	46.2	30.8
	HH	32.2	19	21.1	36.8	42.1
	Overall	25.5	54	18.5	50.0	31.5
0.01%	LL	19.2	14	7.1	64.3	28.6
	LH	29.1	16	18.8	43.8	37.5
	HL	34.1	14	21.4	35.7	42.9
	HH	33.3	23	21.7	30.4	47.8
	Overall	28.2	67	17.9	41.8	40.3
0.02%	LL	20.5	15	20.0	60.0	20.0
	LH	29.1	16	18.8	50.0	31.3
	HL	32.1	18	22.2	38.9	38.9
	HH	38.9	21	23.8	28.6	47.6
	Overall	29.4	70	21.4	42.9	35.7
NEU						
0.005%	LL	21.7	10	10.0	70.0	20.0
	LH	23.6	13	15.4	61.5	23.1
	HL	28.8	15	13.3	46.4	40.0
	HH	42.5	17	23.5	35.3	41.1
	Overall	28.5	55	16.4	50.9	32.7
0.01%	LL	28.6	16	12.5	56.3	31.3
	LH	30.4	17	11.8	47.1	41.2
	HL	30.3	23	21.7	34.8	43.5
	HH	35.1	20	20.0	30.0	50.0
	Overall	31.0	76	17.1	40.8	42.1
0.02%	LL	27.8	22	13.6	59.1	27.3
	LH	30.3	23	17.4	47.8	34.8
	HL	35.9	28	17.9	42.9	39.3
	HH	39.5	30	20.0	33.3	46.7
	Overall	33.3	103	17.5	44.7	37.9

Appendix XXIX Percentage of mutated families for different characters in M_2 generation

Treatment	Percentage of mutated families for							
	days to maturity	plant height	branches/plant	clusters/plant	pods/plant	seeds/pod	100-seed weight	seed yield/ plant
Control	-	-	-	-	-	-	-	-
Gamma rays								
5 kR	17.6	16.0	18.2	22.5	28.3	9.6	10.2	25.1
10 kR	19.9	18.8	19.5	24.3	30.1	10.7	11.8	27.2
20 kR	21.6	23.7	21.9	25.4	31.4	12.0	13.4	28.6
Overall	19.7	19.5	19.9	24.1	29.9	10.8	11.8	27.0
EI								
0.005%	18.4	17.5	19.3	24.1	29.2	10.8	11.3	25.5
0.01%	20.6	19.7	22.7	26.5	32.8	12.2	12.6	28.2
0.02%	23.1	21.8	23.9	28.2	34.9	13.9	14.7	29.4
Overall	20.7	19.7	22.0	26.3	32.3	12.3	12.9	27.7
NEU								
0.005%	21.2	18.6	21.8	25.4	30.6	11.4	13.0	28.5
0.01%	23.7	20.4	23.3	27.8	33.5	13.5	15.1	31.0
0.02%	24.9	23.0	25.2	30.1	36.2	14.6	16.5	33.3
Overall	23.3	20.7	23.4	27.8	33.4	13.2	14.9	30.9

Appendix XXX Percentage of mutated families in different groups of mutagenic damage for various characters in M_2 generation

Treatment		Percentage of mutated families for							
		days to maturity	plant height	branches/ plant	clusters/ plant	pods/plant	seeds/pod	100-seed weight	Yield/ plant
Control		-	-	-	-	-	-	-	-
Gamma rays									
5 kR	LL	7.0	7.0	8.8	14.0	17.5	5.3	7.0	15.8
	LH	14.3	12.2	14.3	20.4	22.4	8.2	8.2	20.4
	HL	20.0	20.0	25.0	27.5	37.5	12.5	12.5	32.5
	HH	34.1	29.3	29.3	31.7	41.5	14.6	14.6	36.6
	Overall	17.6	16.0	18.2	22.5	28.3	9.6	10.2	25.1
10 kR	LL	10.6	11.8	11.8	16.5	23.5	5.9	7.1	20.0
	LH	15.9	15.9	17.4	21.7	26.1	10.1	11.6	23.5
	HL	28.0	24.0	24.0	30.0	36.0	14.0	14.0	34.0
	HH	29.4	26.5	27.9	32.4	38.2	14.7	16.2	35.3
	Overall	19.9	18.8	19.5	24.3	30.1	10.7	11.8	27.2
20 kR	LL	13.2	14.5	13.2	17.1	21.1	6.6	9.2	18.4
	LH	18.6	20.0	20.0	24.3	30.0	11.4	12.9	27.1
	HL	25.0	28.1	26.6	29.7	37.5	14.1	15.6	34.4
	HH	30.1	32.9	28.8	31.5	38.4	16.4	16.4	35.6
	Overall	21.6	23.7	21.9	25.4	31.4	12.0	13.4	28.6
EI									
0.005%	LL	13.0	13.0	13.0	19.6	26.1	8.7	8.7	21.7
	LH	13.8	13.8	15.5	20.7	24.1	8.6	8.6	20.7
	HL	20.4	20.4	20.4	26.5	30.6	12.2	12.2	26.5
	HH	25.4	22.0	27.1	28.8	35.6	13.6	15.3	32.2
	Overall	18.4	17.5	19.3	24.1	29.2	10.8	11.3	25.5
0.01%	LL	11.0	11.0	13.7	16.4	21.9	6.8	9.6	19.2
	LH	18.2	22.2	23.6	27.3	34.5	10.9	9.1	29.1
	HL	26.8	24.6	26.8	31.7	41.5	14.6	14.6	34.1
	HH	29.0	29.3	29.0	33.3	37.7	17.4	17.4	33.3
	Overall	20.6	19.7	22.7	26.5	32.8	12.2	12.6	28.2
0.02%	LL	12.3	13.7	15.1	19.2	24.7	9.6	9.6	20.5
	LH	23.6	21.8	23.6	27.3	34.5	12.7	14.5	29.1
	HL	26.8	25.0	26.8	30.4	39.3	16.1	17.9	32.1
	HH	33.3	29.6	33.3	38.9	44.4	18.5	18.5	38.9
	Overall	23.1	21.8	23.9	28.2	34.9	13.9	14.7	29.4
NEU									
0.005%	LL	15.2	13.0	13.0	19.6	23.9	6.5	6.5	21.7
	LH	18.2	16.4	18.2	21.8	25.5	9.1	10.9	23.6
	HL	23.1	19.2	23.1	26.9	30.8	11.5	15.4	28.8
	HH	30.0	27.5	35.0	35.0	45.0	20.0	20.0	42.5
	Overall	21.2	18.6	21.8	25.4	30.6	11.4	13.0	28.5
0.01%	LL	19.6	16.1	19.6	23.2	30.4	10.7	10.7	28.6
	LH	21.4	17.9	23.2	26.8	33.9	12.5	14.3	30.4
	HL	22.4	19.7	23.7	27.6	31.6	13.2	15.8	30.3
	HH	31.6	28.1	26.3	33.3	38.6	17.5	19.3	35.1
	Overall	23.7	20.4	23.3	27.8	33.5	13.5	15.1	31.0
0.02%	LL	19.0	17.7	20.3	25.3	31.6	11.4	12.7	27.8
	LH	22.4	21.1	22.4	27.6	32.9	14.5	15.8	30.3
	HL	28.2	25.6	26.9	32.1	38.5	15.4	17.9	35.9
	HH	30.3	27.6	31.6	35.5	42.1	17.1	19.7	39.5
	Overall	24.9	23.0	25.2	30.1	36.2	14.6	16.5	33.3

Appendix XXXI : X^2 values for different characters in various populations in M_2 generation

Treatment		Days to maturity	Plant height	Fruiting branches/ plant	Clusters/ plant	Pods/ plant	Seeds/ pod	100-seed weight	Seed yield/ plant
Control		34.9	39.4	44.3	56.1	67.7	26.5	47.8	70.1
Gamma rays :									
5 kR :	LL	65.3**	55.1**	77.3**	78.6**	103.9**	52.7*	66.6*	91.3*
	LH	97.0**	73.9**	97.1**	103.2**	128.6**	67.1**	80.4**	112.5**
	HL	111.2**	81.0**	106.2**	112.8**	145.5**	73.7**	81.5**	128.8**
	HH	115.4**	94.7**	110.2**	120.7**	147.2**	93.8**	88.0**	139.6**
10 kR :	LL	70.2**	78.6**	81.5**	84.4**	105.6**	53.9*	73.4**	94.8**
	LH	99.0**	80.4**	103.4**	108.6**	132.9**	79.4**	106.5**	120.2**
	HL	114.8**	94.1**	112.2**	119.9**	149.5**	90.9**	110.2**	134.5**
	HH	121.5**	105.3**	120.6**	128.5**	152.6**	100.4**	139.4**	144.6**
20 kR :	LL	79.9**	79.9**	89.6**	93.8**	111.2**	56.7*	114.8**	97.2**
	LH	105.6**	83.2**	109.0**	114.7**	134.9**	83.2**	129.1**	125,8**
	HL	119.0**	101.4**	118.4**	122.5**	151.7**	98.3**	131.1**	139.3**
	HH	127.0**	113.8**	133.8**	137.6**	156.3**	109.6**	142.0**	148.6**
EI :									
0.005% :	LL	78.5**	69.3**	80.5**	88.7**	110.6**	59.5*	77.5*	102.5*
	LH	99.4**	77.6**	101.8**	110.5**	135.2**	63.2**	85.8**	118.2**
	HL	114.2**	87.5**	113.2**	123.4**	149.7**	82.8**	99.2**	134.3**
	HH	118.9**	103.2**	122.6**	135.8**	157.8**	113.4**	113.6**	145.7**
0.01% :	LL	82.6**	84.6**	97.2**	99.8**	119.7**	77.2**	121.6**	114.5**
	LH	108.9**	92.2**	115.4**	121.6**	146.2**	89.4**	137.2**	132.8**
	HL	124.6**	108.4**	126.7**	132.5**	156.9**	107.3**	142.8**	145.6**
	HH	135.2**	117.5**	139.5**	146.2**	169.5**	134.7**	149.3**	158.3**
0.02% :	LL	80.3**	81.5**	93.7**	95.1**	121.8**	75.6*	117.7**	108.1**
	LH	104.6**	87.6**	112.1**	117.9**	143.2**	91.3**	132.3**	128.5**
	HL	118.5**	104.2**	121.9**	130.6**	158.5**	105.5**	138.5**	143.6**
	HH	126.7**	115.4**	135.4**	147.8**	165.3**	131.9**	146.2**	154.3**
NEU :									
0.005% :	LL	85.2**	73.5**	89.7**	96.8**	118.5**	75.3**	80.0**	111.3**
	LH	104.6**	81.3**	106.3**	118.5**	143.6**	83.5**	91.2**	126.8**
	HL	119.4**	92.7**	117.5**	131.7**	155.8**	95.5**	105.4**	139.3**
	HH	124.7**	104.9**	128.6**	143.3**	159.2**	115.2**	116.7**	151.7**
0.01% :	LL	92.2**	81.8**	104.3**	110.3**	129.1**	80.6*	129.2**	125.8**
	LH	111.6**	90.7**	121.6**	128.2**	151.8**	97.7**	143.7**	139.3**
	HL	126.5**	102.4**	132.8**	139.6**	166.2**	113.5**	151.3**	153.4**
	HH	133.6**	115.2**	146.6**	153.4**	177.6**	135.2**	157.5**	165.8**
0.02% :	LL	88.3**	76.9**	97.9**	113.6**	138.6**	81.9*	125.5**	117.8**
	LH	108.2**	86.5**	119.3**	125.0**	150.2**	96.9**	137.6**	133.6**
	HL	123.6**	95.7**	134.6**	137.3**	160.3**	110.3**	146.8**	150.5**
	HH	129.5**	110.2**	150.5**	150.8**	170.5**	128.2**	155.2**	166.7**

*,** = Significant at 5% and 1%, respectively.

Appendix XXXII : Percentage of promising families for various characters in different treatments in M_2 generation

Treatment		Days to maturity	Plant height	Branches/ plant	Clusters/ plant	Pod/ plant	Seeds/ pod	100-seed weight	Seed yield/ plant
Control		-	-	-	-	-	-	-	-
Gamma rays:									
5 kR:	LL	0.0	0.0	0.0	1.8	3.5	0.0	0.0	1.8
	LH	2.0	2.0	2.0	4.1	6.1	0.0	0.0	4.1
	HL	5.0	5.0	7.5	10.0	12.5	2.5	2.5	12.5
	HH	12.2	7.3	9.8	12.2	14.6	7.3	7.3	14.6
	Overall	4.3	3.2	4.3	6.4	8.6	2.1	2.1	7.5
10 kR:	LL	1.2	1.2	2.4	3.5	4.7	0.0	0.0	3.5
	LH	4.3	2.9	4.3	5.8	7.2	2.9	2.9	5.8
	HL	8.0	6.0	6.0	10.0	12.0	4.0	4.0	12.0
	HH	8.8	7.4	8.8	11.8	16.2	4.4	5.9	14.7
	Overall	5.1	4.0	5.1	7.4	9.6	2.6	2.9	8.5
20 kR:	LL	2.6	1.3	2.6	3.9	6.6	0.0	1.3	5.3
	LH	5.7	4.3	5.7	7.1	10.0	1.4	2.9	8.6
	HL	7.8	7.8	7.8	10.9	12.5	4.7	4.7	12.5
	HH	9.6	9.6	9.6	12.3	13.7	6.8	6.8	13.7
	Overall	6.4	5.7	6.4	8.5	10.6	3.2	3.9	9.9
EI:									
0.005% :	LL	0.0	2.2	2.2	4.3	6.5	0.0	0.0	4.3
	LH	3.4	1.7	3.4	5.2	6.9	1.7	1.7	5.2
	HL	6.1	4.1	4.1	8.2	10.2	2.0	4.1	8.2
	HH	8.5	6.8	8.5	11.9	13.6	5.1	5.1	13.6
	Overall	4.7	3.8	4.7	7.5	9.4	2.4	2.8	8.0
0.01% :	LL	1.4	1.4	2.7	4.1	6.8	1.4	1.4	5.5
	LH	5.5	3.6	5.5	9.1	10.9	1.8	1.8	10.9
	HL	9.8	9.8	9.8	14.6	17.1	4.9	4.9	14.6
	HH	11.6	8.7	11.6	15.9	15.9	7.2	8.7	15.9
	Overall	6.7	5.5	7.1	10.5	12.2	3.8	4.2	11.3
0.02% :	LL	2.7	1.4	2.7	4.1	5.5	1.4	1.4	4.1
	LH	5.5	5.5	5.5	9.1	10.9	1.8	3.6	9.1
	HL	8.9	7.1	8.9	10.7	16.1	5.4	7.1	12.5
	HH	13.0	9.3	13.0	16.7	18.5	7.4	7.4	18.5
	Overall	7.1	5.5	7.1	9.7	12.2	3.8	4.6	10.5
NEU :									
0.005% :	LL	2.2	2.2	2.2	4.3	4.3	0.0	0.0	4.3
	LH	3.6	3.6	3.6	7.3	7.3	1.8	1.8	5.5
	HL	7.7	5.8	5.8	11.5	11.5	3.8	3.8	11.5
	HH	12.5	7.5	15.0	17.5	20.0	7.5	7.5	17.5
	Overall	6.2	4.7	6.2	9.8	10.4	3.1	3.1	9.3
0.01% :	LL	3.6	1.8	3.6	7.1	10.7	1.8	1.8	8.9
	LH	7.1	5.4	5.4	10.7	12.5	3.6	3.6	12.5
	HL	7.9	6.6	9.2	11.8	11.8	5.3	6.6	13.2
	HH	14.0	10.5	12.3	15.8	17.5	7.0	8.8	17.5
	Overall	8.2	6.1	7.8	11.4	13.1	4.5	5.3	13.1
0.02%	LL	5.1	2.5	3.8	8.9	10.1	1.3	2.5	7.6
	LH	6.6	5.3	5.3	10.5	11.8	3.9	5.3	10.5
	HL	9.0	6.4	9.0	12.8	14.1	5.1	6.4	14.1
	HH	10.5	10.5	11.8	15.8	17.1	6.6	7.9	18.4
	Overall	7.8	6.1	7.4	12.0	13.3	4.2	5.5	12.6

Appendix XXXIII: Block effects in augmented block design for different characters in M_3 generation

Block No.	Characters							
	Days to maturity	Plant height	Fruiting branches/ plant	Effective clusters / plant	Effective pods/plant	Seeds/ pod	100-seed weight	Seed yield/ plant
1	-0.08	-1.53	-0.56	-1.82	-5.09	-0.05	0.14	-0.01
2	1.98	-2.73	-4.73	-20.35	-29.29	-0.08	0.20	-0.87
3	0.38	-0.47	-1.30	2.05	-1.89	-0.03	0.26	0.32
4	-0.59	-2.53	-3.32	-9.31	-15.71	0.01	0.02	-0.27
5	3.65	1.27	3.50	15.85	16.38	-0.02	-0.03	0.64
6	-2.68	-1.20	1.37	-1.08	-0.09	-0.07	-0.33	-0.03
7	-1.62	3.10	3.70	19.25	27.08	0.08	-0.05	0.95
8	-2.24	1.34	5.23	-2.75	2.24	-0.09	-0.30	-0.45
9	0.45	-0.40	-2.43	-0.75	-2.69	0.02	0.34	0.07
10	0.18	-0.66	-2.23	2.32	0.11	-0.06	0.34	0.60
11	0.38	0.54	-2.29	3.78	10.51	-0.06	-0.03	0.09
12	2.72	2.09	2.44	12.25	5.20	-0.02	0.15	0.97
13	-0.95	3.37	-1.08	-2.98	8.98	0.16	0.26	0.57
14	-0.35	0.50	0.97	-1.15	7.38	0.09	0.04	0.46
15	0.52	6.14	0.57	17.92	45.98	-0.01	-0.04	0.76
16	0.35	4.88	5.87	22.91	50.87	0.08	0.24	1.15
17	-4.13	-4.11	-5.90	-19.04	-30.99	-0.18	-0.53	-1.06
18	-2.88	1.00	-0.76	5.45	7.51	-0.14	-0.19	-0.05
19	-2.20	0.95	-2.51	-4.12	1.08	-0.05	-0.24	-0.19
20	-3.88	-0.65	-1.06	2.07	4.87	-0.23	-0.07	0.01
21	0.05	-1.60	1.44	-7.02	-13.49	-0.04	0.18	-0.28
22	-1.68	-1.60	-0.56	2.12	1.11	-0.12	0.50	-0.18
23	0.38	-0.26	0.60	-1.92	-3.22	-0.09	0.25	-0.30
24	1.15	-0.59	-0.60	1.15	-4.29	0.04	0.29	0.07
25	-3.75	0.85	-2.43	-4.02	4.71	0.08	0.01	0.01
26	-1.62	1.80	1.84	-1.95	-3.56	0.10	-0.32	-0.26
27	-2.02	-0.59	-2.03	-7.15	-9.42	-0.02	-0.40	-0.62
28	-2.24	2.13	1.19	-0.68	2.71	0.17	-0.06	0.95
29	0.85	0.34	-0.23	6.25	2.44	0.21	0.34	0.58
30	0.85	-0.39	-1.90	-2.48	-9.09	0.10	0.10	-0.32
31	5.32	3.40	1.70	20.85	33.84	0.28	0.38	1.91
32	3.45	1.40	-1.36	4.65	4.18	-0.02	0.41	0.71
33	5.98	0.54	0.10	-2.22	18.98	-0.03	-0.14	-0.29
34	6.38	2.80	1.44	22.92	29.31	-0.04	0.01	0.93
35	9.32	2.34	0.97	13.65	22.51	-0.01	0.69	1.06
36	7.05	0.63	1.95	17.38	30.89	0.02	-0.13	0.89
37	3.07	-4.63	2.30	-6.18	-10.32	-0.06	-0.65	-0.71
38	1.78	-2.46	2.10	-5.22	-11.22	-0.11	-0.50	-0.67
39	3.18	-3.43	-0.26	-14.88	-22.39	-0.17	-0.85	-1.10
40	4.03	-2.95	-0.19	-5.24	-13.51	-0.01	-0.43	-0.67
41	-0.22	3.94	-0.70	-2.48	-1.16	-0.08	0.11	-0.24
42	0.52	1.47	-1.26	-0.28	0.08	0.01	-0.04	-0.12
43	0.38	2.47	-0.96	0.85	-3.16	-0.06	0.06	-0.07
44	-0.59	3.37	-1.30	0,98	1.60	-0.02	-0.04	-0.18
45	-7.95	-0.13	-0.10	3.98	17.91	-0.06	-0.48	0.18

Contd..

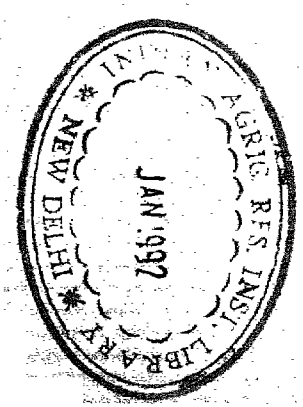
(Appendix XXXIII .....)

Block No.	Characters							
	Days to maturity	Plant height	Fruiting branches/ plant	Effective clusters/ plant	Effective pods/plant	Seeds/ pod	100-seed weight	Seed yield/ plant
46	-7.82	1.60	-0.43	0.45	4.38	-0.04	-0.07	-0.08
47	-8.02	-0.66	3.50	-0.15	4.36	-0.06	-0.03	-0.19
48	-7.82	-0.60	2.37	5.58	1.33	-0.13	-0.07	-0.21
49	-0.13	0.07	3.37	5.28	3.94	0.06	0.01	0.26
50	0.18	-2.00	0.10	-0.68	4.02	-0.06	-0.10	-0.30
51	0.45	-2.73	0.87	-1.43	-1.09	-0.04	0.10	-0.11
52	-0.22	-0.49	-1.14	-1.24	1.51	-0.07	0.07	-0.19
53	-2.35	-2.66	-0.10	2.98	-6.69	-0.01	-0.10	-0.59
54	1.35	-2.53	-1.03	-14.82	-24.76	-0.06	0.45	-0.86
55	1.85	-0.46	0.24	-9.01	-16.29	0.15	-0.08	-0.41
56	5.76	-1.37	0.21	2.92	-6.36	-0.05	-0.12	-0.13
57	3.43	-0.50	1.49	6.50	7.41	-0.09	-0.08	0.16
58	5.95	-1.70	2.04	-5.08	12.72	-0.09	0.35	-0.32
59	2.45	-0.66	2.37	-0.75	-2.82	-0.08	0.45	-0.07
60	2.62	-2.36	1.57	6.27	7.39	-0.05	0.38	0.27
61	-0.88	0.01	-2.03	-2.75	-2.49	0.01	-0.09	-0.22
62	-2.95	3.00	2.37	-0.55	-2.09	-0.05	-0.21	-0.10
63	-2.88	3.74	2.64	4.65	4.58	0.06	-0.19	0.10
64	-2.15	1.96	-3.03	-8.50	-11.42	0.02	-0.09	-0.56
65	-3.62	1.20	2.10	5.18	12.57	0.07	0.15	0.57
66	-5.62	1.47	-2.16	-4.15	-3.29	-0.06	0.25	0.04
67	-4.18	-0.01	-2.61	-14.75	-19.19	-0.13	0.30	-0.51
68	-4.22	0.91	4.30	15.25	11.93	0.11	0.18	1.00
69	-2.52	-3.33	2.10	-6.82	-6.56	0.03	-0.49	-0.63
70	-0.15	-2.66	-1.30	-14.42	-19.89	0.06	-0.48	-0.86
71	-0.48	-3.20	1.17	-10.55	-15.89	-0.04	-0.44	-0.74
72	0.78	-4.93	-1.03	-17.35	-24.16	-0.06	-0.16	-0.87
73	2.78	0.20	-3.36	-0.42	-4.82	0.22	0.36	0.43
74	2.78	-2.33	-2.83	-0.08	-4.02	0.18	-0.01	0.17
75	-0.55	-1.73	-2.09	-8.15	16.89	0.20	0.02	-0.23
76	-2.40	2.14	-3.46	0.01	-7.16	0.12	0.35	0.23
77	-1.35	1.80	-1.10	-2.08	6.91	0.15	0.10	0.48
78	2.58	-1.33	-1.10	-2.68	-5.36	0.19	0.08	0.12
79	6.98	0.47	-1.36	-2.55	-4.82	0.18	0.74	0.34

APPENDIX – XXXIV

Different SE and CD values for various characters in augmented block design

Parameters	Characters							
	Days to maturity	Plant height	Fruiting branches/ plant	Effective peduncles/ plant	Effective pods/ plant	Seeds/ pod	100-seed weight	Seed yield/ plant
SE_1	0.54	0.42	0.43	1.29	1.89	0.02	0.07	0.08
CD_1	1.08	0.84	0.86	2.58	3.78	0.04	0.14	0.16
SE_2	4.82	3.71	3.82	11.50	16.76	0.14	0.63	0.68
CD_2	9.64	7.42	7.64	23.00	33.52	0.28	1.26	1.36
SE_3	5.55	4.28	4.41	13.26	19.33	0.16	0.73	0.78
CD_3	11.1	8.56	8.82	26.52	38.66	0.32	1.46	1.56
SE_4	3.96	3.05	3.14	9.45	13.77	0.12	0.52	0.56
CD_4	7.92	6.10	6.28	18.90	27.54	0.24	1.04	1.12



Where, SE_1 is the standard error between two check variety means

SE_2 is the standard error between two progenies means when both are in the same block

SE_3 is the standard error between two new varieties' means when they are in different blocks

SE_4 is the standard error between a check variety and a new variety means