Genetic Analysis of Induced Polygenic Variation In Microsperma And Macrosperma Lentils (Lens culinaris Medik.)

THESIS

by

Mohinder Pal Sood

Submitted to the Himachal Pradesh Krishi Vishva Vidyalaya in partial fulfilment of the requirements for the degree of

DOCTOR OF PHILOSOPHY

in

PLANT BREEDING

DEPARTMENT OF PLANT BREEDING,
COLLEGE OF AGRICULTURE,
HIMACHAL PRADESH KRISHI VISHVA VIDYALAYA,
PALAMPUR

1983

DEDICATED
TO
PARENTS

"Concern for man himself and his fate must always form the chief interest of all technical endevaours in order that the creation of our minds shall be a blessing and not a curse"

—Albert Einestein

C E R T I F I C A T E I

This is to certify that the thesis entitled " Genetic analysis of induced polygenic variation in microsperma and macrosperma lentil(Lens culinaris Medik.)" submitted in partial fulfilment of the requirements for the award of the degree of DOCTOR OF PHILOSOPHY IN AGRICULTURE (PLANT BREEDING) of Himachal Pradesh Krishi Vishva Vidyalaya, Palampur, is a record of bonafide research carried out by Shri Mohinder Pal Sood under my supervision and no part of the thesis has been submitted for any other degree or diploma.

The assistance and help received during the course of investigation have been fully acknowledged.

(V.P.GUPTA)
Associate Professor
Department of Plant Breeding
H.P. Krishi Vishva Vidyalaya
Palampur-176062 H.P. India

Place: Palampur
Date : 30.8.83

C E R T I F I C A T E II

This is to certify that the thesis entitled, " Genetic analysis of induced polygenic variation in microsperma and macrosperma lentils(Lens culinaris Medik.)" submitted by Shri Mohinder Pal Sood to the Himachal Pradesh Krishi Vishva Vidyalaya, Palampur in partial fulfilment of the requirements of the degree of DOCTOR OF PHILOSOPHY IN AGRICULTURE (PLANT BREEDING) has been approved by the student's advisory committee after an oral examination of the same in collaboration with an external examiner.

22/11/83

Major Advisor

External Examiner

Head of the Department

Dean
College of Agriculture

Dean
Post-graduate Studies

ACKNOWLEDGEMENTS

I steal this most cherished and sacred moment from moving wheel of time, when, with all the good words of dictionary, I acknowledge the grace and perspicacious agility of Dr.V.P.Gupta, Associate Professor, Department of Plant Breeding, Himachal Pradesh Krishi Vishva Vidyalaya, Palampur, Chairman of my advisory committee, for his painstaking pointer, utilitarian exhortation, constructive suggestions, unswerving encouragement and invoking in me the bestir to complete this project. His in-depth knowledge of subject, crisp and prudential scientific insight and humanitarian character were always a moving force behind my all achievements. I owe to him much more than I could care to admit.

My heart-felt thanks are due towards Dr. N.D.Rana, Plant Breeder (Oilseeds), Dr.R.C.Thakur, Associate Professor of Agronomy and Agrometeorology and Dr. G.L.Bansal, Assistant Plant Physiologist, esteemed members of my advisory committee for their constant help, guidance, encouragement and going through the manuscript very critically. I shall always remain thankful to Dr. D.S.Virk, Millet Breeder, Punjab Agricultural University, Ludhiana for extending valuable suggestions in genetic analysis and confirming the validity of certain new formula's proposed.

Grateful acknowledgements are due towards Indian Agricultural Statistical Research Institute, New Delhi, for extending computor facilities for analysing the research data. I am greatly indebted to Dr.K.D.Sharma, Professor and Head, Department of Plant Breeding, Dr.B.R.Tripathi, Dean, College of Agriculture and Dr. O.P.Awasthi, Dean Post Graduate Studies cum Director of Research, Himachal Pradesh Krishi Vishva Vidyalaya Palampur for providing me necessary research facilities and their constant humanitarian encouragement and help in so many ways throughout the course of this investigation.

I gratefully acknowledge, Indian Council of Agricultural Research for the award of Senior Research Fellowship under its Human Resources Development Programme, for the conduct of this study.

Time stops moving, when I think of acknowledging the nice company and unwavering help of my friends, Vinod, Rakesh, Rajinder, Kewal, Jagdish, Hans, Pardeep, Jeevan, Ravinder, Bhupinder, Kamlesh and Ms Sudershna Bhateria, who strengthened my resolve to complete this project and proved the veracity of my facts in various walks of life. Their memories shall always remain most valuable assets to me.

Words are incapable of translating my sincere feelings towards my respected parents, lovely brothers and sisters for their constant moral encouragement lively sentiments, benevolence and eternal affection which led me to accomplish the task with earnest efforts.

Affection, love and benison of Gupta and Negi families and Mr.and Mrs. Kanwaljeet was always a boon for me and it helped me to bear the pangs of long separation from home.

In the end, I specially acknowledge Mr. B.S.Rana for excellent typing of the manuscript.

Any errors or omissions are mine.

Mohinder Sood

(MOHINDER PAL SOOD)

Palampur
Dated : Aug 30 1983

C O N T E N T S

.....
...
.

LIST OF TABLES

-o-

1. INTRODUCTION

INTRODUCTION

Lentil (*Lens culinaris* Medik.) one of man's oldest protein rich food legume crops, having its probable progenitor as *Lens orientalis* with Afghanistan, Turkey and Ethiopia being the most important centres of genetic diversity, originated in the fertile crescent of the Near East and dates back to the beginning of Agriculture itself (Zohari, 1972; Williams *et al*., 1974, and Ladizinsky, 1979). On the basis of physio-morphological traits, cultivated lentil has been further divided into two sub-species namely *microsperma* and *macrosperma* (Papp, 1980). The *microsperma* types are adapted to the Indian sub-continent and the parts in Near East, whereas, *macrosperma* types are mainly specific to Mediterranean region and the New World.

Lentil besides, being a protein rich crop providing more than twice the amount of dietary protein as compared to cereals, has also been mentioned as having various medicinal properties in several old herbals(Webb & Hawtin, 1981) The 16th Century writer Dondonaeus recommended them as part of the diet in monasteries as he believed they dampened the sexual appetite. Nicholas culpepper, a noted 17th century astrologer/physician, wrote that lentil was governed by the planet Venus. He went on to say that when eaten whole, lentil 'blinds the body and stop looseness but the liquid it is boiled in loosens the belly'. Other old herbals report that lentil 'thicken the blood' which may relate to their comparatively high iron content (9.6mg/100g air dry seed as compared to 7.3, 6.0, 6.3 and 3.1 mg/100g air dry seed in chickpeas, faba beans, lupin and wheat, respectively). The straw and pod walls, residues from threshing, have a high feed value (moisture 10.2%, Fat 1.8%, protein 4.4%, carbohydrates 50.0%, fibre 21.4% and ash 12.2%). The seed coat left after decortication are also considered a valuable feed and may contain upto 13% protein. Starch extracted from lentil has a stable viscosity over a wide range

of temperatures, and is sometimes used in the printing and textile industries. The yield of starch from seed is about 28.5% and the residue containing nearly 40% protein, is a valuable animal feed (Kay,1979).

Inspite of its above mentioned valuable attributes, lentil is considered a relatively minor crop on the world scale, as only about 3% of the total world area relegated to pulses, is under lentil. The ratio is, however, higher in several individual countries, particularly, in Asia, the highest being in Jordon(75%) followed by Syria (51%),Turkey (28%), Iran (24%), Bangladesh(20%) and Lebanon (18%). In India the lentil is grown on about one million hectares of land which is 50% of the total world area under lentil and India's contribution to the total world production of lentil is around 37%, which is the highest followed by Turkey, Syria, and USA (Anon.,1981). The countries like India, Jordon, Syria, Iran, Bangladesh and Ethiopia, having large acreage under lentil, have very low productivity per unit area as the yield of lentil per hectare in these countries ranges from 4.2 to 7.4 quintals as compared to 18.3 q/ha in France and 10.5 q/ha in USA, which have low acreage under lentil.

In India, production of lentil and its per unit productivity have remained more or less static over years and has not shown a phenomenal jump as has been achieved in cereals. Recently, a series of varieties of lentil suitable for different parts of country have been mentioned (Jeswani and Saini, 1981), but most of these are land races which have originated through selection under poor agronomic situations leading to a serious genetic drift of elements responding to better management conditions and therefore these varieties may also not lead to a quantum jump in lentil production, which is our immediate need in order to combat the protein malnutrition in the country. Prevalent varieties of lentil in the country, in general, also lack in

resistance to diseases and good seed size for better marketability. However, it is worth mentioning about the two varieties identified at Himachal Pradesh Krishi Vishva Vidyalaya, Palampur having field resistance to rust and lentil blight. One of them HPL-5, which has been released in the name of 'Vipasha' for the general cultivation in Himachal Pradesh, where blight and rust are problems, is free from hard seeds, slightly bold in seed size and has outyielded the standard variety PL9-12 by a considerable margin in the state. Another variety is HPL-4, which is of macrosperma type having average 100-seed weight 6.5g as compared to 2-3g of existing varieties, but the yield potential is more or less the same as of PL9-12. These varieties still needs genetic modification with reference to various quantitative traits in order to improve their adaptability in other parts of the region through appropriate breeding methodology.

A critical appraisal of the lentil breeding work in the country and at the global scale indicates that like other grain legumes, little concerted efforts have been made for its genetic amelioration. The hybridization work undertaken is also very limited and probably it is due to the tedious crossing procedure in this autogamous species because of small and delicate flowers and also due to the problem of non-synchrony of flowering between macrosperma and microsperma lentil. Under such a situation, mutation breeding appears to be of an added advantage. It has been now established that in mutation breeding radiation is as efficient as hybridization in supplying genetic variability (Brock, 1965 and Gregory, 1968).

In hybridization, in order to decide about a suitable breeding method, the basic information on the components of generated genetic variability is imperative (Cockerham, 1961). Similarly in mutation breeding

it is also important to know the nature and magnitude of various components of induced genetic variance to choose appropriate breeding methodology to exploit the nature and magnitude of induced variability to the maximum. Though numerous reports are available on the induction of polygenic variation in many economic crop plants, the partitioning of the variation into additive and dominance components has received very little attention. Recently, Virk et al. (1978), Yonezawa (1979) and Virk and Gupta (1980) have suggested certain biometrical genetic models and in the present study the same have been made use of for the genetic amelioration of both microsperma (HPL-5) and macrosperma (HPL-4) varieties of lentil through mutation with the following objectives:

i. to get the information on the segregation pattern of induced variability between and within lines in M_2, M_3 and M_4 and its persistance over generations under different radiation doses with respect to seed yield and other polygenic traits,

ii to understand the genetic architecture of induced variation under different doses with respect to polygenic traits studied, using biometrical genetic models,

iii. to understand the relationship of different radiation doses with various parameters of induced variability and varieties studied,

iv. to establish the most appropriate selection stage in lentil mutation breeding for various polygenic traits on the basis of segregation pattern and probability estimates for isolating potential mutants excelling parents, and

v. to identify potential mutants with desirable traits.

2. REVIEW OF LITERATURE

REVIEW OF LITERATURE

Natural selection in the presence of existing environments coupled with spontaneous mutations and recombinations has end up with our present day domesticated plants from their wild ancestors. This gradual process of 'evolution' has its genesis on the raw material of available variability for different morphological and physiological traits. For a long time this process went on capitalising the vast reservoirs of natural variability available. The classical discoveries of Muller (1927) and Stadler (1928) which enabled the man to create variation at 'will' opened new vistas for the improvement of crop plants. The mutation technique came as a potential alternative/ supplementary to other breeding methods such as introduction and hybridization.

Mutations are the ultimate source of all variability in organisms. Variability caused by induced mutations is not essentially different from variability caused by spontaneous mutation during evolution. Variation generated following mutagenic treatment is often classified into macro and micro-mutations, although this categorisation is only arbitrary (Gaul,1965) because the genetic nature of the changes are of the same kind. In some cases the classification of mutation into micro and macro depends on the power of observation method, as has been demonstrated by Seyffert (1962, 1963) for colour differences in Mathiola incana. However, so long as we maintain this classification the macro-mutations are those changes which give rise to discontinuous variation and are therefore easily isolated in early generations, while micro-mutations result in continuous variation where segregation persists through advanced generations. The two types of induced variation therefore require different methods of investigation.

The polygenic theory, given by Mather (1941, 1943 and 1954) involved 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.

Synthesis and discussion on the theory about the inheritance of characters with continuous variation have been given by Lerner (1958), Scossiroli (1960) and Gaul (1965). Any quantitative trait is the result of the joint action of many single genes whose individual substitution produces small phenotypic effects and of the environmental influences. Usually different genes cooperating to determine the same traits are kept together in blocks intermingled with genes cooperating to influence other traits. Such 'Polygenic blocks' are the result of a natural selection process but they may be broken by recombination. Therefore one may say that in such blocks a genetic variation is stored which represents the potential to face ecological requirements at different locations and in different years to face evolutionary trends or to provide variability for artificial selection.

Evidence for the spontaneous mutability of the genetic factors underlying quantitative characters has been provided by several workers in the past. According to Gaul (1967) the report of Johannsen in 1913 might be considered first to prove the existence of spontaneous mutations for quantitative traits even if de Vries (1901) speaking of characters which are of quantitative nature quoted "many mutations are smaller than differences between extreme variants". Baur (1924) and Stubbe (1934) described spontaneous mutations for quantitative characters in Anthirrinum majus, East (1935) in tobacco and Schuler and Sprague (1956) in corn.

micro-mutations (Swaminathan, 1965). Gaul (1965) has envisaged the importance of micro-mutations in two ways. First that they occur more frequently than macro-mutations and secondly that they do not affect the vitality so adversely as the macro-mutations do.

The theoretical expectations of induced random micro-mutation in a self fertilizing species with the large number of genes each having small individual positive or negative effect on a particular character (Brock,1965) would depend on the total number of genes involved, on the relative proportion of genes with positive or negative effects and on the degree to which the genes of the parental genome operate as a balanced set. In such cases random mutation would be expected to increase the variance and to shift the mean away from the direction of previous selection. In characters not subjected to previous selection induced mutations do not follow a particular trend but would be random. Highly the selected or adapted trait, greater will be the shift in mean and also greater asymmetry of distribution of variances. If the extreme limits are not reached in the parental genome, effective selection would be possible in either direction.

Developments in the genetic analysis of induced polygenic variation

The first and extensive report involving the deliberate selection of mutations in quantitatively inherited traits following irradiation with ionizing radiations came from Gregory's work in 1955, 1956, 1957 and 1961 in peanut. He concluded that mutations affecting quantitative characters in a crop plant can be induced by radiation and that phenotypic selection can accumulate positive mutations to produce better strains. Various other workers did a good work in this direction and induced polygenic variation successfully in many economic crop plants (Oka et al.,1958 in rice; Moes, 1958 and Gaul,1961

in barley; Rawlings et al.,1958 in soybean; Wittemer, 1960 in tobacco; Daly, 1960 in subterranean clover; Krull and Frey, 1961 in oats; Scossiroli, 1962 in Maize; Bhatia and Swaminathan, 1962 in wheat; Pate and Duncan,1963 in cotton; Palenzona, 1964 in wild tomato and Gupta and Swaminathan,1967 in brassica).

While many experiments have been conducted to assess the amount of induced genetic variation in self-fertilising plants, the genetical interpretation of the variation has received little attention. Such genetic defination of induced polygenic variation is of paramount importance as it is the accurate basis for deciding appropriate breeding methodology to exploit the valuable variability generated and thus achieve the desired breeding goal. The difficulty is not in deriving biometrical genetic expectations but of equating them to the kind of data that are generated without having to make untestable assumption or alternatively having to restrict the analysis to only part of data. A few attempts have been carried in this direction which are briefly reviewed here and further advance awaits assessment of the biometrical methods for manipulating induced variation.

As a consequence of the pecularity of phenotypic manifestation of quantitative characters the only method available to detect the induction of new variation coming from mutagenic treatment is that given by mean and variance comparisons.

Many workers (Jinks, 1954; Hayman,1954, 1958; Scossiroli,1962; Palenzona, 1965; Lawrence, 1965 and Scossiroli et al.,1966) using different biometrical analysis have clearly demonstrated that the increase of phenotypic variation in generations following irradiation particularly in self pollinated plants is mainly due to an increase in genetic component and it may be accounted for by the effects of mutations on the genetic factors influencing

quantitative characters. The genetic nature of the increased variation, as well as the role and importance of radiation in plant breeding has been stressed by experiments of selection performed according to classical methods in different crop plants (Borojevic, 1965; Brock and Latter, 1961; Gaul, 1964 and 1965; Goud, 1967; Oka et al., 1958; Scossiroli, 1965 and 1966). In some instances the improvement in yield obtained through radiation breeding were not obtained by the standard method of plant breeding, that is selection following hybridization. It has been demonstrated and clearly stated by different workers that radiation is as efficient as hybridization in supplying genetic variability (Gregory, 1956, 1968; Frey, 1965 and Brock, 1965).

Kao et al. (1960) took the first step in this direction and based their genetic analysis on the assumption that allele 'A' mutates to 'a' at the rate 'p', when an individual (AA) is treated. They defined the M_1 population as consisting of entirely (1-p)AA and (p)Aa plants. They omitted the possibility that both 'A' alleles can mutate to the same or different alleles.

Aastveit and Gaul (1967) avoided the above necessity by using the M_2 derived by selfing M_1 plants as the starting point. They then allowed the three kinds of individuals in respect of a single gene locus i.e. AA, Aa, aa to arise in M_2 with arbitrary frequencies of p, q and r, respectively. They concentrated on statistics of a single rank in successive generations rather than on different ranks in the same generation. To accomplish this, all M_2 M_3 and M_4 have to be grown in the same year to eliminate bias due to genotype x environment interaction. The genetic variance and co-variances of the M_2, M_3 and M_4 population are partitioned into components which more directly reflect the genic effect of individual genes.

Noticing the inconvenience of growing three generations in same year Virk et al.(1978) proposed another method which requires a single generation of a population with hierarchical pedigree system. They confine their attention to the variation that arise within progenies of individual M_1 plants treating different M_1 plants more or less as replicates. Each M_1 plant can be regarded as F_1 between hypothetical parents which in successive generation of selfing yield progenies whose progenies can be completely specified since $M_2 = F_2$, $M_3 = F_3$ etc. whose means, variances and co-variances are well known (Mather and Jinks, 1971). In this way the analysis of contribution to the variation of loci which have become heterozygous in the F_1 as a result of the mutagenic treatment can be obtained.

Following mutagenic treatment of a pure breeding line any single M_1 plant will be heterozygous at a number of loci,'K' either for original allele 'A' and a mutant allele 'a' or for both mutant allele 'a' and 'a_2' on selfing each of these 'K' loci will segregate with the expectations typical of an F_2

$$V_{M_2} = V_{F_2} = 1/2 \sum_{i=1}^{K} d^2_i + 1/4 \sum_{i=1}^{K} h_i^2 \text{ (Mather and Jinks,1971)}$$

Now if the selfing continues and at the same time a hierarchical structure is retained, the contribution of this segregation to the variance of rth rank in the nth generation (VrMn) is given by the general formula of Mather and Jinks (1971).

$$V_r M_n = V_r F_n = (1/2)^r D + (1/2)^{2n-r-1} H$$

where $$D = \sum_{i=1}^{K} d_i^2$$

$$H = \sum_{i=1}^{K} h_i^2$$

The corresponding parent offspring co-variances WrMn(n-1) is given by

$$WrMn(n-1) = WrMn(n-1) = (1/2)^{r}D + (1/2)^{2n-r-2}H$$

The formulae apply directly to the variances and co-variances derived from the progenies of any one M_1 plant. To extend them to the average variances and co-variances obtained from the progenies of all M_1 plants, the defination of 'D' and 'H' as given by Dickinson and Jinks (1956) are required to be modified. Thus, if it is assumed that in the M_1 generation the three kinds of individuals AA, Aa and aa in respect of any one locus arise with arbitrary frequencies 'α', 'β' and 'γ' as a result one of both 'A' alleles mutating to 'a' or vice-versa, then summing over 'K' such loci only a proportion 'β' will be contributing to the variation defined by the general formulae and the definations of 'D' and 'H' becomes $\sum_{i=1}^{K} 2\beta_i d_i^2$ and $\sum_{i=1}^{K} 2\beta_i h_i^2$, respectively, where $\alpha_i + \beta_i + \gamma_i = 1$.

On the other hand, if it is assumed that 'A' mutates to 'a' with a frequency of 'v' and that mutation at each allele is independent so that 'AA' mutates to 'aa' with a frequency of 'v^2', then summing over 'K' such loci only a proportion '2 uvv' will be contributing to the variation defined by the general formulae and the definations of 'D' and 'H' become $\sum_{i=1}^{k} 4 u_i v_i d_i^2$ and $\sum_{i=1}^{k} 4 u_i v_i h_i^2$, respectively, where $u_i = (1-v_1)$.

Thus, it is clear that any assumption about gene and genotype frequency in the M_1 can be accomodated by adjusting the coefficients of d^2 and h^2. The coefficient will always be twice the frequency of heterozygotes in M_1 and it will be identical for d^2 and h^2. Thus the estimates of 'D' and 'H' and the relative values of the estimates is independent of any assumptions about gene and genotype frequencies in the M_1 generation. The general

formulae, however are based on a frequency of heterozygotes in the $F_1 = M_1$ of one, where as in these models it is β or 2 uv and the maximum frequency that could be obtained, with the random model (u,v) is half when u=v. To put it other way, both additive and non-additive or dominance components of variance in these models are half of those expected from the general formulae if the general definations of 'D' and 'H' are used in the general formulae no matter which model it is, if these formulae are used for statistics averaged over the progenies of all M_1 plants.

There are two ways of making the adjustment. We can maintain the convention that rank 1(r-1) in the selfing series refers to the variation among $F_2(M_2)$ individuals, in which case we must substitute (r+1)for 'r' in the general formulae or we can recognize that in the special case we are considering the highest hierarchy (rank 1) is the variation among $F_1(M_1)$ individuals in which case the highest rank specified by the general formula is not r=1 but r=2.

To get the expectations of rank zero i.e. variation among M_1 plants, some additional parameters are required to be introduced. If we assume arbitrary genotype frequencies of 'α', 'β' and 'γ' for allele AA(+d) Aa(h) and aa(-d) then the mean = $\alpha d + \beta h - \gamma d$ and variance

$$VOM_1 = \alpha d^2 + \beta h^2 + \gamma d^2 - (\alpha d + \beta h + \gamma d)^2$$

$$= 1/2 \times 2[4\alpha\gamma + \beta(1-\beta)]d^2 + 1/2(2\beta)h^2 - 1/4(4\beta^2)h^2 - 1/2[4\beta(\alpha - \gamma)]dh$$

$$= 1/2D_1 + 1/2H - 1/4\, H_1 - 1/2\, F_1$$

where $D_1 = \sum_{i=1}^{k} 2\, Z_i d_i^2$

$$H_1 = \sum_{i=1}^{k} 4\beta_i{}^2 h^2$$

$$F_1 = \sum_{i=1}^{k} 4\beta_i (\alpha_i - \gamma_i)dh$$

where $Z = [4\alpha_i \beta_i + \beta_i(1+\beta_i)]$

If however, we use the genotype frequencies u^2, $2uv$ and v^2 which assumes that alleles at the same locus mutate independently, we need to introduce only two parameters.

$$H_1 = \sum_{i=1}^{k} 16\, u_i^2 v_i^2 h_i^2$$

and

$$F_1 = \sum_{i=1}^{K} 8\, u_i v_i (u_i - v_i) d_i h_i$$

since D_1 will then equal D.

The complete specification requires five genetical components and at least one and usually two or more environmental components. By including both D and D_1 in the specifications no assumption about the gene and genotype frequencies is required and we can always subsequently test the validity of the assumption that leads to $D = D_1$.

Infact there are two strategies for reducing the number of genetical components to the level where they may be readily estimated. The first was proposed by Aastveit and Gaul (1967) who by confining attention to rank zero statistics could omit 'D' and combine 'H' and 'H_1' into a single parameter with the composition ($H - 1/2\ H_1$). Virk et al.,(1978) proposed to omit rank zero statistics and thereby remove the need for 'D_1', 'H' and 'F_1'. The first obviously makes better use of the data from early generations but it requires one more statistics for estimating the additional parameters whereas the latter makes much better use of data from later generations, has one less parameter and estimates parameters which are more simply interpreted in terms of gene action.

However, the analysis of Virk et al.(1978) as proposed above has certain shortcomings like:

i. Their idea is not applicable before the M_4 generation unless the mutagenic treatment is applied to zygotic cells or at a very early stage of embryo development. As discussed earlier the seeds of the higher plants are multicellular at the time of treatment.

ii. The method does not provide an estimate of the multiplicative component of the A-D gene effects which is necessary not only in predicting the efficiency of artificial selection but also to provide information about the association of dominant genes in the parental lines.

iii. Thehierarchical pedigree structure may lead to genetic drift.

As a result Yonezawa (1979) proposed another method for predicting the additive and dominance components of induced variation which are practicable up to M_3 generation since the M_3 is regarded as being the best generation to start selection for breeding (Yonezawa,1975). According to them as the M_1 plants are genetically chimeric at the level of both spike and whole plant therefore, the genetical segregation in M_1 spike and plant progenies is different from that in the progeny of F_1 individuals. For example if we consider a single locus at which the parental allele 'G' mutates to mutant allele 'g' the mutation rate G-g being 'm' and assuming independent occurrence of mutations, the expected frequencies of GG, Gg and gg cells in mutagenically treated embryos are $(1-m)^2$, $2m(1-m)$ and m^2, respectively. Since mutation rate 'm' is of the order of 10^{-3} or lower (Yonezawa and Yamagata,1977) these values can be approximated by 1-2m, 2m and zero respectively. So if M_1 spike primordia consists of initial cells at the time of mutagenic treatment,

the frequency of the primordia, which are of the Gg genotype for 'i' cells among the 'c' is given by $(C_i)(2m)^i(1-2m)^{c-i}$. Since the number 'c' is much smaller than $1/m^3$ this formula can be approximated by

$1-2Cm \ldots\ldots\ldots i = 0$

$2Cm \ldots\ldots\ldots i = 1$

$0 \ldots\ldots\ldots i \geq 2$

because if M_1 spike primordia consist of 'c' initial cells at the time of mutagenic treatment, the frequency of primordia which are of Gg genotype for 'i' cells among the 'C' is given by

$$^cC_i(2m)^i\ (1-2m)^{c-i}$$

so if $i = 0$

$$^cC_0(2m)^0(1-2m)^{C-0}$$

$$= 1-2cm$$

similarly if $i = 1$

$$^cC_i(2m)^1(1-2m)^{c-1}$$

$$= 2cm$$

and if $i = 2$

we get $^cC_2(2m)^2(1-2m)^{c-2} = 0$

Hence for this locus, there is no segregation in the 1-2cm of the total M_1 spiked derived M_2 lines and the remaining 2cm lines segregate with the ratio

$$\frac{4c-3}{4c}\ GG:\ \frac{1}{2c}\ Gg\ :\frac{1}{4c}\ gg$$

Which indicates that a ratio of 1/4:1/2:1/4 as assumed by Virk et al. (1978) does not hold unless c=1. If 'c' is made equal to the total number of the initial cells contained in an embryo, the above ratio represents the

segregation in M_1 plant derived M_2 lines. Genotypic frequencies of M_2 population as a whole are independent of the cell number, and are given by (1-3/2m) GG: mGg : 1/2m gg. With 'k' genes concerned with the character at issue, the number of mutations occuring simultaneously in a single cell is expected to be subject of the 'Poission' distribution with mean 2km which is likely to be smaller than unity. This is another characteristics of induced variation that mutant individuals carrying two or more mutant genes will be very infrequent, indicating that effects of linkage, if any would be much less than in genetic variation caused by hybridization.

Yonezawa (1979) defined and estimated the different genetic parameters by using the additive-dominance model (Mather and Jinks,1971) and the genotype frequencies formulated in the preceeding section the mean and the genetic variance of M_2 populations are described as

$$\bar{M}_2 = \bar{M}_0 - 2(d)m + (h)m$$

and by omitting the terms with the second power of the mutation rate 'm'

$$V_{M_2} = 3Dm + Hm - 2Fm, \text{ respectively, where}$$

$\bar{M}_0$ = mean of the parent used

$(d)m = \Sigma \pm md (d \geq 0)$

$(h)m = \Sigma mh$

$Dm = \Sigma md^2$

$Hm = \Sigma mh^2$

$Fm = \Sigma \pm mdh$

The symbols $(d)_m$ and $(h)_m$ are similarly defined as in Mather and Jinks (1971). The plus and minus sign in the summation of (d)m and Fm correspond to whether the original alleles of the parent have larger or

smaller effects than the respective mutant alleles. The summation in this case is over all the 'k' genes affecting the character at issue.

When the M_2 population is made up of the M_2 lines derived from different M_1 plants or spikes, the variance VM_2 can be partitioned into two statistically independent components i.e. between and within M_2 line variances, which are:

$$\overline{VM}_2 = \frac{2}{c} Dm + \frac{1}{2c} Hm - \frac{2}{C} Fm \text{ and}$$

$$\overline{VM}_2 = (3-\frac{2}{c})Dm + (1 - \frac{1}{2c})Hm - 2(1 - \frac{1}{c}) Fm, \text{ respectively.}$$

The corresponding statistics of the M_3 population are formulated by

$$\overline{M}_3 = \overline{M}_0 - 2(d)m + 1/2(h)m$$

and $$VM_3 = 1/2Dm + 1/2Hm - Fm$$

when the M_3 population consists of the M_3 lines derived from different M_2 plants VM_3 is divided into

$$V\overline{M}_3 = 3Dm + 1/4Hm - Fm \text{ and}$$

$$\overline{V}M_3 = 1/2Dm + 1/4Hm$$

If the M_3 population is hierarchically structured by M_1 plants the variance $\overline{VM}_3$ can be further partitioned into the two components i.e. the variance between M_3 groups derived from different M_1 plants and the variance between M_3 lines from the same M_1 plants, which are presented by

$$V_{\overline{M}_{3B}} = \frac{2}{C}Dm + \frac{1}{8C} Hm - \frac{1}{c} Fm \text{ and}$$

$$V_{\overline{M}_{3W}} = (3 - \frac{2}{c})Dm + (1/4-1/8c)Hm - (1-1/c)Fm, \text{ respectively.}$$

Co-variance between the M_2 and M_3 generation may provide additional

source for parameter estimation. The genetic co-variance between M_2 plants and their M_3 progeny means is given by

$W\bar{M}_3/M_2 = 3\ Dm + 1/2\ Hm - 3/2Fm$ and that between M_2 lines and M_3 group is

$$W\bar{M}_3/\bar{M}_2 = \frac{2}{C} Dm + \frac{1}{4C} Hm - \frac{3}{2C} Fm$$

By using the M_2 and M_3 populations, we have two sources for the estimation of the two first degree parameters, (d)m and (h)m. Theoretically seven sources $V\bar{M}_2$, $\bar{V}M_2$, $V\bar{M}_3B$, $V\bar{M}_3W$, $\bar{V}M_3$, $W\bar{M}_3/M_2$ &$W\bar{M}_3/\bar{M}_2$ are available for the three second degree parameters 'Dm', 'Hm' and 'Fm'. Among these seven however, those statistics that are based on the hierarchical pedigree structure originating from M_1 spikes or plants, namely $V\bar{M}_2$, $\bar{V}M_2$, $V\bar{M}_3B$, $V\bar{M}_3W$ and $W\bar{M}_3/\bar{M}_2$, include the cell number 'c' and therefore should not be used unless the value of 'c' is precisely known in advance. In practice 'c' appears to differ with M_1 spikes (Sarvella et al.,1962) and its estimate is influenced by the haplontic and diplontic selection against mutations (Yonezawa and Yamagatta, 1975). The co-variance $W\bar{M}_3/M_2$ would also be unsuitable, its estimates may be much biased by both measurement error and genotype x year interaction since M_2 plants can neither be replicated nor grown in the same year as their M_3 progenies.

Hence only three variances $\bar{V}M_2$, $V\bar{M}_3$ and $\bar{V}M_3$ are reliable sources of estimates of the three second degree parameters. Then applying the perfect fit solution, the estimates of the parameters are obtained by

$$(d)m = 1/2\ (\bar{M}_0 + \bar{M}_2 - 2\bar{M}_3)$$

$$(h)m = 2(\bar{M}_2 - \bar{M}_3)$$

$$\hat{Dm} = -1/4\ \hat{\bar{V}}M_2 + 1/2\ \hat{V\bar{M}}_3 + 1/2\ \hat{\bar{V}}M_3$$

$$Hm = 1/2\ \hat{\bar{V}}M_2 - \hat{\bar{V}}M_3 + 3\ \hat{\bar{\bar{V}}}M_3,$$

$$FM = -5/8\ \hat{\bar{V}}M_2 + 1/4\ \hat{\bar{V}}M_3 + 9/4\ \hat{\bar{\bar{V}}}M_3$$

where $\bar{\bar{M}}_0$, $\bar{\bar{M}}_2$ and $\bar{\bar{M}}_3$ are of course estimated by the total mean of the respective populations.

A simple equation to test the adequacy of additive-dominance model to account for the induced variability has also been suggested by Virk and Gupta (1980) as $2\bar{\bar{M}}_2 + \bar{\bar{M}}_4 - 3\bar{\bar{M}}_3 = 0$, but it was modified in consultation with Dr. D.S.Virk (1983) as $2\bar{\bar{M}}_4 + \bar{\bar{M}}_2 - 3\bar{\bar{M}}_3 = 0$ and was made use in present analysis. If the value is significantly less than or equal to zero than the additional variability following mutagenesis can be explained on a simple additive-dominance model, otherwise the role of interactions has to be analysed as one of the possible reasons of variability.

Yonezawa (1979) has further given some methods to predict the genetic nature and selection efficiency in later generations using the estimates of the first and second degree parameters defined above.

Some rough estimates on the degree of dominance and gene distribution can be obtained by the use of the estimates. Supposing that each gene is alike in both genetic effect and mutation rate, the parameters may then be written as

$$(d)m = mkr_1 d$$

$$(h)m = mkr_2 (h)$$

$$Dm = mkd^2$$

$$Hm = mkh^2$$

$$Fm = mkr_3 d/h$$

where coefficient 'r' corresponds to the degree of gene asscciation of Mather and Jinks (1971), which in this case assumes $\pm$ 1, 0 and -1 according to whether all, half and none of the parental genes have larger contributions to the

phenotype than mutant genes. The coefficient 'r_2' measures the isodirectionality of dominance taking the values of +1, 0 and -1 if all, half and none of the alleles with increasing effect are dominant to the ones with decreasing effect respectively. The coefficient 'r_3' shows the degree of association of dominant genes, the value of which is +1, 0 and -1 when all, half and none of the parental alleles are dominant to mutant ones.

As in case of the populations obtained by crossing between two inbred lines, the ratio $\sqrt{\frac{Hm}{Dm}} = \frac{|h|}{d}$ gives the average degree of dominance.

The coefficients r_1 and r_2 cannot be estimated uniquely but their signs i.e. the signs of (d)m and (h)m together with the ratio

$$\frac{(h)m}{\sqrt{Hm}} \Big/ \frac{(d)m}{\sqrt{Dm}} = \frac{r_2}{r_1}$$

may in some cases give some idea on the balance sheet of gene association and isodirectionality of dominance. For example, the situation of (h)m 0 and r_2/r_1 1 strongly suggests that r_1 - and r_2 1, namely about half of the parental genes have increasing effect compared to mutant genes, dominance being positively directed for most of the genes concerned. The validity of this speculation would be confirmed if the value of 'r_3' calculated as

$$\frac{Fm}{\sqrt{Dm\ Hm}} = r_3 \text{ is around zero.}$$

In the case where two parental lines with significantly different phenotypes, say P_1 and P_2 are available, the mutation rate can be estimated by

$$\frac{(d)m_1 - (d)m_2}{\bar{P}_1 - \bar{P}_2} = \frac{2 \sum^{k'} \pm md}{2 \sum^{k'} \pm d} = m$$

Where $\bar{P}_1$ and $\bar{P}_2$ = means of P_1 and P_2, $(d)m_1$ and $(d)m_2$ = (d)m of P_1 and P_2
k' = number of genes for which the two parents carry different alleles.

Mutation Studies in Lentil

Very few mutation studies have been conducted in grain legumes specifically in lentil and that too in the direction of genetic analysis following mutagenesis. However, the available reports are briefly reviewed here.

Sharma and Chatterji (1962) while investigating the genomic influence on radiosensitivity found that genus Lens is more radiosensitive than Lathyrus and Pisum genera because of its low chromatin content, thus opening new optimism towards potential mutation breeding in lentil which is one of the first crops demesticated by man (Zohari, 1972; Youngman, 1968) and is difficult to hybridise on account of small, fragile and cleistogamous flowers. Uhlik (1972) was the first person to come out with a study concerning the cytogenetic effects of thermal neutrons in lentil and found a linear relationship between the doses and frequency of bridges and fragments after irradiation. The frequency of fragments was found in linear dependence on the doses of the thermal neutrons only in the range of lower and medium doses of irradiation, whereas it was linear even at higher doses for bridges. A linear relationship between chromosome aberration and irradiation doses was also established.

Sinha and Godward (1972a) reported that variety macrosperma is more radiosensitive than variety microsperma. At varying doses of gamma radiation studied in three successive generations, they found that in 8 kR dose the mean value of height, number of primary branches, number of pods increased whereas at 12, 16 and 20 kR doses there was decrease in mean value as compared to control. The mean values of pods per plant were more or less the same as that of 4 and 8 kR, whereas at 12, 16 and 20 kR, the values were clearly less than control. Number of seeds per plant showed a definite

tendency to decrease with an increase in dose. Induced variation in the population increased with the dose.

Sinha and Godward (1972b) found various cytological abnormalities in the M_1 and M_2 generations following mutation of both micro and macrosperma lentil. The frequency of abnormalities was lower in M_2 than in M_1 but pollen and seed sterility were higher in the M_2 than in the M_1.

Moursi et al.,(1974)in lentil studied the effect of gamma rays in inducing mutations and reported that pre-sowing irradiation of air dried seeds of lentil gave rise to range of mutations in the M_2 generation, some of which may be of value for improving yield. Shaikh (1975) reported that some of the lentil mutants showed good promise with regard to yield in Bangladesh.

Significant mean differences in M_3 and M_4 generations of lentil were reported by Uhlik and Urban (1976) for various morphological traits like plant height, whole plant weight, height of the lowest pod, number of pods and 100-seed weight.

Sharma and Sharma (1978) obtained true breeding mutants with pods large or larger than those of parents in the M_2 generation following exposure of L 235 seeds to 6kR gamma rays. In 10kR treatment the size of pods decreased. Significant correlation was found between pod surface area and 1000-seed weight, indicating that pod size may be used as selection criterion for seed weight. All the mutations were found to be recessive and monogenically controlled.

Tirdea (1978) studied the effect of gamma-rays upon lentil seeds derived from three small and three large seeded varieties subject to eight

different doses of radiation and found that the effect of irradiation was small in the small seeded varieties and it tended to reduce the number of pods per plant.

Sharma and Sharma (1979) explained the pattern of induced mutability in different genotypes of lentil. The mutation frequency and mutation spectrum were greater following treatment with NMU than gamma rays. Mutations affecting plant height and pod characters were chiefly affected by gamma rays.

Ravi et al.,(1979) in lentil reported that five high yielding progenies selected in the M_4, two progenies in M_5, four in M_6 derived from irradiated material at 10, 20, 30 kR and one EMS derived progeny outyielded the control in M_4, M_5 and M_6 generations for the four quantitative traits under study viz., plant height, number of primary branches, number of pods and seeds per plant. The study also revealed that higher doses of mutagen (20kR) employed in this study are not suitable for increasing variability. They also practised selection for these four traits and reported that delayed selection in M_3 to M_5 generations were found to be more efficient than M_2 selection when plants with multiple mutant loci are to be obtained, as deletirous mutations are generally eleminated in early generations (Rao et al.,1960).

Hussain and Adalla (1979) in field bean showed that some of the mutants surpassed their control significantly in two successive generations while other showed fluctuating results from M_4 to M_5 for seed yield. Shaikh et al.,(1979) recorded mutants of lentil with greater seed yield and protein contents than original varieties.

Sharma and Sharma (1981) while studying the effects of mutagens in the character association in lentil reported that correlation coefficient

differences are attributed to the effects of mutagens on linkage and changed effects of mutated genes. Sharma and Sharma (1982) further studied the mutagenic effects of gamma rays and NMU on four quantitative traits in M_1 to M_3 generations of lentil variety L 235. The mean value and coefficient of variation increased in M_1 generation for all traits except 1000-grain weight. In M_2 mean values increased in case of gamma rays treatment but remained below the level of control value in the NMU treatments. The mean values of all characters were comparable to the control in all the mutagen treatments in M_3 generation. Barring 1000-seed weight in 6kR gamma rays and 0.005% NMU and seed yield in 0.005% NMU, the variability for all the traits in all the treatments increased in M_2 generation and genetic parameters continued to be higher in the treated populations as compared to the control. The induced genetic variability was probably due to mutations in the genes having additive effect. Different characters responded differently to the mutagenic treatments with regard to induced variation in M_2 and M_3. Thus selection seems to depend upon character and nature of inheritence of a trait.

Sen (1982) reported the successful mutation in B 77 variety of lentil and obtained promising mutants with early maturity, good ideotype and increased 1000-seed weight. One of the mutant S 256 yielding on an average 22.81 q/ha was recommended for cultivation in West Bengal.

Kalia (1982) conducted a study to understand the nature and magnitude of induced variation, its relationship with different doses and genotypes used alongwith judging the efficiency of augmented design superimposed on randomized block design for handling large progenies in M_3 generation of <u>microsperma</u> (HPL-5) and <u>macrosperma</u> (HPL-4) varieties of

lentil by using 5, 10, 15, 20 and 25 kR doses of gamma rays with respect to seed yield components and phenological traits. It was concluded that sufficient genetic variability was induced for most of the polygenic traits in both types of lentil. High magnitude of increased induced variation within progeny with high heritability and genetic advance suggested that in mutation breeding programme, selection in M_3 generation would be more effective both between and within lines. Augmented design superimposed on completely randomized block design was found to be more efficient for evaluating large number of mutation progenies in M_3 and later generations. The variety macrosperma was found to be more radiosensitive than microsperma. Shift in population mean and induced genetic variance was dependent upon specific genotype-trait combination. High yielding and early maturing mutants in both types were isolated.

3. MATERIALS AND METHODS

MATERIALS AND METHODS

The present investigation on the genetic analysis was carried out in two varieties of lentil (*Lens culinaris* Medik) at the experimental farm of department of Plant Breeding, Himachal Pradesh Krishi Vishva Vidyalaya Palampur, situated at 1280m above mean sea level and at $32^{\circ}6'$ North latitude and $76^{\circ}3'$ East longitude. This part of the state is a sub-temperate mid-hill zone having high monsoon rainfalls.

3.1 Materials

The varieties used in the present study were HPL-5, a *microsperma* type adapted to a wide range of environments and HPL-4, a *macrosperma* type specifically adapted to sub-temperate mid-hill zone of Himachal Pradesh. *Microsperma* type mainly adapted to the Indian sub-continent and parts of the Near-East, has smaller seeds with orange or yellow cotyledons. It is more polymorphous as a group but the plant is generally shorter, more pigmented and has smaller pods, leaves and leaflets than *macrosperma*. *Macrosperma* type is adapted to Mediterranean region and the new world, has large seeds normally yellow cotyledons with no or little pigmentation in the flowers or vegetative structure.

The experimental material consisted of M_2, M_3 and M_4 generations of these two varieties. Two hundred dry seeds of each variety were got irradiated with different radiation doses *viz.* 5, 10, 15 and 20kR from Co_{60} source at IARI, New Delhi. These were raised during 1980-81 as M_1 generation and from this generation, only normal looking plants, free from sterility and physio-morphological abnormalities were selected and bulked to provide the seed for M_2 population in each dose and in each variety. The lines in M_3 and M_4 generations were selected from the earlier generated material under same dose of radiation of the above mentioned varieties (Kalia, 1982). The

criteria of selecting these lines were again on the basis of normal looking plants in the whole line and without any sign of sterility and abnormality. In M_3 and M_4 generation, seed of each line was a random bulk tracing back to individual plants in M_1 generation raised during Rabi, 1978. At no stage selection was practised within lines, which constituted the M_3 and M_4 generation of present study.

3.2. Layout of the experiments

Independent experiments were raised for each dose and variety during 1981-82. For each experiment the M_2, M_3 and M_4 generations under each dose of the two varieties were simultaneously raised alongwith parents (control), in randomised block design with two replications. Each plot within a replication consisted of a single row of 2 meter length with row to row spacing of 30cm and within row, plant to plant spacing of 7-8 cm. Thus, each plot consisted of 25 plants. The recommended dose of fertilizer at the rate of 20 kg N and 40 kg P_2O_5 per hectare was applied at the time of sowing. In all, there were eight experiments raised. The number of lines raised generation wise and dose wise for each variety are given below:

Dose	Number of lines					
	microsperma (HPL-5)			macrosperma (HPL-4)		
	M_2	M_3	M_4	M_2	M_3	M_4
5 kR	17	89	61	7	17	38
10kR	13	44	27	9	18	26
15kR	18	28	49	17	6	22
20kR	6	7	20	5	5	7

3.3. Data recording

For recording of the data, ten random plants in each row and replications were tagged for taking the observations on the following traits:

1. Grain yield(g)/plant: It was recorded in grams as weight of seeds per plant on Sartorius 2355 top pan balance.

2. Biological yield(g)/plant: It was recorded as weight of the whole plant excluding roots after harvesting and sun drying on Sartorius 2355 top pan balance.

3. Harvest index(%): Harvest index for each plant was calculated as the ratio of grain yield to biological yield and expressed as percentage.

4. Number of pods/plant: The number of pods were counted for each plant.

5. 100-seed weight(g): Weight of 100 seeds was recorded for each plant.

6. Number of Primary branches/plant: Primary branches in each plant were recorded.

7. Plant height(cm): Each plant was measured from ground level to the tip of the uppermost branch at maturity.

8. Days to maturity: Days taken were recorded for each plant from the date of sowing to physiological maturity.

3.4. Statistical analysis

Data recorded on individual plants for all the traits, all the generations over different radiation doses was analysed to have the generation means (first degree statistics) and variances (second degree statistics) as per the analysis requirements of Yonezawa (1979) to know the nature and magnitude of induced variation for polygenic traits. The variance within 10 plants of each row was also worked out to have the comprehensive genetic background and basis for deciding the effective stage of selection in lentil under the mutation breeding programme for maximum genetic gains.

3.4.1. Analysis of variance

Dose wise analysis based on individual plant analysis of each row and each generation based on 10 plants was carried out for both microsperma (HPL-5) and macrosperma (HPL-4) varieties of lentil for various polygenic traits to get the mean performance and respective standard error of each line in different generations. In M_3 and M_4 generations, within line mean and variance analysis was also carried out for the individual lines.

The variance analysis of M_2, M_3 and M_4 in each dose was carried out as suggested by Yonezawa (1979) as per the ANOVA table given below:

ANOVA

Item	d.f.	M.S.	E.M.S.
Blocks	r-1	MS_{BI}	$\sigma^2 W + b\,\sigma^2_{BxL} + ab\,\sigma^2 BI$
Lines	a-1	MS_L	$\sigma^2 W + b\,\sigma^2_{BxL} + br\,\sigma^2 L$
Block x lines	(a-1)(r-1)	MS_{BxL}	$\sigma^2 W + b\,\sigma^2 B \times L$
Within line	ar(b-1)	MS_W	$\sigma^2 W + \sigma^2 e$
Error (parental variance)		MS_P	$\sigma^2 e$

Where

r = Number of replications

a = Number of lines of each generation under different doses.

b = Number of plants recorded in each line.

Variance of different lines was tested against parental variance variance within lines and variance due to line x block interaction, so as to obtain the realistic estimates of genetic variation induced after eleminating all other factors.

For comparing the two means belonging to different generations paired 't' test was used as per Panse and Sukhatme (1978).

3.4.2. Estimates of coefficients of variation and heritability (broad sense)

Phenotypic coefficients of variation (C.V.) due to lines was worked out by eleminating line x block interaction as:

$$\sqrt{\frac{MS_L - MS_W}{rb} + MS_P} \Big/ \bar{x} \times 100$$

Where

$\bar{x}$ = mean of the respective population.

Phenotypic coefficient of variation within lines was estimated as

$$\sqrt{MS_W} / \bar{x} \times 100$$

Heritability estimates (broad sense) were also worked out by general formula

$$H = \sigma^2_g / \sigma^2_P \times 100$$

Where σ^2_g = genotypic variance

σ^2_P = phenotypic variance

The estimates were calculated due to lines by eleminating line x block interaction as:

$$\sigma^2_g = MS_L - MS_{BxL} - MS_W / rb$$

$$\sigma^2_P = \sigma^2_g + MS_W$$

thus $H = \sigma^2_g / \sigma^2_P \times 100$

Heritability due to lines was also calculated by ignoring lines x block interaction as

$$\sigma^2_g = MS_L - MS_P / r$$

$$\sigma^2_P = \sigma^2_g + MS_P$$

and $H = \sigma^2_g / \sigma^2_p \times 100$

Heritability within lines was also worked out as:

$$\sigma^2_g = MS_w - MS_p$$

$$\sigma^2_p = \sigma^2_g + \text{Parental variance}$$

thus $H = \sigma^2_g / \sigma^2_p \times 100$

3.4.3 Genetic component analysis for induced variation

By considering the variation that arises within the progenies of individual M_1 plants and treating different M_1 plants more or less as F_1 replicates between hypothetical parents, one can analyse the contribution to the variation of those loci which have become heterozygous following mutagenic treatment of a pure breeding line. The properties of the selfed progenies of the individual M_1 plants can then be specified by using usual selfing series formulae of Mather and Jinks (1971) since $M_2 = F_2$, $M_3 = F_3$ and so on. Genetical expectations of the means ($\bar{M}n$) for the 'n'th generation produced by selfing following mutagenic treatment of a pure breeding line (n=0) as per Mather and Jinks (1971) and further suggested by Yonezawa (1979), are as:

$$\bar{M}n = m + (d)_i + (1/2)^{n-1}(h)_i$$

where $(d)_i = \sum_{i=1}^{k} (u_i - v_i)d_i$

$(h)_i = \sum_{i=1}^{k} 2 u_i v_i h_i$

in a u, v system, where frequencies of three genotypes viz., AA, Aa and aa in respect of a single gene difference are u^2, 2 uv and v^2 and 'm' is parental mean.

3.4.3.1 Scaling test for adequacy of additive - dominance model

Using the Mather and Jinks (1971) approach of scaling test the following equation was used to test the adequacy of additive - dominance model for the induced polygenic variation under each dose in each variety. The equation will hold ture only in the absence of non-allelic interaction.

$$2\bar{M}_4 + \bar{M}_2 - 3\bar{M}_3 = 0$$

The standard error of the above equation for testing its deviation from zero was worked out as:

$$\pm\sqrt{4\,V\bar{M}_4 + V\bar{M}_2 + 9\,V\bar{M}_3}$$

Significant deviation of above equation from zero led to the conclusion for the inadequacy of additive-dominance model and thus probable presence of non-allelic interaction for the induced variation.

Virk and Gupta (1980) did also suggested earlier such type of scaling test but due to some mistakes in the equation, it was required to be modified as above after presonal discussion with Dr. D.S. Virk.

3.4.3.2 Estimation of genetic components

The genetic components were estimated by using first degree and second degree statistics as per the following procedure given by Yonezawa (1979) and their respective standard errors were worked out by imperical way. By using first degree statistics, the additive (dm) and dominance (hm) effects were worked out as:

$$(d)_m = 1/2\,(\bar{M}_0 + \bar{M}_2 - 2\bar{M}_3)$$

and

$$(h)_m = 2\,(\bar{M}_2 - \bar{M}_3)$$

Where

$\bar{M}_o$, $\bar{M}_2$ and $\bar{M}_3$ are the mean values of parents (control), M_2 and M_3 generations. For testing their significance, the standard error's were worked out as;

$$S.E. \text{ of } (d)_m = \pm\sqrt{1/4\ (V\bar{M}_o + V\bar{M}_2 + 4\ V\bar{M}_3)}$$

and

$$S.E. \text{ of } (h)_m = \pm\sqrt{4\ (V\bar{M}_2 + V\bar{M}_3)}$$

Average degree of dominance was calculated as ratio of $(h)_m/(d)_m$.

By using second degree statistics, the additive (Dm), dominance (Hm) and Fm variances were worked out as,

$$\hat{Dm} = -1/4\ \hat{V}M_2 + 1/2\ \hat{V}\bar{M}_3 + 1/2\ \hat{\hat{V}}M_3$$

$$\hat{Hm} = 1/2\ \hat{V}M_2 - \hat{V}\bar{M}_3 + 3\ \hat{\hat{V}}M_3$$

and

$$\hat{Fm} = -5/8\ \hat{V}M_2 + \hat{V}\bar{M}_3 + 9/4\ \hat{\hat{V}}M_3$$

where,

$\hat{V}M_2$ = Variance due to M_2 lines

$\hat{V}\bar{M}_3$ = Variance between lines in M_3

$\hat{\hat{V}}M_3$ = Variance within lines in M_3.

Average degree of dominance was calculated as ratio of $\sqrt{Hm/Dm}$.

The ratio of coefficients 'r_1' which corresponds to the degree of gene association of Mather and Jinks (1971) and 'r_2' which measures the isodirection ality of dominance, was worked out as per Yonezawa (1979) as:

$$r_2/r_1 = \left(\frac{(h)m}{\sqrt{Hm}}\right) \Big/ \frac{(d)m}{\sqrt{Dm}}$$

The coefficient 'r_3' which shows the degree of association of dominant genes, was worked out as,

$$r_3 = \frac{Fm}{\sqrt{Dm \cdot Hm}}$$

3.4.4 Estimates of normal probability integrals

Estimates of normal probability integrals values for isolating potential mutants falling outside the parental range were computed by following Jinks and Pooni (1976) as,

$$x = \frac{\bar{P} - m}{dm}$$

Where, $\bar{P}$ = parental mean value

m = expected mean of a mutation generation

and

dm = additive genic effect

Normal Probability integrals corresponding to 'x' value were obtained as per Fisher and Yates (1938). The probability estimates for isolating potential mutants were also worked out by taking environmental effects also in addition to additive one as:

$$x' = \frac{\bar{p} - m}{dm + e}$$

The normal probability integral values corresponding to x' were obtained as above.

4. RESULTS

EXPERIMENTAL RESULTS

Results obtained from the present investigation on the Genetic analysis of induced polygenic variation in M_2, M_3 and M_4 generations of both microsperma (HPL-5) and macrosperma (HPL-4) varieties of lentil under different radiation doses viz. 5, 10, 15 and 20 kR for different polygenic traits are presented below:

4.1. Analysis of variance

The results obtained from the analysis of variance for the induced variation for various polygenic traits namely seed yield, biological yield, harvest index, number of pods, 100-seed weight, number of primary branches, plant height and days to maturity in M_2, M_3 and M_4 generations under different radiation doses viz., 5, 10,15 and 20kR for both microsperma and macrosperma varieties of lentil are incorporated in Tables 1 to 4. Dose wise and within dose variety wise results obtained are presented in the following pages.

4.1.1. Analysis of variance under 5kR

The results obtained from the analysis of variance under 5kR (Table 1) are presented below variety wise:

Analysis of variance under 5kR for microsperma (HPL-5) lentil: Analysis of variance in microsperma (HPL-5) under 5kR showed that variance due to within lines was significant in M_2, M_3 and M_4 generations for seed yield and number of pods, whereas, it was significant in M_2 and M_3 for days to maturity and only in M_2 for plant height and in M_4 for 100-seed weight when it was tested against parental variance. For seed yield the variances due to lines and line x block interaction were significant both against parental as well as within lines variance. Biological yield exhibited significant variance due to line x block interaction in M_2 and due to lines in M_4 when tested against

Table 1. Analysis of variance for induced genetic variation for various polygenic traits in M_2, M_3 and M_4 generations of microsperma (HPL-5) and macrosperma (HPL-4) varities of lentil under 5kR

Traits/ variety	M_2 m.s. due to			M_3 m.s. due to			M_4 ms. due to			Error m.s.
	L	LB	WL	L	LB	WL	L	LB	WL	Parental variance
HPL-5 d.f.	16	16	306	88	88	1602	60	60	1098	18
SY	1.5*@	3.1*@	0.5*	23.9*@	25.1*@	0.7*	2.6*@	1.8*@	0.3*	0.1
BY	16.9	42.3*	3.6	14.1	11.5	4.9	25.8*	9.9	4.8	8.8
HI	38.9	117.8	50.5	139.5	135.5	37.3	157.3	97.9	49.9	154.5
NP	623.1*@	367.2*@	121.6*	701.6*@@	451.9*@	133.9*	726.4*@@	452.8*@	99.7*	10.6
SDW	0.60*	0.2	0.1	0.7*	0.2	0.1	0.6*@	0.2	0.8*	0.2
NPB	15.8*	8.6*	1.7	19.0*	11.1*	2.5	17.8*	11.8*	2.1	2.8
PH	17.3*@@	23.2*@	7.2*	23.3*	13.2*	4.9	31.6*	20.4*	4.8	5.9
DM	24.7*@	18.8*	12.2*	159.4*@@	41.4*@	10.4*	107.4*	39.8*	7.1*	7.3
HPL-4 d.f.	6	6	126	16	16	306	38	38	702	18
SY	2.3*	3.7*	0.3	2.0*@	1.5*@	0.8*	0.5*	0.4	0.3	0.6
BY	11.4*	9.8	5.2*	25.0*@	9.2	7.4*	16.5*	6.3	3.8	4.9
HI	109.3	51.2	55.5	122.8	81.3	53.7	141.7	129.8	48.8	91.7
NP	120.7*@	73.8	52.8*	107.9*	167.9*@	69.4*	1522.8*@@	536.91*@	490	7.5* 31.7
SDW	0.3*	0.2*	0.3*	0.9*@@	0.3*	0.5*	1.4*@	0.8*@	0.5*	0.1
NPB	3.5*	5.2*	7.3*	8.1*	3.3*	12.3*	30.5*@@	17.1*@	10.3*	1.0
PH	53.5*@	35.5*	17.5*	22.6*	16.0*	19.6*	71.5*@@	31.4*@	15.7*	5.8
DM	77.6*	13.6	13.1	64.2*	31.4	16.5	52.6*	32.81*	12.3	16.6

SY- Seed yield(g), BY-Biological Yield(g), HI-harvest index(%) NP-Number of pods, SDW-100-seed weight(g), NPB- Number of primary branches, PH- Plant height(cm), and DM-Days to maturity.

L- Lines, LB - Lines x blocks and WL- within lines.

* Significant at 5% level, when tested against within line parental m.s.

*@Significant at 5% level when tested also against significant within line m.s of respective generation

*@@Significant at 5% level, when tested also against significant m.s. due to blocks x lines interaction.

parental variance. Variance due to lines and line x block interaction were significant against both parental and within lines variances in M_2, M_3 and M_4 generations, whereas variance due to lines was also significant against significant line x block interaction in M_3 and M_4 generations for number of pods. Hundred seed weight exhibited significant variance due to lines when tested against parental variance in all the generations, however, in M_4 it was also significant against within line variance. Variance due to lines and line x block interaction was significant against within lines variance in all the generations for number of primary branches, plant height and days to maturity. However, plant height exhibited significant variance due to lines and line x block interaction when tested against within lines variance, but variance due to lines in M_2 was also significant against significant line x block interaction. Variance due to lines for days to maturity was also significant when tested against variance within lines in M_2 and also against significant line x block interaction in M_3.

Analysis of variance under 5kR for macrosperma(HPL-4) lentil: Analysis of variance for macrosperma (HPL-4) revealed that within lines variance was significant for number of pods, 100-seed weight, number of primary branches and plant height in all the three generations. Within lines variance was significant for biological yield in M_2 and M_3 and for seed yield in M_3 only. Variances due to lines and line x block interaction were significant for seed yield in all the generations when tested against parental variance but in it was also significant within line variance. Biological yield exhibited significant variance due to lines in all the generations when tested against parental variance, however, in M_3, variance due to lines was also significant against within lines variance. Number of pods exhibited significant variance

due to lines and line x block interaction in M_3 and M_4 against parental variance but in M_2 variance due to lines was significant when tested against both parental variance and line x block interaction variance. Variance due to line x block interaction in M_3 and M_4 was significant for number of pods. Variance due to lines in M_4 was significant against variances due to parent, within lines and line x block interactions. Variances due to lines and line x block interaction were significant in M_2, M_3 and M_4, when tested against parental variance for 100-seed weight, moreover, variance due to lines in M_3 was also significant against variance due to within lines and line x block interactions and it was significant against within lines variance in M_4. Variances due to lines and line x block interaction were significant against parental variance for number of primary branches in M_2, M_3 and M_4 but in M_4 variance due to lines was also significant when tested against significant variance due to within lines and line x block interaction. For plant height, in M_2 variance due to lines was significant against variances due to parent and within line and variance due to line x block interaction was significant against parental variance, in M_3 the variances due to lines and line x block interaction were significant against parental variance; and in M_4 variance due to lines was significant against variance due to parent , within lines and line x block interaction.

4.1.2. Analysis of variance under 10 kR

The results obtained from the analysis of variance under 10 kR (Table 2) are presented below variety wise:

Analysis of variance under 10kR for microsperma (HPL-5) lentil: Analysis of variance (Table 2) revealed that variance due to within lines was significant for seed yield, biological yield, number of pods and plant height in all the

Table 2. Analysis of variance for induced genetic variation for various polygenic traits in M_2, M_3 and M_4 generations of microsperma(HPL-5) and macrosperma(HPL-4) varieties of lentil at 10kR

Trait/ variety	m.s. due to M_2			M_3			M_4			Error m.s.
	L	LB	WL	L	LB	WL	L	LB	Wl	Parental variance
HPL-5 d.f.	12	12	234	43	43	792	26	26	486	18
SY	1.9*@	1.2*@	0.6*	4.7*@	3.8*@	1.4*	1.6*@	1.1*@	0.3*	0.1
BY	13.3*@	16.3*@	5.6*	69.6*@@	14.9*@	13.1*	9.8*@	7.6*@	3.6*	2.2
HI	104.2	183.3*	33.2	98.3	92.6*	40.4	94.5*	100.6*	31.9	51.2
NP	876.9*@	947.6*@	443.0*	978.7*@@	564.6*@	440.3*	526.3*@	600.5*@	245.3*	134.3
SDW	0.5*@	0.4*	0.6*	0.5*	0.1	0.1	0.3*	0.3*	0.1	0.1
NPB	18.8*	14.7	4.3	30.1*	11.1	5.6	16.5*	14.9*	2.7	8.2
PH	66.6*@	109.4*@	8.1*	63.8*@	34.3	10.3*	36.6*@	22.2*@	7.1*	3.7
DM	92.4*	37.3*	5.8	93.2*	89.4*	4.1	95.5*	78.5*	4.0	8.7
HPL-4 d.f.	8	8	162	17	17	324	25	25	468	18
SY	4.8*@	2.4*@	0.7*	1.4*@	0.1	0.5*	2.0*@@	0.7*@	0.5*	0.2
BY	38.8*@@	10.6*	7.7*	26.6*@	3.8	8.2*	29.6*@	6.1	5.0*	3.3
NP	1303.6*@	1070.3*@	116.8*	191.2*	143.2	135.9*	272.5*@	121.3	121.2*	80.5
HI	176.5*@	102.3*	56.3*	111.3*@	94.6*	66.9*	99.7*@	158.4*@	46.5*	37.2
SDW	1.1*@@	0.3*	0.3*	0.6*	0.3*	0.5*	1.2*@	1.1*@	0.3*	0.1
NPB	15.8*@	9.5*@	3.4*	4.9*	3.3*	6.8*	10.7*@	8.7*@	5.3*	0.8
PH	61.5*@	61.1*@	16.2*	27.3*@	13.8*	16.0*	43.4*@@	17.1*@	11.1*	4.6
DM	31.9*@	11.6	10.0*	14.2	15.0	9.2*	15.8*	11.5	7.4	7.5

SY- Seed yield(g), BY-Biological Yield(g), HI-harvest index(%) NP-Number of pods, SDW-100-seed weight(g), NPB-Number of primary branches, PH-Plant height(cm), and DM-Days to maturity.

L - Lines, LB - Lines x blocks and WL-within lines.

* Significant at 5% levelm when tested against within line parental m.s.

*@Significant at 5% level when tested alsc against significant within line m.s. of respective generation

*@@Significant at 5% level, when tested also against significant m.s. due to blocks x lines interaction.

generations, whereas, for 100-seed weight it was so only in M_2. Variance due to lines was significant against parental and within lines variances in M_2,M_3 and M_4 for seed yield, biological yield, number of pods and plant height, whereas, it was so only in M_2 for 100-seed weight. Biological yield and number of pods in M_3 also exhibited significant variance due to line x block interaction. Variance due to lines was significant against parental variance fof harvest index in M_4, 100-seed weight in M_3 and M_4 and for number of primary branches and days to maturity for all the generations. Variance due to line x Block interaction was significant both against parental and within lines variances in all the generations for seed yield, biological yield and number of pods,however, it was so only in M_2 and M_4 for plant height. Variances due to line x block interaction was significant against parental variance in M_2, M_3 and M_4 generations for harvest index and days to maturity, in M_2 and M_4 for 100-seed weight and only in M_4 for number of primary branches.

Analysis of variance under 10kR for macrosperma (HPL-4) lentil: Analysis of variance in M_2, M_3 and M_4 generations for macrosperma under 10kR revealed significant within lines variance for all the traits in all the generation except for days to maturity where it was significant only in M_2 and M_3 generations. Seed yield exhibited significant variance due to line and lines x block interaction when tested against parental and within lines variances for all the generations except in M_3 where line x block interaction variance was found to be non-significant. Variance due to lines was significant against parental and within lines variance for biological yield, harvest index and plant height in M_2, M_3 and M_4, for number of pods, 100-seed weight and number of primary branches in M_2 and M_4 and for days to maturity in M_2 only.

Biological yield and 100-seed weight in M_2 and seed yield and plant height in M_4 also exhibited significant variance due to lines when tested against their respective significant variance due to line x block interaction. Number of pods, 100-seed weight and number of primary branches exhibited significant variance due to line when tested against parental variance in M_3. Line x block interaction variance was found to be significant when tested against both parental and within lines variances in M_2 and M_4 for seed yield, number of primary branches and plant height; in M_4 for harvest index and 100-seed weight and in M_2 for number of pods. Harvest index and 100-seed weight in M_2 and M_3, biological yield in M_2, number of primary branches and plant height in M_3 exhibited significant variance due to line x block interaction when tested against parental variance.

4.1.3. Analysis of variance under 15kR

The results obtained from the analysis of variance under 15kR (Table 3) are presented below variety wise:

Analysis of variance under 15 kR for microsperma (HPL-5) lentil: Analysis of variance revealed that variance within lines was significant for all polygenic traits studied, except for 100 seed weight in M_2 and seed yield and plant height in M_4. Harvest index, number of pods and number of primary branches exhibited significant variance due to lines and line x block interaction against both parental and within lines variances in all the generations under study. Seed yield and plant height also showed significant variance due to lines and line x block interaction against both parental and within lines variance. Biological yield, 100 seed weight and days to maturity also exhibited significant variance due to lines and line x block interaction

Table 3. Analysis of variance for induced genetic variation for various polygenic traits in M_2, M_3 and M_4 generations of microsperma(HPL-5) and macrosperma(HPL-4) varieties of lentil under 15 kR

Trait/ variety	m.s. due to M_2			M_3			M_4			Error m.s.
	L	LB	WL	L	LB	WL	L	LB	WL	Parental variance
HPL-5 d.f.	17	17	324	27	27	504	48	48	882	18
SY	1.6*@	1.1*@	0.5*	1.5*@@	0.7*@	0.4*	0.7*	0.7*	0.3	0.3
BY	8.5*	11.1*@	5.2*@	18.6*@@	9.6*@	5.1*	8.4*@	17.4*@	3.8*	3.3
HI	109.9*@	110.0*@	42.4*	99.6*@	106.6*@	62.4*	76.7*@	81.7*@	41.1*	30.0
NP	671.0*@	704.9*@	240.9*	1556.3*@@	698.6*@	360.7*	937.6*@	1056.5*@	268.6*	228.1
SDW	0.6*	0.5*	0.1	0.2*@@	0.5*@	0.2*	0.3*@	0.3*@	0.2*	0.1
NPB	7.1*@	5.8*@	2.4*	14.1*@	9.3*@	2.7*	368.8*@	354.5*@	8.4*	1.0
PH	32.1*@	44.2*@	6.8*	38.5*@@	12.2*@	6.5*	9.6*	14.6*	5.2	5.5
DM	17.1*@	6.2	7.9*	70.1*@	11.4	9.5*	668.6*@	623.0*@	560.6*	7.5
HPL-4 d.f.	16	16	306	5	5	108	21	21	396	18
SY	1.6*@	1.1*@	0.2*	1.0*@	0.9*@	0.3*	3.7*@@	0.9*@	0.4*	0.2
BY	8.8*	9.0*	4.3	36.3*@	3.1	4.9*	65.8*@@	8.6*@	5.8*	4.5
HI	356.4*@@	128.2*@	46.3*	69.5	156.5*@	46.6*	134.6*@	124.4*@	50.8*	34.3
NP	402.1	218.8	67.5	334.3	36.1	116.2	678.9*	173.9	102.3	256.3
SDW	2.7*	1.5*	0.3	0.9*@	1.2*@	0.4*	1.3*	2.3*	0.3	0.3
NPB	11.6*@@	4.8*@	2.2*	12.3*@	3.8	4.5*	9.0*@	5.1*@	2.9*	2.2
PH	64.6*@	33.8*@	10.6*	36.8*@	49.1*@	16.0*	37.1*@	49.7*@	11.1*	4.6
DM	59.2*@	30.0*@	8.9*	32.6*@	6.3	14.5*	38.0*@	29.0*@	13.8*	5.2

Note: Symbols carry same meaning as explained in foot note of Table 1.

against both parental and within line variances in M_3 and M_4 except for days to maturity, where variance due to line x block interaction was non-significant in M_3 and for biological yield where variance due to lines was significant against parental variance in M_2. Hundred seed weight in M_2, seed yield and plant height in M_4 exhibited significant variance due to lines and line x block interactions when tested against variance due to parent. Besides above, the Table 3 further showed that variance due to lines in M_3 for seed yield, biological yield, number of pods and plant height was also significant against their respective significant variance due to line x block interaction.

Analysis of variance under 15kR for macrosperma (HPL-4) lentil: Analysis of variance revealed significant within lines variance in M_2, M_3 and M_4 generations for seed yield, harvest index, number of primary branches, plant height and days to maturity, in M_3 and M_4 for biological yield and in M_3 for 100 seed weight. Seed yield showed significant variances due to lines and line x block interaction in M_2, M_3 and M_4 when tested against both parental and within lines variances except in M_4 where variance due to lines was also significant against its significant line x block interaction. Variances due to lines and line x block interaction for biological yield were significant against parental variance for M_2 and M_4, whereas, in M_3 variance due to lines was significant against both parental and within lines variance. Variances due to lines in M_4 for biological yield was also significant when tested against its significant line x block interaction. Harvest index had significant variance due to lines and line x block interaction when tested against their parental and within lines variances in M_2 and M_4. Variance due to lines in M_2 for harvest index was also significant when tested against significant line x block interaction. Number of pods did not

exhibit significant variance in all the generations except in M_4 where variance due to lines was significant against parental variance. Hundred seed weight exhibited significant variances due to lines and line x block interaction in M_2, M_3 and M_4 when tested against parental variance and in M_3 the variances were also significant when tested against respective within lines variances. Number of primary branches, plant height and days to maturity had significant variance due to lines and line x block interactions in M_2, M_3 and M_4 when tested against respective parental and within lines variances except variance due to line x block interaction which was non-significant for number of primary branches and days to maturity in M_3.

4.1.4. Analysis of variance under 20kR

The results obtained from the analysis of variance under 20kR (Table 4) are presented below variety wise:

Analysis of variance under 20 kR for microsperma (HPL-5) lentil: Analysis of variance revealed that variance within lines was significant when tested against parental variance for all traits in M_2, M_3 and M_4 except for days to maturity and seed yield in M_2 and M_4 and number of pods in M_4. Seed yield had a significant line x block interaction variance in M_2 when tested against parental variance and in M_3 against both parental and within lines variances. Variances due to lines and line x block interaction was significant for biological yield in M_2 and M_3 when tested against parental and within lines variances and in M_4 these were significant only when tested against parental variance. Harvest index also exhibited significant variance due to lines and line x block interactions against both parental and within lines variances in M_2 and M_4. Number of pods showed significant variances due to lines and line x block interaction against both parental and within lines

Table 4. Analysis of variance for induced genetic variation for various polygenic traits in M_2, M_3 and M_4 generations of microsperma (HPL-5) and macrosperma (HPL-4) varieties of lentil under 20kR

Trait/ variety	m.s. due to M_2			M_3			M_4			Error m.s.
	L	LB	WL	L	LB	WL	L	LB	WL	Parental variance
HPL-5 d.f.	5	5	108	6	6	126	19	19	360	18
SY	0.5	1.4*	0.2	0.5	1.1*©	0.3*	0.1	0.2	0.1	0.3
BY	19.0*©	14.4*©	2.8*	13.8*©	27.4*©	6.6*	4.9*	5.3*	2.3*	0.01
HI	274.8*©	162.3*©	44.2*	44.2	45.3	41.7*	132.6*©	155.5*©	42.8*	23.9
NP	720.9*©	360.4	202.0*	2878.5*©	223.5	179.2*	609.7*	533.2*	133.3	171.2
SDW	0.2*©	0.1*©	0.1*	0.1	0.1	0.1*	0.2*©	0.1*©	0.1*	0.1
NPB	3.6	0.9	2.1*	13.2*©	0.9	2.3*	8.8*©	10.5*©	2.3*	1.7
PH	35.9*©	15.9*©	3.4*	47.6*©©	5.5*	7.6*	19.8*©	7.2*©	6.6*	0.1
DM	56.9*	27.6	13.2	30.5	46.7*	13.8	43.8*	19.1*	10.2	15.5
HPL-4 d.f.	4	4	90	4	4	90	6	6	126	18
SY	0.1	0.5	0.3*	1.3*©	0.3	0.5*	0.3	0.2	0.1	0.3
BY	11.5*	0.5	6.9*	32.4*©	11.3*	8.9*	23.1*	1.9	3.0*	2.7
HI	51.1*	32.2	32.8*	18.5	18.2	39.2*	41.8	73.3*	45.2*	16.6
NP	106.3	197.3	45.6	191.7	247.2	82.6	177.0	133.2	45.4	118.9
SDW	1.9*©	1.8*©	0.3*	6.3*©	1.2*©	0.3*	7.0*©	4.1*©	0.3*	0.1
NPB	1.4	5.3	3.2	3.9	1.6	3.1	9.5	4.5	3.5	7.5
PH	26.2*	35.4*	17.5*	13.9*	112.6*©	10.6*	77.4*©	29.5*©	12.9*	4.7
DM	37.4*©	23.8*©	8.1*	43.9*©	76.9*©	7.5*	33.2*©	15.6*©	12.9*	4.7

Note: Symbols carry same meaning as explained in foot note of Table 1.

variances in M_2 and M_4. Number of pods showed significant variances due to lines and line x block interaction against both parental and within lines variances in M_2 and M_3, however, these variances in M_4 were significant against parental variance only. Hundred seed weight had significant variances due to lines and line x block interaction in M_2 and M_4 when tested against both parental and within lines variances. Number of primary branches exhibited such a trend for variance due to lines in M_3 and for variances due to lines and lines x block interaction in M_4. Plant height showed significant variance due to lines and line x block interaction in M_2, M_3 and M_4 when tested against both parental and within lines variances respectively except in M_3, where line x block interaction was significant only against parental variance. Days to maturity exhibited significant variance due to lines in M_2 and M_4 and line x block interaction variance in M_3 and M_4 against parental variance.

Analysis of variance under 20kR for macrosperma(HPL-4) lentil: Within lines variance was significant for all the generations studied for biological yield, harvest index, 100-seed weight, plant height and days to maturity, however, for seed yield it was significant in M_2 only. For seed yield, variance due to lines was significant only in M_3 when tested against both parental as well as within lines variances. Biological yield exhibited significant variance due to lines when tested against parental variance in M_2 and M_3. In M_4, it was significant when tested against within lines variance. Line x block interaction variance was significant against parental variance only in M_3. Harvest index exhibited significant variance due to lines in M_2 and significant line x block interaction in M_4 when tested against parental variance. Hundred seed weight and days to maturity exhibited significant variances due to lines and line x block interaction in all the generations

when tested against both parental and within lines variances except for days to maturity in M_4 where variance due to line x block interaction was significant against parental variance only. Plant height exhibited significant variances due to lines and line x block interaction when tested against both parental and within lines variances in M_4 and against parental variance in M_2 and M_3, however line x block interaction variance in M_3 was also significant against significant within lines variances.

4.2. Estimates of coefficient of variation (C.V.)

The C.V. at phenotypic level between lines (eleminating line x block interaction) and within lines was estimated to know the extent of induction of polygenic variation in M_2, M_3 and M_4 generation under various radiation doses viz., 5, 10, 15 and 20 kR in comparison to parental c.v. with respect to microsperma and macrosperma varities of lentil. The results obtained on c.v. due to lines (eleminating line x block interaction), within lines and parents are given in Tables 5 to 8. The dose wise and within dose, variety wise results obtained are given below:

4.2.1 Estimates of C.V. under 5 kR

The results obtained on the estimates of C.V. due to lines, within lines and parents (HPL-5 and HPL-4) as given in Table 5 are presented below variety wise:

. Estimates of C.V. under 5 kR for microsperma (HPL-5) lentil

Estimates of C.V. due to lines (eleminating line X block interaction) and within lines, revealed that, in general, the variation present in M_2, M_3 and M_4 was more as compared to parental variation indicating thereby the induction of variation following radiations. The C.V. due to lines was high for seed yield and biological yield in M_2. M_3 and M_4 was moderate for

Table 5. Estimates of phenotypic coefficients of variation(%) for various polygenic traits in parents, M_2, M_3 and M_4 generations in microsperma(HPL-5) and macrosperma (HPL-4) varieties of lentil under 5kR

Tnait/ variety	M_2		M_3		M_4		Parents
	BL*	WL**	BL	WL	BL	WL	WL
HPL-5							
Seed yield(g)	46.90	52.95	97.89	65.15	59.26	67.42	23.41
Biological yield(g)	50.46	31.07	52.57	33.74	58.46	33.99	32.45
Harvest index (%)	25.84	9.74	24.52	9.31	34.49	12.33	16.00
Number of pods	34.77	9.53	42.92	11.46	42.39	11.70	11.96
100-seed weight(g)	10.00	16.66	11.21	18.10	11.98	19.30	17.31
No.of primary branches	37.41	27.48	46.24	31.82	48.89	34.50	24.30
Plant height(cm)	12.84	7.58	11.77	7.25	12.17	7.24	11.26
Days to maturity	2.05	1.07	2.40	1.02	1.97	0.92	1.57
HPL-4							
Seed yield(g)	61.66	82.40	82.93	83.68	58.84	77.25	54.49
Biological yield(g)	51.10	32.90	58.09	33.25	47.05	31.23	25.26
Harvest index (%)	36.92	13.21	33.93	12.15	32.92	11.90	18.40
Number of pods	43.17	15.51	55.09	18.83	51.87	16.61	32.63
100-seed weight(g)	8.20	11.23	11.46	13.23	11.95	13.42	3.26
No.of primary branches	70.53	43.43	74.23	39.97	69.61	37.09	23.06
Plant height(cm)	18.98	8.83	21.29	10.08	19.06	8.82	11.53
Days to maturity	2.04	0.96	2.20	1.02	1.98	0.97	2.14

* Between lines eleminating line x block int.(BL)

**Within lines (WL).

harvest index, number of pods and number of primary branches in all the generations. The estimates of C.V. within lines was sufficiently high for seed yield in all the generation whereas, it was moderate for biological yield and number of primary branches in all the generations but it was, low for harvest index, 100 seed weight, plant height and maturity days.

Estimates of C.V. under 5 kR for macrosperma (HPL-4) lentil

Estimates of C.V. due to lines were in general high as compared to parental C.V. and it was also larger than within lines C.V. except for seed yield in all the generations. Moderate values of C.V. due to lines was observed for harvest index, whereas, 100 seed weight, plant height and maturity days exhibited low C.V. Within lines C.V. was high for seed yield only in all the generations, moderate for biological yield and number of primary branches and low for rest of the traits.

4.2.2 Estimates of C.V. under 10 kR

The results obtained on the estimates of C.V. due to lines, within lines and parents (HPL-5 and HPL-4) are given in Table 6 and presented below variety wise.

Estimates of C.V. under kR for microsperma (HPL-5) lentil

Estimates of C.V. due to lines were higher than the parental C.V. though within lines C.V. in some cases was marginally lower than the parental C.V.. C.V. due to lines was high for seed yield in all the generations under study. C.V. was moderate for biological yield except in M_3 where it was high for harvest index, numbers of pods and number of primary branches and it was low for 100 seed weight, plant height and days to maturity. Within lines C.V. in M_2 and M_4 was high for seed yield which was large than C.V. due

Table 6. Estimates of phenotypic coefficients of variation(%) for various polygenic traits in parents M_2,M_3 and M_4 generation in microsperma(HPL-5) and macrosperma (HPL-4) varieties of lentil under 10kR

Trait /variety	M_2		M_3		M_4		Parents
	BL	WL	BL	WL	BL	WL	WL
HPL-5							
Seed yield(g)	50.53	54.18	72.80	63.06	62.23	73.77	38.35
Biological yield(g)	38.41	29.13	55.10	26.28	38.96	27.13	28.25
Harvest index (%)	25.58	10.13	29.52	11.22	28.59	12.05	13.33
Number of pods	44.77	9.53	48.86	10.35	40.79	10.02	29.35
100-seed weight(g)	10.75	18.14	10.94	18.41	10.79	19.61	10.44
No.of primary branches	36.55	23.47	43.09	25.36	36.14	25.11	24.71
Plant height(cm)	12.96	6.59	14.63	7.27	12.55	6.98	8.35
Days to maturity	1.80	0.88	1.65	0.80	1.67	0.81	0.70
HPL-4							
Seed yield(g)	69.12	65.77	72.42	80.72	60.47	67.41	37.48
Biological yield(g)	42.19	23.86	61.86	34.64	42.84	25.63	31.88
Harvest index(%)	40.12	13.92	37.04	12.74	34.01	12.66	27.25
Number of pods	52.89	13.10	51.84	15.03	47.43	13.87	21.20
100-seed weight(g)	9.34	11.66	11.25	12.97	8.98	11.41	5.73
No.of primary branches	49.20	33.25	61.35	38.17	55.05	35.60	22.94
Plant height(cm)	15.14	2.63	16.05	7.91	13.69	7.00	8.65
Days to maturity	1.69	0.90	1.57	0.88	1.42	0.84	1.37

BL - Between lines eleminating line x block int.

WL - Within lines

to lines. Moderate estimates of C.V. within lines were noticed for biological yield and number of primary branches.

Estimates of C.V. under 10 kR for macrosperma (HPL-4) lentil

Estimates of C.V. due to lines and their comparison with parental C.V. showed that variation was induced for various polygenic traits, however, the extent of induction varied and it was quite pronounced for seed yield, number of pods and number of primary branches. C.V. due to lines was high for seed yield and number of primary branches for all the generations for number of pods in M_2 and M_3 and for biological yield in M_3. It was moderate for harvest index in M_2, M_3 and M_4 and for biological yield in M_2 and M_4. For biological yield and number of primary branches in all the generations C.V. was moderate.

4.2.3 Estimates of C.V. under 15 kR

The results obtained on the estimates of C.V. due to lines, within lines and parents (HPL-5) and HPL-4) are given in Table 7 and presented below variety wise:

Estimates of C.V. under 15 kR for microsperma (HPL-5) lentil: The estimates of C.V. due to lines were higher than the parental C.V. except for 100 seed weight in M_4 generation. C.V. due to lines was high for seed yield but within lines C.V. was still higher. Biological yield, harvest index, number of pods showed that C.V. was moderate in M_2, M_3 and M_4 and for number of primary branches it was moderate in M_2 and M_3 and was high in M_4. Hundred seed weight, plant height and maturity days showed low C.V. The induction of variation was quite prominent for seed yield, biological yield, number of pods and number of primary branches. Within lines C.V. was moderate for biological yield and number of primary branches and it was low for rest of the traits.

Table 7. Estimates of phenotypic coefficients of variation(%) for various polygenic traits in parents, M_2,M_3 and M_4 generations in microsperma(HPL-5) and macrosperma(HPL-4) varieties of lentil under 15 kR

Trait/variety	M_2		M_3		M_4		Parents
	BL	WL	BL	WL	BL	WL	WL
HPL-5							
Seed yield (g)	66.82	74.29	51.90	60.60	46.56	60.73	29.88
Biological yield(g)	41.49	27.01	43.31	27.07	36.21	25.11	25.91
Harvest index(%)	35.51	13.39	35.69	12.53	31.80	12.29	21.83
Number of pods	38.99	9.48	46.57	9.89	36.41	8.95	23.90
100-seed weight(g)	12.69	19.17	16.29	21.32	13.54	20.59	14.28
No.of primary branches	28.78	22.07	31.91	22.52	79.89	26.44	13.60
Plant height(cm)	11.59	6.58	12.28	6.89	9.99	6.48	9.53
Days to maturity	1.62	0.94	1.99	0.98	13.29	2.72	1.55
HPL-4							
Seed yield (g)	56.22	70.01	56.64	72.00	66.34	69.50	36.93
Biological yield(g)	40.01	27.09	55.32	32.39	53.51	28.01	31.00
Harvest index (%)	41.84	14.02	30.86	11.66	36.62	13.19	33.94
Number of pods	42.77	13.35	53.45	15.57	50.75	13.97	34.40
100-seed weight(g)	10.22	11.57	10.69	13.05	8.75	11.21	8.68
No.of primary branches	44.88	33.33	52.96	34.83	44.88	32.68	26.43
Plant height(cm)	14.13	6.99	18.13	8.77	13.98	7.24	8.36
Days to maturity	1.70	0.87	1.96	0.98	1.96	0.97	1.15

BL- Between lines eleminating block x line int.

WL- Within lines.

Estimates of C.V. under 15 kR for macrosperma (HPL-4) lentil: Estimates of C.V. due to lines in comparison to parental C.V. were high for all the traits in all the generations except for harvest index in M_3, where it was slightly low. Induction of variability was quite pronounced for seed yield, number of pods and number of primary branches. Seed yield in all the generations, biological yield and number of pods in M_3 and M_4 and number of primary branches in M_3, showed high amount of C.V. due to lines, whereas, moderate C.V. was noticed for harvest index in all the generations, for biological yield and number of pods in M_2 and for number of primary branches in M_2 and M_4. Within lines C.V. was very high for seed yield which was higher than C.V. due to lines. Biological yield and number of primary branches exhibited moderate within lines C.V. Rest of the traits i.e. harvest index, number of pods, 100 seed weight, plant height and maturity days showed low within lines C.V.

4.2.4 Estimates of C.V. under 20 kR

The results obtained on the estimates of C.V. due to lines, within lines and parents (HPL-5 and HPL-4) are given in Table 8 and presented below variety wise:

Estimates of C.V. under 20 kR for microsperma (HPL-5) lentil: The estimates of C.V. indicated the induction of sufficient variability for all the traits following radiation. However, C.V. was more pronounced for seed yield, biological yield, number of pods and number of primary branches. The C.V. due to lines was high only in M_3 for biological yield and number of pods. Seed yield, harvest index and number of primary branches exhibited a moderate C.V. due to lines in all the generations, whereas, it was so only in M_2 and M_4 for biological yield and number of pods and low for 100 seed weight, plant height and days to maturity in all the generations.

Table 8. Estimates of phenotypic coefficients of variation(%) for various polygenic traits in parents, M_2, M_3 and M_4 generations in microsperma (HPL-5) and macrosperma (HPL-4) varieties of lentil under 20 kR

Trait/variety	M_2		M_3		M_4		Parents
	BL	WL	BL	WL	BL	WL	WL
HPL-5							
Seed yield(g)	39.52	55.12	42.94	56.26	35.66	56.77	26.72
Biological yield (g)	40.21	27.37	48.16	29.20	38.91	30.56	1.10
Harvest index(%)	30.92	10.69	27.71	10.89	30.35	11.28	19.47
Number of pods	42.65	10.65	63.79	13.17	43.10	11.64	30.60
100-seed weight(g)	9.23	17.81	9.22	17.83	9.45	18.01	7.87
No.of primary branches	29.33	23.99	39.17	28.54	37.31	28.35	18.60
Plant height(cm)	10.49	6.35	15.62	8.36	12.80	7.61	1.52
Days to maturity	2.55	1.09	2.40	1.12	2.43	1.02	2.27
HPL-4							
Seed yield(g)	40.60	57.80	71.04	61.08	41.46	52.63	40.15
Biological yield(g)	48.02	25.66	77.38	29.41	78.41	31.28	24.34
Harvest index(%)	30.81	11.39	30.60	11.89	32.40	11.02	23.60
Number of pods	42.99	12.82	43.28	13.56	56.54	13.92	20.85
100-seed weight(g)	16.41	11.67	28.07	11.30	28.25	11.02	5.38
No.of primary branches	38.60	31.72	40.19	28.47	66.35	35.51	27.54
Plant height(cm)	17.24	7.54	14.15	7.28	24.95	7.04	8.40
Days to maturity	2.24	0.85	2.22	0.83	1.97	0.96	1.09

BL- Between lines eleminating block x lines int.

WL- Within lines.

Within lines C.V. was high only for seed yield where its value was greater than the C.V. due to lines. A moderate estimate of C.V. due to within lines was observed for biological yield and number of primary branches Rest of the traits exhibited a low value of within lines C.V.

Estimates of C.V. under 20 kR for macrosperma (HPL-4) lentil: As indicated by the estimates of C.V., sufficient variability was induced for all the traits under study. C.V. due to lines was quite high for biological yield in all the generations, for seed yield in M_3 and for number of primary branches in M_4 and it was moderate for harvest index in all the generations, for seed yield in M_2 and M_4, for number of pods in M_2 and M_3, for 100-seed weight in M_3 and M_4, for number of primary branches in M_2 and M_3 and for plant height in M_4. Within lines C.V. was higher for seed yield only and in M_2 and M_4 it was even higher than the C.V. due to lines. Biological yield and number of primary branches showed moderate within lines C.V. Rest of the traits exhibited a low amount of within lines C.V.

4.3. Estimates of heritability (broad sense)

Heritability was estimated in broad sense, firstly, with respect to induced variation due to lines by eleminating as well as by ignoring line x block interaction and induction of variation within lines for various polygenic traits in M_2, M_3 and M_4 generations under various radiation doses studied for microsperma and macrosperma varieties of lentil. The results obtained on various estimates of heritability are incorporated in Tables 9 to 12. The dose wise and within dose variety wise results obtained are presented below in the following pages.

4.3.1. Estimates of heritability under 5kR

Results obtained on the estimates of heritability under 5 kR are given in Table 9 and presented below variety wise:

Estimates of heritability under 5kR for microsperma(HPL-5) lentil: Heritability estimates indicated that in general heritability was high between lines when variance due to line x block interaction was ignored as compared to one, when it was eleminated. Heritability within lines capitalising on heterozygous gene loci following mutagenesis was substantial for seed yield and number of pods in all the generations and in M_4 only for 100-seed weight. Heritability between lines after eleminating line x block interaction was quite large for seed yield in M_2 and moderate for 100-seed weight and number of primary branches in all the generations. Heritability computed after ignoring Line x block interaction was very high for seed yield, number of pods, number of primary branches, plant height and maturity days for all the generations under study, whereas, it was moderate for 100-seed weight in M_2, M_3 and M_4: and in M_4 only for biological yield. Rest of the traits under various generations either exhibited very low or nil heritability.

Heritability estimates under 5kR for macrosperma (HPL-4) lentil: Within lines heritability estimates were high for 100 seed weight, number of primary branches and plant height in M_2, M_3 and M_4 generations and number of pods in M_4, where heritability estimates were moderate in M_2 and M_3 generations. Heritability estimates as observed in *microsperma* were inflated when computed by ignoring line x block interaction. However, heritability after eleminating line x block interaction was high in M_2 for biological yield and moderate for number of pods, plant height and maturity days. In M_3 and M_4, all the traits except

Table 9. Estimates of heritability(broad sense) for induced variation for various polygenic traits in M_2,M_3 and M_4 generations of microsperma (HPL-5) and macrosperma(HPL-4) varieties of lentil under 5kR

Trait/ variety	M_2			M_3			M_4		
	BLe	BLi	WL	BLe	BLi	WL	BLe	BLi	WL
HPL-5									
Seed yield (g)	69.4	91.1	75.0	23.2	99.4	97.7	26.9	94.8	94.6
Biological yield(g)	19.0	-	-	18.7	-	-	18.2	48.9	-
Harvest index (%)	-	-	-	12.6	-	-	27.0	-	-
No.of pods	17.5	96.8	83.8	17.5	97.0	85.2	23.9	97.1	80.7
100-seed wt. (g)	32.0	46.9	-	29.6	51.1	-	24.6	48.8	58.5
No.of primary branches	28.7	70.3	-	24.7	74.7	-	27.1	73.2	-
Plant height (cm)	16.6	49.5	10.0	15.8	59.8	-	21.4	68.7	-
Days to maturity	4.9	54.5	25.2	4.2	91.2	17.6	4.1	87.3	-
HPL-4									
Seed yield (g)	-	66.4	-	16.7	61.7	26.7	13.7	5.9	-
Biological yield(g)	56.7	39.2	2.00	16.1	66.7	19.5	14.5	53.5	-
Harvest index (%)	-	-	-	16.1	-	-	18.7	-	-
No.of pods	26.3	58.4	25.1	26.9	54.6	37.3	14.3	99.4	98.7
100-seed wt. (g)	-	72.9	68.7	14.6	90.4	82.1	6.9	92.9	83.3
No.of primary branches	-	54.7	75.4	-	77.4	84.5	8.9	93.5	81.8
Plant height (cm)	19.3	80.8	51.0	19.8	59.9	55.1	15.1	84.4	46.8
Days to maturity	19.8	64.9	-	12.6	59.1	-	12.9	52.3	-

Ble - Between lines eleminating line x block int.

Bli - Between lines ignoring line x block int.

WL - Within lines

number of primary branches in M_3, showed a moderate to low estimates of heritability. Heritability estimates were high when computed by ignoring interaction variance for number of pods, 100-seed weight, number of primary branches, plant height and maturity days in all the generations. For biological yield the estimates were high in M_3 and M_4 but moderate in M_2, whereas for seed yield, these were high in M_2 and M_3 and low in M_4.

4.3.2. Estimates of heritability under 10kR:

Results obtained on the estimates of heritability under 10kR are given in Table 10 and presented below variety wise:

Estimates of heritability under 10kR for microsperma (HPL-5) lentil: Heritability estimates indicated within lines heritability were high for seed yield in all the generations, for biological yield and number of pods in M_2 and M_3 and for 100 seed weight in M_2. Plant height exhibited a moderate amount of heritability within lines for all the generations, whereas, it was so only in M_4 for biological yield and number of pods. Heritability between lines by ignoring interaction variance was as usually more, being very high for seed yield, biological yield, number of pods, 100-seed weight, plant height and maturity days in all the generations and in M_3 for number of primary branches. It was moderate for primary branches in M_2 and M_4 generations. Harvest index exhibited a moderate heritability only in M_4. Heritability estimated by eleminating line x block interaction variance was high only for maturity days in all the generations whereas, it was moderate for number of pods, in M_2, M_3 and M_4 and for 100 seed weight and plant height in M_2 and M_3 generations.

Estimates of heritability under 10kR for macrosperma (HPL-4) lentil: Heritability estimates within lines of different generations were very high for seed yield and number of primary branches, whereas, it was so only in M_3 for 100-seed weight

Table 10. Estimates of heritability(broad sense) for induced variation for various polygenic traits in M_2,M_3 and M_4 generations of microsperma(HPL-5) and macrosperma(HPL-4) varieties of lentil under 10kR

Trait/ variety	M_2			M_3			M_4		
	BLe	BLi	WL	BLe	BLi	WL	BLe	BLi	WL
HPL-5									
Seed yield (g)	19.9	85.7	60.5	19.6	93.9	80.9	14.9	83.3	42.3
Biological yield (g)	16.4	70.9	42.8	17.8	93.7	70.6	17.9	62.7	23.3
Harvest index(%)	19.6	-	-	16.7	-	-	18.0	29.7	-
No.of pods	34.7	73.4	53.4	35.8	75.8	53.2	35.4	59.3	29.2
100-seed wt.(g)	25.8	74.2	78.9	25.6	73.8	-	13.1	54.3	-
No.ofPrimary branches	14.4	38.9	-	17.9	56.9	-	20.2	33.3	-
Plant height(cm)	26.4	89.2	36.6	26.6	88.9	46.6	17.1	81.4	31.0
Days to maturity	42.5	82.8	-	52.2	82.9	-	53.1	83.3	-
HPL-4									
Seed yield (g)	21.4	93.2	62.6	26.6	78.3	54.7	13.4	84.6	49.2
Biological yield (g)	16.7	84.1	39.5	16.2	77.6	41.9	19.6	79.6	19.9
Harvest index(%)	19.6	65.2	20.5	19.3	49.9	28.6	15.4	45.6	11.1
No. of pods	33.7	88.4	18.4	-	40.7	25.6	35.9	54.4	20.2
100 seed weight (g)	10.3	78.9	43.5	10.5	67.5	61.8	14.1	80.6	36.6
No. of Primary branches	15.3	90.6	62.9	-	72.5	79.6	14.9	86.5	74.2
Plant height(cm)	12.2	86.1	55.8	-	71.2	55.4	12.7	80.9	41.5
Days to maturity	9.9	61.7	14.0	-	-	10.1	5.4	35.5	-

Ble - Between lines eleminating line x block int.

Bli - Between lines ignoring line x block int.

WL - Within lines.

and M_2 and M_3 for plant height. Moderate heritability within lines was found for biological yield in M_2 and M_3, harvest index and number of pods in M_3, 100 seed weight and plant height in M_4. None of the trait in any generation showed high amount of heritability computed after eleminating line x block interaction, however, moderate estimates were found for number of pods in M_2 and $M_4$and seed yield in M_3. Other traits exhibited low to nil heritability. Heritability estimates computed by ignoring interaction variance were very high in all the generations for seed yield, biological yield, harvest index, 100-seed weight, number of primary branches and plant height. It was also high for number of pods in M_2 and M_4 and for days to maturity in M_2. Moderate estimates were found for number of pods in M_3 and days to maturity in M_4.

4.3.3. Estimates of heritability under 15kR

Results obtained on the estimates of heritability under 15kR are given in Table 11 and presented below variety wise:

Estimates of heritability under 15kR for microsperma (HPL-5)lentil: Estimates of heritability within lines were very high for number of primary branches and maturity days in M_4. Generally, the lines exhibited moderate to low heritability. Heritability estimates within lines were moderate for number of primary branches in M_3 and M_4 and for harvest index in M_3. Heritability estimates after eleminating variance due to line x block interaction was high only for number of primary branches in M_4. Generally, all other traits under different generations showed a low heritability. Estimates of heritability obtained after ignoring line x block interaction was quite high for seed yield, biological yield, harvest index, number of pods, 100-seed weight, number of primary branches and days to maturity in all the generations and in M_2 and M_3 only in case of plant height where heritability was moderate in M_4.

Table 11. Estimates of heritability (broad sense) for induced variation for various polygenic traits in M_2, M_3 and M_4 generations of microsperma (HPL-5) and macrosperma (HPL-4) varities of lentil under 15kR

Trait/ variety	M_2			M_3			M_4		
	BLe	BLi	WL	BLe	BLi	WL	BLe	BLi	WL
HPL-5									
Seed yield (g)	9.7	63.6	21.3	12.4	63.1	7.9	16.9	35.8	-
Biological yield (g)	-	44.0	22.7	11.8	69.9	21.2	15.6	43.8	7.9
Harvest index(%)	7.4	57.1	17.0	2.9	53.6	35.0	4.1	43.7	15.6
No. of pods	18.2	49.2	2.7	14.2	74.4	22.5	11.2	60.9	8.1
100 seed weight (%)	15.2	62.6	-	18.2	79.7	24.3	15.7	45.1	9.7
No. of Primary branches	19.0	74.5	39.5	17.5	86.3	45.3	68.1	99.4	78.0
Plant height(cm)	15.2	70.9	11.4	19.7	75.1	8.7	14.1	27.6	-
Days to maturity	5.5	38.8	2.4	24.1	80.6	11.6	9.5	97.7	97.3
HPL-4									
Seed yield (g)	20.7	76.2	8.3	18.5	64.2	15.4	27.9	88.9	32.3
Biological yield (g)	25.1	32.7	-	24.2	77.9	4.2	34.3	87.2	12.2
Harvest index(%)	25.8	82.4	14.8	23.8	-	15.1	17.6	59.3	19.3
No. of pods	19.8	-	-	18.6	-	-	20.7	45.2	-
100 seed weight (g)	28.4	78.6	-	25.9	46.8	9.6	16.8	59.7	-
No. of primary branches	17.7	68.4	0.2	17.9	69.9	34.9	19.5	60.9	13.9
Plant height(cm)	20.2	86.6	39.1	26.1	77.6	55.0	19.5	77.7	40.9
Days to maturity	21.9	83.8	26.4	5.9	72.4	47.0	8.1	76.1	45.4

Ble - Between lines eleminating line x block int.

Bli - Between lines ignoring line x block int.

WL - Within lines.

Estimates of heritability under 15kR for macrosperma(HPL-4)lentil: Heritability estimates indicated a moderate to low heritability within lines in all the generations for various polygenic traits. These estimates were moderate in M_3 for seed yield and number of primary branches and in M_2 and M_4 for plant height and maturity days. Moderate to low heritability estimates were found for various traits when heritability between lines was computed after eleminating variance due to line x block interaction. It was moderate for seed yield in M_4, for biological yield in all the generations, for harvest index in M_2, for 100 seed weight in M_2 and M_3, for plant height in M_3. Heritability estimates obtained after ignoring interaction was very high for seed yield, 100-seed weight, number of primary branches, plant height and days to maturity in all the generations, for biological yield in $M_3$and M_4, for harvest index in M_2 and M_4 and moderate for biological yield in M_2 and number of pods in M_4.

4.3.4. Estimates of heritability under 20 kR

Results obtained on the estimates of heritability under 20kR are given in Table 12 and presented below variety wise:

Estimates of heritability under 20kR for microsperma(HPL5) lentil: A very high heritability estimates within lines was obtained for biological yield and plant height in all the generations, whereas a moderate value was obtained for harvest index in all the generations. Heritability estimates obtained after eleminating line x block interaction variance was moderate for biological yield in all the generations, for harvest index in M_2 and M_4, for number of pods in M_3 and for plant height in all the generations. Heritability values estimated after ignoring line x block interaction were high for biological yield, number of pods and plant height in all the generations, for harvest index, 100-seed weight and maturity days in M_2 and M_4 generations.

Table 12. Estimates of heritability (broad sense) for induced variation for various polygenic traits in M_2, M_3 and M_4 generations of microsperma (HPL-5) and macrosperma (HPL-4) varities of lentil under 20 kR

Trait/ variety	M_2			M_3			M_4		
	BLe	BLi	WL	BLe	BLi	WL	BLe	BLi	WL
HPL-5									
Seed yield (g)	-	-	-	-	-	5.0	-	-	-
Biological yield (g)	22.1	99.9	99.5	25.2	99.9	99.8	25.3	99.7	99.4
Harvest index (%)	20.7	83.9	29.9	-	-	27.1	19.5	69.4	28.4
No. of pods	11.4	61.6	8.2	42.9	88.7	2.2	14.8	56.1	-
100 seed weight(g)	17.6	50.9	7.1	-	-	14.7	11.8	60.3	7.1
No. of primary branches	-	-	9.6	18.9	76.8	14.7	12.7	67.5	13.7
Plant height(cm)	32.1	99.1	91.8	28.7	99.3	96.2	19.1	98.5	95.6
Days to maturity	14.2	56.9	-	5.7	-	-	1.1	47.7	-
HPL-4									
Seed yield (g)	-	-	16.1	50.0	68.2	27.7	42.2	-	-
Biological yield (g)	-	61.0	42.6	56.9	84.1	52.3	76.7	78.5	4.5
Harvest index(%)	-	50.8	32.6	-	-	40.3	-	-	46.1
No. of pods	-	-	-	-	-	-	59.2	-	-
100 seed weight (g)	70.1	88.8	49.5	91.3	96.3	42.1	91.3	96.7	46.1
No. of primary branches	-	-	-	-	-	-	46.8	-	-
Plant height	-	69.6	57.7	-	49.5	38.5	71.3	88.5	46.7
Days to maturity	71.2	77.7	26.9	69.2	80.7	22.8	43.9	75.2	46.8

Ble - Between lines eleminating line x block int.

Bli - Between lines ignoring line x block int.

WL - Within ; lines.

Estimates of heritability under 20kR for macrosprama(HPL-4)lentil: Heritability estimates within lines were high for 100-seed weight and number of primary branches in M_2, for biological yield, harvest index and 100-seed weight in M_3 and harvest index, 100 seed weight, plant height and days to maturity in M_4. Moderate heritability estimates within lines variance were obtained for seed yield in M_3, for harvest index in M_2 and M_3, for plant height in M_3, for maturity days in M_2 and M_3. Heritability estimates obtained by eleminating line x block interaction variance were quite high for 100-seed weight and days to maturity in all the generations,for seed yield and biological yield in M_3 and M_4 and for number of pods, number of primary branches and plant height in M_4 generation. Estimates of heritability obtained after ignoring line x block interaction were quite high for biological yield, 100 seed weight, plant height and days to maturity in all the generations, for seed yield in M_3 and for harvest index in M_2.

4.4. Estimates of individual line mean and within line analysis of variance in M_3 and M_4 generation

In M_3 and M_4 generations, estimates of means were obtained for all the lines studied individually for various polygenic traits under different radiation doses studied for both microsperma and macrosperma varieties of lentil in order to isolate the desirable mutant lines in comparison to parents (Control). The results obtained on the estimates of individual line mean are given in Tables 13 to 20. In order to know the magnitude of induced variation within line, analysis of variance within line was also carried out for all the lines in M_3 and M_4 generations under all radiation doses for both the varieties. The actural results obtained are available in records and here in order to avoid lengthy tables, the lines which showed significant within line variance are marked with star(*) in Tables 13 to 20. The lines in these tables having

their mean values marked with star(*) indicate that for these lines within line variance is significant at 5 per cent level. The mean values marked with '@' indicate that these values are significantly deviating from their parental mean in the desired direction. The desired direction for all the traits except days to maturity is positive shift from the parental values. The dose wise and within dose variety wise results obtained on the estimates of individual line mean and within line analysis of variance in M_3 and M_4 are given below:

4.4.1. Estimates of individual line mean and within line analysis of variance under 5 kR

The variety wise results obtained on the estimates of line mean and within line analysis of variance under 5 kR are given in Tables 13 and 14 and presented below:

Estimates of individual line mean and within line analysis of variance(Table 13) under 5 kR for microsperma (HPL-5) lentil

Analysis was done at individual plant level in M_3 and M_4 to assess the shift in mean of different lines at micro level and also to reveal the segregation pattern of mutant loci. Line mean analysis indicated that only one line out of 89 lines in M_3 and none of the lines out of 61 lines in M_4 showed significantly positive shift in mean for seed yield. The line showing significant shift was HPLM 74 which showed a 280.5 per cent increase over control. For biological yield 5 lines in M_3 and 7 lines in M_4 exhibited superiority over control. 15 and 4 lines for number of pods, 8 and 4 lines for 100 seed weight showed a significant positive shift in M_3 and M_4, respectively. For number of primary branches only 3 lines in M_3 were found to be superior as compared to control. None of the lines exhibited superiority for harvest index, plant height and days to maturity.

Table 17. Estimates of line mean alongwith within line analysis of variance in M_3 and M_4 generations of microsperma (HPL-5) variety of lentil under 5kR

Progeny/ generation	Seed yield per plant (g)	Biological yield per plant	Harvest index per plant (%)	Number of pods per plant	100-seed weight (g)	Number of primary branches per plant	Plant height (cm)	Days to maturity
1.	2.	3.	4.	5.	6.	7.	8.	9.
M_3								
HPLM 1	1.32*	4.70	28.03	30.05*	2.98	5.05	20.50	174.05
2	1.09*	6.04*@	27.05	24.95*	3.14@	4.10	19.87	174.25
3	1.014	3.71	24.72	31.00*	2.87	4.90	21.12	173.95
4	1.11*	4.54	28.04	37.30*@	2.59	5.45	22.10	175.20
5	1.05*	3.85	22.97	28.80*	2.82	3.95	19.70	174.35
6	1.15	3.88	26.69	30.00*	2.61	4.55	21.17	175.00*
7	1.25	4.77	25.49	29.55*	2.63	3.90	21.57	171.00
8	0.88*	3.45	26.78	27.20*	2.80	4.05	20.51	174.75
9	1.18*	3.96	26.15	25.65*	2.48	2.70	21.10	175.65*
10	1.08*	4.19	24.31	30.50*	2.78	4.15	20.20	175.05
11	1.40*	4.16	28.28	28.25*	3.13@	3.90	20.40	175.65
12	1.71*	5.82@	30.65	36.15*	2.90	4.80	23.25	175.50*
13	1.51*	4.52	29.60	36.10*	3.36@	3.90	20.95	174.65*
14	1.53*	4.30	28.96	32.05*	2.76	4.10	20.22	175.75
15	1.29*	4.28	29.91	24.00*	2.68	2.40	19.50	175.95
16	0.72	2.35	26.95	23.55*	2.88	2.55	19.45	176.00
17	1.08*	4.01	26.12	28.55*	2.87	4.15	21.25	178.85
18	2.03*	7.06*@	28.21	38.15*@	2.94	5.10	21.07	172.00*
19	1.37*	5.15*	24.69	29.70*	2.75	4.75	21.17	176.90
20	1.71*	5.31	28.45	42.40*@	2.81	3.80	22.17	175.15
21	1.33*	4.00	29.14	26.65*	2.64	5.25	21.65	175.50

Contd

Table 13 Contd.

1.	2.	3.	4.	5.	6.	7.	8.	9.
22	1.69*	5.49	26.37	44.35*@	2.77	3.95	21.35	175.60
23	1.40*	4.96	29.13	34.35*	3.00	3.55	20.87	175.80*
24	1.28*	4.25	28.05	3[illegible]35*@	2.72	5.10	20.32	174.90
25	1.44	5.17	27.31	37.70*@	2.65	5.05	20.65	174.50
26	1.59*	5.52	29.54	38.40*@	2.72	5.15	22.12	175.70*
27	1.48	4.82	29.04	35.90*	3.02	4.70	21.37	174.15*
28	1.18	4.23	26.82	29.55*	2.79	3.55	20.02	176.35
29	1.33*	4.71	27.22	33.70*	2.90	4.50	21.97	174.30
30	1.41*	4.54	27.79	29.40*	2.93	4.30	21.95	172.85
31	1.48*	4.77	29.43	25.90*	2.97	4.25	21.00	173.00
32	1.38*	5.86@	23.87	32.95*@	2.70	4.85	21.07	174.15
33	0.91*	3.29	24.76	22.15*@	2.78	3.90	18.97	173.55
34	0.78	2.89	26.69	22.55*	2.72	3.15	20.95	174.25
35.	1.29	4.62	27.62	34.85*	2.54	4.05	20.50	175.05
36	1.09*	3.63	28.55*	32.15*	2.81	3.65	20.45	176.05
37	1.58*	5.37	28.64	24.80*	2.81	3.90	20.30	174.80
38	1.37*	4.65	26.30	28.60*	2.94	1.95	21.00	173.80
39	1.11*	3.46	27.03	38.20*@	2.89	3.90	21.57	175.10*
40	1.09*	3.77	24.67	27.25*	2.83	3.80	21.30	176.60
41	1.03*	3.95	25.33	26.65*	2.82	2.25	20.95	177.85
42	1.46*	4.41	30.28	23.20*	2.68	3.25	20.30	176.55
43	1.45*	5.74	24.45	29.95*	2.74	4.05	19.90	175.50
44	1.19*	4.80	26.32	34.90*	2.97	4.70*	19.66	176.05*
45	1.33*	4.73	26.16	31.20*	3.07	4.45	20.92	177.60*
46	1.40*	4.83	28.92	37.00*@	3.28@	5.75@	19.72	172.90

Table13 Contd.

1.	2.	3.	4.	5.	6.	7.	8.	9.
47	1.25*	3.84	26.89	21.35*	2.94	3.45*	19.40	175.30
48	1.53*	5.16	27.46	19.55*	2.85	3.45	18.35	171.65
49	1.02*	3.48	28.59	22 3*	2.89	3.00	18.8C	178.15
50	1.08	4.27	20.90	29.95*	2.99	3.60	21.50	181.00
51	1.20*	4.64	24.29	27.05*	2.75	4.45	20.07	181.30.
52	1.33*	4.85	27.83	29.20*	2.93	3.65	20.45*	174.55
53	1.32*	3.98	28.22	20.60*	2.98	2.90	20.97*	184.40*
54	1.45*	4.98	28.36	32.75*	2.71	4.15	21.12	173.80
55	1.48*	4.32	30.15*	27.95*	2.75	3.65	20.37	171.00
56	1.15*	4.13	28.68	22.50*	3.18@	2.70	22.22	172.70
57	0.99*	3.53	27.50	31.60*	2.87	3.45*	21.80	179.6C
58	1.24*	4.35	28.29*	26.30*	3.00	3.55*	18.07	176.30
59	1.63*	5.27	27.96*	33.35*	2.54	3.85*	19.87	180.75
60	1.07*	4.31	22.95	30.65*	2.99	4.90*	20.42	177.95
61	1.26*	3.95	26.28	26.40*	2.75	3.95	19.70	175.85
62	1.31*	3.47	28.52	31.20*	2.91	4.95	19.82	177.65
63	1.22*	3.52	26.89	22.00*	2.82	2.75*	20.00	180.50
64	1.41*	4.85	26.93	2[illegible].50*	2.93	3.95	19.57	179.10
65	1.24*	4.42	24.71	29.75*	2.68	3.20	18.77	177.90
66	1.19*	4.67	26.21	21.25*	2.96	3.80	19.15*	174.10
67	1.36*	4.71	27.98	27.20*	2.24	4.00	20.65*	176.05
68	0.88	3.40	27.07	29.75*	2.90	4.25	19.87	175.40
69	1.43*	3.54	29.74	30.40*	2.99	4.60	20.17	173.25
70	1.30*	5.06*	26.10	31.25*	2.75	3.25	20.25	175.00
71	0.76	3.02	24.28	20.00*	2.43	1.95	17.50*	175.60

Contd,...

Table 15 Contd.

1.	2.	3.	4.	5.	6.	7.	8.	9.
72	1.39*	4.48	23.28	30.65*	3.09	3.05*	20.10	177.65
73	1.40*	5.34	21.14*	29.00*	2.84	4.20	18.45	180.50
74	14.30@*	4.74	20.53	38 .0*@	2.90	5.05	20.72	173.65
75	2.13*	6.11@	20.21	43.95*@	3.01	6.65@	22.05	171.40
76	0.89	2.63	29.25	18.10*	2.70	1.10	19.07	180.20
77	0.88	2.54	28.99	20.85*	2.95	2.35	20.52	182.30
78	1.13	3.86	27.20	22.90	2.99	2.30	20.45	171.00
79	1.21	3.36	31.34	20.95	3.17@	2.60	20.37	181.65
80	0.80	3.00	26.98	14.90	2.90	3.75	19.30	180.55
81	1.13*	4.51	18.22	31.05*	2.97	4.70	21.22	181.80
82	1.62*	5.04	24.20*	43.60*@	3.07	6.65*@	22.57	175.30
83	1.22	4.65	24.34	34.60	3.04	5.05	22.65	176.80
84	1.36*	4.08	19.87*	28.65*	2.72	4.00	20.50	178.85
85	1.98*	5.43	22.16	36.80*@	3.29@	4.80	21.80*	178.70
86	1.292*	4.42	23.57	33.65*@	3.38@	4.10	20.22	180.70
87	1.43*	4.44	21.32	29.65*	2.85	3.90*	19.85	181.95
88	1.29*	4.95*	24.02	30.85*	2.75	3.10	19.02*	175.65*
89	0.87	3.32	22.25*	.80*	2.86	3.20	18.77	175.65*
M4								
90	1.94	6.02@	23.27	34.20*	2.70	4.00	20.27	178.0
91	1.98	6.38@	18.11	31.00*	2.54	3.70	20.30	178.7
92	1.98	5.87@	23.10	43.30*@	2.61	4.35	22.55	177.65
93	1.97	5.08	18.19	36.95*@	2.72	4.80	23.22	174.50*
94	1.97	3.33	23.91	34.20*	2.74	3.40	19.62	177.25
95	1.96	5.44	19.54	37.85*@	2.56	5.00	20.65	177.80

Contd...

Table13 Contd.

1.	2.	3.	4.	5.	6.	7.	8.	9.
96	1.99	5.38	23.06	29.40*	2.62	4.80	20.72	177.90
97	1.98	4.95*	27.98	32.55*	2.60	3.25	21.72	175.75
98	1.97	4.94	19.60	34.95*	2.64	5.10	20.77	180.70
99	1.96	5.31	21.74	34.35*	2.65	4.95	20.57	176.15*
100	1.96	4.15	22.67	34.70*	2.65	2.70	20.37	177.80
101	1.97	3.88	25.38	32.05*	2.65	4.40	22.05	179.80
102	1.97	5.61	23.20	31.50*	2.55	4.25	20.57	177.75
103	1.96	5.06	25.43	28.60*	2.80	3.40	21.45	178.10
104	1.90	4.25	22.74	28.80*	2.98	3.85	20.52	178.45
105	1.06*	4.43	22.26	28.20*	2.77	3.60	20.60	177.60
106	1.01*	3.32	22.15	29.83*	2.71	4.15	21.40	179.10
107	1.08*	4.70	19.95	32.80*	2.82	4.30	19.77	175.20
108	1.23*	4.45	21.93	27.85*	2.86	3.55	19.95	180.00
109	1.28	5.02*	21.61	27.55*	2.80	3.05	19.17	179.40
110	1.02*	3.65	26.42	25.75*	2.80	3.55	18.80	179.20
111	1.62*	5.15	23.47	29.50*	2.91	3.10	20.55	180.35
112	1.11	3.94	22.83	28.50*	2.73	3.35	21.25	174.45
113	1.17*	5.87*@	21.57	33.45*	2.56	4.85	22.72	176.55
114	1.70*	5.95@	20.97	35.05*	2.93	3.40	20.95	178.25
115	1.31*	4.27	27.47	31.30*	2.94	3.95	22.00	180.10
116	1.20*	4.17	22.53	29.55*	2.75	4.15	21.52	177.70
117	1.13*	4.08	23.14	29.85*	2.77	5.15	20.90	179.20
118	1.21*	4.04	21.27	29.90*	3.25@	2.90	19.82	178.80
119	1.28*	5.48	19.26	26.65*	2.90	2.50	20.90	177.80
120	1.35*	5.46*	19.37	27.85*	2.52	3.30	21.50	178.05
121	0.66	3.21	20.76	23.10	2.62	2.95	21.30	174.05

Contd...

Table13 contd.

1.	2.	3.	4.	5.	6.	7.	8.	9.
122	1.32	4.05	26.81	18.40*	2.55	1.85	20.82	176.20
123	1.19*	4.46	21.45	29.05*	3.10@	4.15	22.67*	180.55
124	0.97	3.26	27.69	27.25*	3.05	3.75	22.85	178.10
125	1.16*	4.49	20.86	33.20*	2.83	4.10	21.47	179.15
126	1.19*	3.59	21.00	25.70*	3.06	3.60	20.65	179.45
127	1.27*	4.00	24.58	28.25*	2.94	4.15*	20.22	178.10
128	1.67	2.74	19.22	25.25*	2.79	3.60	19.95	174.70*
129	0.86	2.95	20.29	22.70*	2.85	2.60	20.32	175.20
130	0.70	3.28	17.31	20.75*	2.81	2.20	19.97	173.20
131	0.79*	2.65	20.67	20.15*	2.78	3.35	19.66	173.95
132	1.62	3.07	17.34	25.25*	2.92	3.65	20.70	173.80
133	0.83	3.58	20.85	21.25*	3.06	2.70	21.45	174.05
134	1.37*	5.98@	21.03	32.05*	2.78	4.00	20.12	173.10
135	1.69	2.69	20.29	20.00	2.96	2.80	19.25	173.40
136	1.63*	6.73*@	20.14	17.25*	3.02	1.95	21.17	173.80
137	1.67	2.69	21.74	26.10*	2.94	3.20	18.15*	174.15
138	1.63	2.41	20.74	13.20*	2.72	2.80	19.70	174.55*
139	1.64	2.49	19.71	21.50*	2.76	2.35	17.87	173.40
140	1.51	2.60	17.46	22.15*	3.32@	3.70*	15.92	174.95
141	1.64	2.35	19.78	17.05*	3.13@	2.05	20.70	179.95*
142	0.72	3.17	24.59	20.55*	2.79	3.40	19.80	177.80
143	1.63	2.80	20.66	21.45*	2.78	2.20	19.97	179.35
144	1.69	2.94	17.96	22.85*	2.74	3.30	19.72	180.30
145	1.60	3.22	17.83	17.85@	2.62	2.45	19.92	180.55
146	0.84	3.12	19.27	25.70*	2.86	4.40	18.47	180.45
147	1.07	4.76	15.98@	20.35*	2.53	2.80	20.52	178.90*

Contd...

Table 13 Contd.

1.	2.	3.	4.	5.	6.	7.	8.	9
148	1.05*	4.35	18.21	19.90*	2.70	3.10	18.67	179.60
149	0.96	3.62*	21.46	18.70*	2.68	2.10	21.27	178.30
150	0.84	3.65	20.44	20.25*	2.92	2.65	20.67	175.25
HPL-5 (control)	1.13	3.61	27.02	27.30	2.71	3.75	21.50	172.30
Parental S.E ±	0.06	0.66	2.78	0.73	0.11	0.37	0.54	0.60
Line mean S.E ±	0.87	0.97	2.71	5.96	0.18	0.96	1.15	2.63
Pooled S.E ±	0.65	1.15	3.87	4.71	0.20	0.93	1.19	2.28
Lines falling outside the parental range	M_3 1	5	0	1.5	.8	3	0	0
	M_4 0	7	0	4	4	0	0	0

* indicates lines with significant within line variance.

@ indicates lines showing significant shift in desired direction.

Within line analysis of variance revealed that for seed yield 70 out of 89 lines in M_3 and 22 out of 61 lines in M_4 showed significant within lines variance in the segregating population following mutagenesis of homozygous loci of true breeding lines. Similarly, the number of lines exhibiting significant within lines variance in M_3 and M_4, respectively, were 5 and 6 for biological yield, 8 and zero for harvest index, 85 and 57 for number of pods, 10 and 2 for number of primary branches, 7 and 2 for plant height and 14 and 7 for days to maturity. For 100-seed weight none of the lines in M_3 and M_4 exhibited significant within lines variance.

Estimates of individual line mean and within line analysis of variance(Table 14) under 5 kR for macrosperma (HPL-4) lentil:

Line mean analysis of macrosperma showed that three lines out of 17 in M_3 and 9 lines out of 38 in M_4 had a positive shift in mean for seed yield. Line HPLM 326 was the best line isolated in M_3 (128% increase over control) followed by HPLM 328 and HPLM 329. In M_4 the top yielding line was HPLM 365 (140.2% increase over control) followed by HPLM 366, 348, 349, 350, 354 380, 364, and 355. None of the lines in M_3 and M_4 exhibited a desirable shift for maturity, harvest index and 100-seed weight. For biological yield 7 lines in M_3 and 6 lines in M_4 showed a significant superiority over control, the top most line being HPLM 326 in M_3 and HPLM 379 in M_4. In M_4 three lines for number of pods, eight lines for number of primary branches and six lines for plant height showed a significant positive shift in mean.

Within lines analysis of variance in M_3 and M_4 revealed that 5 out 2 lines exhibited significant within line variance for seed yield in M_3 and M_4 generation, respectively. Number of lines exhibiting significant within lines variance in M_3 and M_4, respectively were 2 each for seed yield, 6 and 9 for number of pods, 17 and 36 for seed weight, 17 and 35 for number of primary branches, 15 and 26 for plant height and 8 and 16 for days to maturity.

Table 14. Estimates of line mean alongwith within line analysis of variance in M_3 and M_4 generations of macrosperama lentil (HPL-4) under 5 kR

Progeny/ generation	Seed yield per plant(g)	Biological yield per plant(g)	Harvest index per plant (%)	Number of pods per plant	100-seed weight (g)	Number of primary branches	Plant height (cm)	Days to maturity
1.	2.	3.	4.	5.	6.	7.	8.	9.
M_3								
HPLM326	1.87*@	7.54*@	24.43	20.80*	6.86*	5.00*	20.37*	196.75
327	1.16	5.57*@	20.43	16.15	6.63*	4.60*	20.57*	197.05
328	1.63*@	6.05*@	25.69	11.70	6.35*	3.80*	19.27	196.90
329	1.37*@	6.18@	21.66	16.70*	6.34*	6.15*	22.27*	199.20*
330	0.86	4.12	21.07	15.50	6.30*	5.10*	23.02*	195.35
331	0.92	5.06	17.36	18.70*	6.46*	3.65*	22.07*	195.60*
332	0.92	3.90	26.54	13.85	6.35*	4.00*	20.91*	198.90*
333	0.87	3.64	23.63	14.95	5.88*	4.25*	20.59*	196.55
334	0.98*	4.41	21.69	16.00*	6.13*	4.80*	20.95*	196.80*
335	1.11	5.40@	20.51	17.05	6.30*	4.60*	20.95*	194.05*
336	1.20	5.48@	20.76	14.15	6.31*	4.85*	20.60*	199.20*
337	0.78	4.29	18.85	16.60*	6.26*	5.85*	20.72*	199.85*
338	1.14	4.76	23.97	13.65	6.44*	4.45*	19.90*	197.65
339	1.59*	5.69@	20.46	15.[illegible]*	6.20*	4.50*	22.22*	198.25*
340	0.72	3.05	23.46	11.55	6.29*	4.50*	19.20	200.95
341	1.22	5.26	24.33	14.20	6.56*	4.70*	19.75*	199.25
342	1.03	3.86	24.02	13.85	6.65*	4.70*	21.32*	197.60
M_4 343	0.61	3.40	17.43	16.10	6.31*	5.95*	20.90	198.85
344	0.85	3.92	19.84	20.10	6.31*	4.95*	21.67*	194.95*
345	0.99	4.87	18.70	18.65	6.45*	4.40*	23.57*	196.40*
346	1.02	4.53	26.12	17.15	6.69*	6.60*@	19.85*	195.05*
347	0.97	4.71	22.58	16.30	6.62*	5.00*	25.00*	198.45

Contd...

Table 14 Contd.

1.	2.	3.	4.	5.	6.	7.	8.	9.
348	1.78@	4.37	20.14	16.20	6.28*	4.25*	23.43*	195.95*
349	1.94@	4.76	20.03	18.25*	6.21*	4.85*	21.42*	197.70*
350	1.94@	3.97	20.31	16.75	6.63*	8.25*@	21.05*	199.15*
351	0.88	3.39	24.34	14.90	6.57*	4.20*	22.40*	196.25*
352	1.25	5.45@	25.88	16.95	6.12*	5.25*	20.27*	199.10*
353	0.97	4.34	22.23	19.20	6.33*	2.85	20.02	196.45
354	1.83@	3.50	24.63	10.45	6.52*	2.50	21.57*	195.75
355	1.86@	3.66	24.58	17.45	6.54*	4.00*	19.72*	195.35*
356	1.01	4.44	25.28	16.70	6.58*	6.40*@	21.40	195.55*
357	0.86	3.97	25.10	16.90	6.75*	4.55*	21.12*	196.45
358	0.77	4.09	18.92	16.85	6.79*	3.55*	21.65*	197.60*
359	0.83	3.77	22.26	15.65	6.34*	5.45*	20.85	197.10*
360	0.85	3.18	24.16	17.50	6.00*	4.15*	21.92	196.65
361	0.99	4.05	23.86	19.50*	6.18*	5.30*	24.15	195.25*
362	0.60	3.40	25.03	19.40*	5.96*	4.60*	24.20*@	194.95*
363	1.06	4.52	23.14	23.30*@	6.28*	6.60*@	20.70	195.35*
364	1.92@	4.43	23.70	20.15	6.20*	6.30*@	21.40	195.15
365	1.97@	4.86	19.39	18.75*	6.27*	6.40*@	19.70	196.40*
366	1.95@	4.23	22.84	16.05	6.80	3.70*	26.70*@	199.80
367	1.04	4.10	21.03	14.25	6.06*	2.75	23.77*@	195.25
368	0.95	4.24	23.67	13.85	6.07*	3.50*	22.10*	198.85
369	0.97	3.44	23.78	11.40	6.47*	3.80*	20.67	198.80
370	1.16*	3.73*	26.91	13.95	6.87*	6.40*@	24.12*	197.90
371	1.02	4.55	20.09	17.50*	6.16*	5.60*	22.82*	195.85
372	0.84	3.99	24.42	21.80*	6.28*	4.65*	22.70	197.45

Contd....

Table 14 Contd.

1.	2.	3.	4.	5.	6.	7.	8.	9.
373	1.19	5.38@	25.48	16.55	6.08*	3.25*	23.42*	198.65
374	0.99	5.12	20.07	14.65	6.20*	4.80*	25.35*	195.10
375	1.30*	6.10*@	20.06	14.85*	6.97*	6.10*	21.60*	196,75
376	1.30	5.18	24.53	16.35	6.60*	6.40*@	22.40*	200.65
377	1.01	6.01@	21.39	20.40	6.74*	3.65*	26.27@	197.25
378	1.15	4.06	20.70	12.75	5.96*	4.95*	23.45*	200.50
379	1.19	7.49@	19.80	33.85*@	6.39*	5.25*	26.20*@	197.90
380	1.79@	6.29@	18.05	22.60@	6.41	4.30*	25.47*@	196.85
HPL-4 (Control)	0.82	3.33	23.71	17.25	6.86	4.40	20.67	190.00
Parental SE ±	0.15	0.50	2.19	1.26	0.05	0.23	0.53	0.91
Line mean SE ±	0.22	0.97	2.61	2.17	0.25	1.09	1.69	1.67
Pooled S.E.±	0.26	1.03	3.38	2.42	0.21	0.93	1.56	1.82
Lines M_3 falling outside parental range	3	7	0	0	0	0	0	0
Lines M_4 falling outside parental range	9	6	0	3	0	8	6	0

* Indicates lines with significant within line variance.

@ Indicates lines showing significant shift in desired direction.

4.4.2 Estimates of individual line mean and within line analysis of variance under 10 kR:

The variety wise results obtained on the estimates of line mean and within line analysis of variance under 10 kR are given in Tables 15 and 16 and presented below:

Estimates of individual line mean and within line analysis of variance (Table 15) under 10 kR for microsperma (HPL-5) lentil:

Line mean analysis revealed that as much as 19 lines out of 44 lines in M_3 and 2 lines out of 27 lines in M_4 exhibited a desirable shift in mean for seed yield. The top most performance was shown by HPLM 189 in M_3 and HPLM 196 in M_4 which surpassed their parents by a margin of 211.8 and 105.9%, respectively. None of the lines in M_3 and M_4 exhibited desirable shift for maturity. In M_3, 12 lines for biological yield, one line for harvest index, 3 lines each for number of pods, 100 seed weight and number of primary branches and 8 lines for plant height showed a positive shift in mean. In M_4 one line each for number of pods and plant height showed a desirable shift in mean. Within line analysis of 44 lines in M_3 and 27 lines in M_4 indicated that a total of 39 and 11 lines for seed yield, 32 and 2 for biological yield, 3 and zero for harvest index, 34 and 7 for number of pods, 2 and 1 for 100 seed weight, 2 and zero for number of primary branches, 27 and 9 for plant height and 2 and zero for days to maturity respectively in M_3 and M_4 populations showed significant variance.

Estimates of individual line mean and within line analysis of variance (Table 16) under 10 kR for macrosperma (HPL-4) lentil:

Screening of 18 lines in M_3 and 26 lines in M_4 for their mean performance w.r.t. various polygenic traits showed that only one line HPLM 391 in M_3 exhibited superior performance (70% increase over control) for seed yield. In M_4 four lines had a superior shift in mean, the best performer being HPLM 423, which surpassed the control by a margin of 79%. None of the lines in M_3 and M_4 showed a desirable shift in mean for days to maturity and harvest

Table 15. Estimates of line mean alongwith within line analysis of variance in M_3 and M_4 generation of micro-sperma lentil(HPL-5) under 10 kR

Progeny/ generation	Seed yield per plant (g)	Biological yield per plant(g)	Harvest index per plant (%)	Number of pods per plant	100-seed weight (g)	Number of primary branches per plant	Plant height (cm)	Days to maturity
1.	2.	3.	4.	5.	6.	7.	8.	9.
M_3								
HPLM 151	1.01	6.34*	18 30	32.70	2.49	3.55	25.35*	174.20
152	1.31*	5.55	20.36	33.10	2.58	3.85	26.32*@	183.60
153	1.37*	5.48	21.70	41.60*	2.48	5.10	22.82*	173.70
154	2.09*@	8.20*@	23.54	50.75*	2.79*	6.25	27.45*@	175.60
155	2.64*@	9.90*@	23.67	59.05*@	3.04@	8.05	28.02*@	179.10
156	1.59*	7.07	22.86	41.45*	2.87	7.90@	22.82	175.70
157	1.67*	6.59*	22.80	50.25*	2.78	5.95	25.32*	178.50
158	1.11	6.06	22.26	40.30*	2.57	5.05	25.00	178.90
159	1.45*	7.19*	22.17	46.56*	2.70	5.95	25.07*	179.80
160	1.93*@	8.27*@	22.58	40.00	2.48	5.15	27.97*@	179.05
161	1.35*	6.50*	22.29	46.80*	2.61	5.70	23.55*	178.80
162	1.51*	6.31	21.60	45.65*	2.82	5.35	24.97*	173.10
163	1.05	5.91*	18.61	32.65	2.86	4.30	25.45*	174.50
164	1.59*	6.60	22.57	43.752*	2.57	7.35	24.35*	175.40
165	1.21*	5.09*	20.46	32.70	2.51	4.95	22.82*	175.10
166	1.21*	5.16*	23.18	39.10	2.67	5.40	21.75*	174.70
167	1.63*	6.60	19.83	53.40*@	2.80	5.05	24.27*	177.40
168	1.47*	6.38*	21.21	49.70*	2.75	6.40	24.40*	179.00
169	1.60*	5.68	19.91	55.30@	2.60	6.15	24.65*	176.90*
170	1.39*	5.69*	25.76	37.70*	2.62	4.90	22.84	177.65
171	1.71*	6.65*	22.67	41.75*	2.63	7.15	22.87*	177.70
172	1.25*	6.76*	20.69	32.25*	2.69	6.90	23.00	177.30

Contd.

Table 15 Contd.

1.	2.	3.	4.	5.	6.	7.	8.	9.
173	1.14*	5.93*	20.45*	27.25	2.58	5.80	21.67	177.95
174	1.93*@	9.27*@	22.64	47.75*	2.79	7.50	24.87*	177.60
175	2.46*@	8.00*@	23.80	44.05*	2.77	7.20	25.85	177.10
176	1.93*@	8.02*@	23.63	47.05*	2.77	5.70	25.22	176.70
177	1.62*	6.32*	23.36	49.75*	2.68	6.85	22.65	175.40
178	1.15	6.17	19.02	51.85*	2.86	6.85	23.75	179.70
179	1.41*	7.63	21.79	37.65*	2.70	4.10	25.60	179.40
180	1.36	7.60*	21.02	49.70*	2.87	6.70	24.70	177.70
181	1.78*@	7.94*@	22.07	50.60*	2.84	5.95	22.92*	179.50
182	1.73*@	8.50*@	25.10	50.20*	2.75	7.80@	24.60	170.10
183	1.96*@	6.60*	24.54	50.00*	2.90	5.60	24.97	177.70
184	2.04*@	7.88*	25.12	46.20*	2.90	6.35	23.47*	179.30
185	1.85*@	6.31*	24.71	46.65*	2.86	6.50	26.60@	178.30
186	1.81*@	12.66*@	26.62	50.70*	2.92	6.55*	22.87	179.50
187	2.61*@	7.12*	27.21@	49.55*	2.94*	6.95	27.67*@	175.00
188	2.24*@	11.98*@	24.81*	36.45*	3.00@	5.05	25.27*	177.05
189	3.15*@	8.93*@	24.12	38.55	2.85	10.00*@	28.60*@	178.90
190	2.13*@	6.21*	21.21	51.85*	3.25@	6.15	25.15*	174.00*
191	2.41*@	13.35*@	22.78*	41.20	2.81	5.55	22.67	175.10
192	2.67*@	6.66*	23.22	44.15*	2.95	5.05	27.62*@	175.00
193	1.97*@	4.84	20.15	43.95*	2.95	6.65	24.20*	175.20
194	1.46*	4.80	18.83	42.05*	2.66	5.70	22.00	171.80
M_4								
195	1.26*	6.31*	25.44	44.70*	2.55	7.00	27.45*@	174.40
196	2.08*@	7.23*	22.75	47.30*	2.69	7.35	25.37*	172.80

Contd...

Table 15 Contd.

1.	2.	3.	4.	5.	6.	7.	8.	9.
197	1.31*	5.70	19.36	44.70	2.76	4.60	25.00	173.90
198	1.59	4.59	23.03	38.20	2.61	5.25	23.17	171.95
199	1.05	5.49	21.25	38.00	2.83	4.70	25.27*	174.80
200	0.87	4.95	17.23	44.65*	2.44*	5.50	24.05	175.00
201	0.95*	5.97	20.23	32.15	2.75	4.40	24.10*	174.15
202	1.20*	5.16	19.09	42.85*	2.61	5.25	22.85	173.80
203	1.98*©	5.46	19.09	45.60	2.65	5.65	22.77	174.95
204	1.15*	5.33	17.48	35.40	2.60	4.85	22.97*	173.85
205	1.68	5.04	18.05	37.10	2.70	4.80	23.05	173.90
206	1.00	5.05	18.62	53.30@	2.63	6.30	24.17	173.60
207	0.88	4.68	15.91	40.70	2.60	5.10	22.62	174.80
208	0.88	4.85	16.85	38.35	2.64	5.15	22.40	174.90
209	0.86	5.08	18.02	41.45	2.38	5.45	22.45	174.90
210	0.87	5.25	18.79	41.85	2.58	5.25	22.97	175.00
211	1.34*	5.14	18.84	36.60	2.41	3.80	22.70	173.75
212	1.04*	5.00	17.55	40.05	2.50	5.40	22.77	173.90
213	1.11	5.07	20.44	29.50	2.51	2.80	22.40*	178.30
214	0.91	4.29	20.46	33.05	2.48	4.50	22.32	179.10
215	0.86	3.43	22.76	34.95	2.39	4.80	22.47*	175.80
216	0.63	4.25	21.69	36.45	2.59	4.15	20.95*	178.60
217	1.11*	4.64	21.04	34.25	2.49	5.00	22.22	178.25
218	0.93	5.04	20.63	38.35	2.77	5.75	22.50	178.25
219	1.02*	4.81	20.75	37.75*	2.63	4.70	24.15*	179.30
220	0.94	4.94	19.11	41.45*	2.64	5.90	23.20	178.30

Contd...

Table 15 Contd.

1.	2.	3.	4.	5.	6.	7.	8.	9.
221	1.07	4.61	19.14	38.55*	2.61	5.05	25.22	180.10
HPL-5 (Control)	1.01	5.31	21.47	39.50	2.71	5.25	23.22	173.55
Parental S.E.±	0.09	0.34	1.60	2.39	0.06	0.64	0.43	0.66
Line Mean S.E.±	0.42	1.53	2.20	6.40	0.14	1.11	1.64	2.17
Pooled S.E.±	0.36	1.32	2.68	6.33	0.14	1.23	1.46	1.99
Lines falling outside M_3	19	12	1	3	3	3	8	0
parental range M_4	2	0	0	1	0	0	1	0

* Indicates lines with significant within line variance.

@ Indicates lines showing significant shift in desired direction.

Table 16. Estimates of line mean alongwith within line analysis of variance in M_3 and M_4 generations of macrosperma (HPL-4) variety of lentil under 10kR

Progeny/ generation	Seed yield per plant (g)	Biological yield per plant(g)	Harvest index per plant (%)	Number of pods per plant	100-seed weight (g)	Number of primary branches per plant	Plant height (cm)	Days to maturity
1.	2.	3.	4.		6.	7.	8.	9.
M_3								
HPLM 381	1.12	5.15*	22.20	21.90	6.82@	4.00*	23.90	196.20
382	0.83	3.66	22.70	18.95	6.79*@	4.35*	25.72	196.00
383	0.91	5.05	19.55	21.70	6.38*	4.55*	26.05*	197.30
384	1.23*	5.46*	21.10	19.35	6.53*	4.40*	26.27	197.20
385	1.44*	6.90*	21.22	26.95@	6.73*@	3.55*	25.70*	196.25*
386	1.07	5.36*	18.80*	21.70	7.00*@	4.40*	28.47*@	195.80
387	0.57	2.90	18.29	21.75*	6.51*	4.25*	26.97*	195.95
388	1.15*	5.36*	23.45	28.45*@	6.57*	4.65*	25.57*	196.60
389	1.11	5.01	22.52	26.00@	6.50*	4.50*	25.77*	197.15
390	1.15*	5.85*	20.03*	26.75@	6.62*	4.70*	24.50*	197.75
391	1.87*@	3.67*	22.79	25.80*@	6.49*	3.50*	23.90*	198.20
392	0.81	3.18	24.13*	19.95	6.46*	4.20*	25.20*	195.75
393	1.62*	7.04*	23.66	23.55	6.99*@	4.80*	25.12*	195.00
394	1.13*	4.91*	25.57	.50@	6.43*	5.00*@	25.17*	196.25
395	0.85	3.58	24.34	20.70*	6.68*	4.15*	24.00*	196.90
396	1.22*	5.03*	26.89*	20.35	6.65	4.45*	25.02*	195.90
397	1.48*	5.47*	25.16	18.50	6.71@	3.10*	25.40*	195.30*
398	0.95	4.38	21.77	21.15	6.48	3.75*	23.90*	196.95
M_4								
399	1.03	5.83	18.90	20.85	6.37*	3.70*	25.37*	196.90
400	0.85	5.95	18.16	22.25	6.12*	3.35*	25.07	198.20
401	1.10*	4.39	21.26	19.80*	6.39	3.35*	24.70	196.10

Contd...

Table 16 Contd.

1.	2.	3.	4.	5.	6.	7.	8.	9.
402	0.88	4.03	21.88	20.10	6.48	3.55*	24.12	195.55
403	1.40	5.33	21.64	23.45	6.33	4.85*	25.40*	196.05
404	1.55*	6.73*	21.79	21.70	6.38	5.15*@	25.87*	195.90
405	1.85*@	6.60	24.95*	28.05@	6.42	5.15*@	28.09	196.95
406	1.84*@	6.40	23.61	23.95	6.35*	3.70*	25.75*	198.20
407	0.87	4.97	17.48	25.05*@	5.75*	4.35*	28.87*@	198.25
408	1.03	6.39	16.88	21.90	6.44	5.20*@	27.47	197.05
409	0.84	4.27	19.41	20.65	6.76@	4.45*	25.77*	195.80
410	1.16	4.72	22.06	23.00	6.62*	4.95*	25.25*	197.55
411	1.09*	4.23	20.98	21.60	6.46*	3.70*	26.65	196.75
412	1.22	6.03*	21.52	22.45	6.22	3.85	26.85*	197.35
413	0.94	4.83*	21.58	19.15*	6.48*	2.85*	24.07	196.70
414	1.35*	5.41	23.61	30.00*@	6.58	4.15*	26.45	197.95
415	1.11*	8.87@	16.22	31.15@	6.48	4.55*	25.51*	196. 0
416	1.10*	6.67	17.05	24.55	5.81*	3.90*	25.12	196.75
417	1.96*@	8.33@	22.62	32.60*@	6.59	5.20*@	30.65*@	198.30*
418	1.51*	6.65	20.83	25.85@	6.85*@	4.35*	26.15	196.40
419	1.42	6.59	20.89	27.65@	6.56	5.05@*	26.70*	196.90
420	1.48	6.97	19.82	25.55@	6.09	4.50*	26.85*	197.15
421	1.44	6.99	21.39	26.35@	6.30	5.60*@	25.65*	198.15
422	1.42	6.50	22.47	24.75	6.26	4.70*	25.52*	195.25
423	1.97@	6.12	19.39	18.80	6.34	3.45	24.95	196.75
424	1.16	4.57	20.45	20.85	6.45*	3.60*	24.70	196.05
HPL-4(control)	1.10	5.75	22.39	17.40	6.29	3.85	24.77	195.80
Patental S.E+	0.09	0.41	1.36	2.01	0.08	0.19	0.48	0.61
Line mean $\overline{SE}$+	0.30	1.19	2.28	3.46	0.22	0.65	1.36	0.87
Pooled S.E.+	0.27	1.12	2.56	3.85	0.21	0.59	1.80	1.04
Line falling M_3 outside parental range M_4	1 4	0 2	0 0	6 9	6 2	1 6	1 2	0 0

* Indicates lines with within line significant variance.
@ Indicates lines showing significant shift in desired direction.

index. However, 6 lines each for number of pods and 100 seed weight and one line each for number of primary branches and plant height had a positive shift in mean in M_3 generation. In M_4,2 lines each for biological yield, 100 seed weight and plant height, 6 lines f number of primary branches and 9 lines for number of pods showed a desirable shift in mean.

Within lines analysis of 18 and 26 lines in M_3 and M_4,respectively showed that most of the lines exhibited the presence of significant amount of variance. Table indicates that 9 and 10 lines for seed yield, 11 and 3 lines for biological yield, 4 and 1 line for harvest index, 4 and 4 lines for number of pods, 14 and 10 lines for 100 seed weight, 18 and 24 lines for number of primary branches, 15 and 14 for plant height and 2 and 1 line for days to maturity in M_3 and M_4 respectively, exhibited significant variance.

4.4.3 Estimates of individual line mean and within line analysis of variance under 15 kR

The variety wise results obtained on the estimates of line mean and within line analysis of variance under 15 kR are given in Tables 17 and 18 and presented below:

Estimates of individual line mean and within line analysis of variance (Table17) under 15 kR for microsperma (HPL-5) lentil:

Individual line analysis revealed that none of the 28 lines in M_3 and 49 lines in M_4 showed a desirable shift in mean for seed yield, biological yield, harvest index, number of pods, number of primary branches and days to maturity. However, as much as 19 lines out of 28 in M_3 and 40 lines out of 49 in M_4 exhibited a desirable shift for 100 seed weight, the top most lines being HPLM 249 in M_3 (36.6% increase over parent) and HPLM 262 in M_4 (27.5% increase over parent). Only one line HPLM 224 showed a significant shift for plant height in M_3.

Table 17. Estimates of line mean alongwith within line analysis of variance in M_3 and M_4 generations of microsperma(HPL-5) variety of lintil under 15 kR

Progeny/ generation	Seed yield per plant(g)	Biological yield per plant (g)	Harvest index per plant (%)	Number of pods per plant	100-seed weight (g)	Number of primary branches per plant	Plant height (cm)	Days to maturity
1.	2.	3.	4.	5.	6.	7.	8.	9.
M_3								
HPLM 222	0.91	3.76	19.69	..+.70	2.87	3.95*	22.82	175.65*
223	1.90	7.32	23.97	66.05	3.45@	6.75*	24.37	179.05
224	1.65	6.74	22.41*	47.40*	3.31@	7.00*	27.62*@	177.00
225	1.20	5.37	19.65	41.15	3.04@	6.10	23.77	179.10
226	1.94*	8.04*	21.40*	46.60	2.50	6.15*	22.55	176.25
227	1.23	5.31	22.02	41.00	2.58	5.40*	22.87	176.25
228	1.75	6.83	25.73	56.45*	2.33	7.00*	24.60	177.20
229	1.22	4.92	22.35	50.80	2.79	6.20*	22.60	175.85
230	0.93	3.98	21.90*	32.10	3.32*@	4.10*	22.35	178.80
231	1.46	5.95*	24.78	35.55	2.85	4.75	21.40	175.20
232	1.18	4.78	23.66	41.55	3.12@	5.35*	21.72	177.50
233	0.97	5.07	18.71	50.05	2.74	6.00	22.62	179.70*
234	1.20	5.41*	22.95	43.10	3.16@	5.70*	21.52	178.25
235	1.58	6.31	26.10	37.05	3.37@	5.35*	22.32	178.85
236	1.19	4.95	22.50*	52.50	3.43@	6.35*	23.90	179.40
237	1.43	5.61	25.47*	39.80	2.11	4.65*	23.80	179.10
238	1.15	5.23	20.65	39.70	2.56	6.30*	22.02*	178.30
239	1.13	5.22	20.44	33.95	3.15@	4.60*	23.12	178.60
240	1.32	4.98	25.80*	46.55	3.44@	5.90*	23.72	179.70
241	1.03	4.41	18.10*	37.10	3.36*@	5.20*	22.65	177.85
242	1.08	4.77	19.98*	38.45	3.28@	5.45	23.45	176.65*
243	1.32	5.09	24.32	40.30	3.58@	5.30*	21.67	175.30*
244	1.54	6.03	21.73*	48.45	3.29*@	6.00*	24.05	178.65

Contd...

Table 17 Contd.

1.	2.	3.	4.	5.	6.	7.	8.	9.
245	1.30	5.67	21.69	53.25*	2.98@	6.65*	23.85	173.40
246	1.03	5.09	22.59*	44.35	3.22@	6.00	21.10	175.50
247	1.26	5.33*	25.17*	35.05	3.07*@	4.80*	22.65	176.70*
248	1.46	6.33	20.97*	50.55*	3.41@	6.55*	24.48*	176.45*
249	1.62*	6.51	24.33*	57.70*	3.63*@	6.60*	25.42	178.50
250	1.55	5.40*	22.09	42.95*	3.42@	5.45*	23.40	177.30
251	1.04	5.39	17.61	38.90	3.13@	5.30*	23.15	177.30
252	1.39	5.36*	24.18	47.05	3.32@	6.10	25.47	179.50
253	1.71	7.10	23.23*	53.65*	3.01@	6.05*	23.85	178.50
254	1.20	5.97	20.99	52.40*	3.25@	6.80*	24.77	178.50
255	1.76	7.16	25.80*	57.95	3.22@	6.90	24.42	217.70*
256	1.35	6.70	20.49	54.10	2.93	5.15	23.92	177.90
257	1.32	5.17	21.61*	46.45	2.96	5.70*	23.80	179.40
258	1.22	6.19	19.43	49.60	3.21@	7.20	22.27	178.50
259	1.39	7.05	19.57	68.10	3.08@	6.85	23.47	177.30
260	1.30	6.02	19.36	46.75	3.20@	7.05	22.97	179.70
261	1.01	5.36	17.86	50.35	3.09@	5.10	23.00	178.75
262	1.13	4.97	21.30	3[illegible]10	3.34@	5.60	22.62	179.20
263	1.30	5.91	21.99*	49.45	2.90	5.50*	23.55	176.65
264	1.24	5.68	20.90	44.05	3.12@	5.60	23.77	178.20
265	1.20	5.99*	20.64*	38.20	3.16@	4.50	23.12	176.20
266	1.44	5.68	24.00*	32.80	2.89	4.75*	22.45	177.90
267	1.10	5.38	20.79	42.35	3.21@	6.25*	22.77	178.00
268	1.06	4.72	19.43	44.85	3.15@	6.00	23.62	179.10
269	1.12	4.85	20.57	44.90	3.02@	6.15*	23.32	177.55
270	1.10	5.72	19.19	53.05	3.09@	7.40	22.75	178.35

Contd....

Table 17 Contd.

1.	2.	3.	4.	5.	6.	7.	98.	9.
271	1.18	5.72	20.34	46.10	3.30@	5.10*	23.05	178.85
272	1.27	5.85	21.23	44.30	3.23*@	5.80	23.35	175.05*
273	1.03	5.70	19.67	44.80	2.86	6.00	23.27	179.10
274	1.99	4.96	20.58	46.[illegible]	2.81*	5.85	23.72	182.90*
275	1.33	6.03	21.42	43.35	3.22@	5.70	23.97	177.35
276	0.91	4.42	20.16	45.35	3.03@	5.45	22.27	178.25
277	1.22	5.99*	20.47	44.10	3.16@	5.80*	23.90	179.40
278	1.07	4.67	20.83	37.60	3.08@	5.35	22.45	176.85*
279	0.88	4.89	16.44	44.40	3.13@	5.25	22.85	177.65
280	1.13	5.65*	18.19	42.85	3.08@	6.35*	23.15	179.85
281	0.99	5.35	17.55	41.25	3.18@	6.55	23.20	178.80
282	0.97	4.90	20.47	45.60	3.09@	5.90*	23.37	178.20
283	1.30*	5.40	17.68	48.60	3.01@	6.50	23.32	177.65
284	1.02	5.67	17.53	48.30	2.90	5.35*	23.40	178.85
285	1.21	5.15	23.42	53.96*	3.07@	5.55	22.62	178.05
286	0.96	4.95	18.61	48.55	3.12@	5.60	23.00	178.40
287	1.30	5.22	21.69	44.85	3.05@	5.75*	23.55	179.70*
288	1.37	5.94	24.72	35.30	3.04@	5.60*	22.55	177.75
289	1.34	6.03	21.22	36.00	3.13@	6.45	23.05	176.60*
290	1.14	5.76	20.31	46.55	2.22	6.50*	22.92	177.30*
291	1.40*	6.46*	21.41	53.60*	3.00@	6.30*	22.30	175.15*
292	1.21	5.13	20.08*	41.35	2.43	3.90	24.15	176.10
293	1.14	4.83	20.46*	44.50	2.95	5.30	23.25	177.50
294	0.99	4.17	20.25	25.35	3.13@	5.05	21.92	178.95
295	1.17*	5.82	18.02*	45.60	3.05@	5.80	22.10	177.80
296	1.23	5.57*	21.80	44.05	3.06@	5.50*	23.12	177.95*

Contd..

Table 17 Contd.

1.	2.	3.	4.	5.	6.	7.	8.	9.
297	1.55	6.08*	22.39	42.10	3.08@	5.50	22.47	179.25
298	1.20	5.67	21.27	39.35	3.14@	6.30	24.02	178.15
HPL-5 (control)	1.98	7.01	25.11	6[illegible].20	2.62	7.50	24.52	177.20
Patental S.E±	0.14	0.41	1.22	3.38	0.08	0.23	0.52	0.61
Line mean S.E.±	0.23	0.78	2.06	7.61	0.18	3.47	1.00	4.76
Pooled S.E.±	0.26	0.83	2.31	7.74	0.18	2.60	1.07	2.68
Lines falling M_3 outside	0	0	0	0	19	0	1	0
parental M_4 range	0	0	0	0	40	0	0	0

* Indicates lines with significant within lines variance.

@ Indicates lines showing significant shift in desired direction.

Analysis table indicated that except for harvest index and number of primary branches most of the 28 and 49 lines studied in M_3 and M_4, respectively, did not exhibited occurrance of significant within lines variance for rest of the traits. The number of lines showing significant variance for harvest index and number of primary branches were 13 and 9, 23 and 19, respectively, in M_3 and M_4 generations. The number of lines with significant within lines variance in M_3 and M_4 generations were 2 and 3, 4 and 8, 5 and 5, 5 and 2, 3 and zero and 6, 9 for seed yield, biological yield, number of pods, 100 seed weight, plant height and days to maturity, respectively.

Estimates of individual line mean and within line analysis of variance (Table 18) under 15 kR for macrosperma (HPL-4) lentil:

Line mean analysis indicated that none of the lines in M_3 had desirable shift in mean for seed yield and days to maturity. However, line HPLM 436 in M_4 exhibited 89.7% increase over control for seed yield, lines HPLM 435 and 444 showed a desirable shift for days to maturity. Three lines in M_3 and four lines in M_4 showed significantly better performance over parents for harvest index.

Within lines variance analysis of 6 and 22 lines in M_3 and M_4 generations, respectively, showed that most of the lines were non-significant for many polygenic traits except for plant height and days to maturity where the number of significant lines was 5 and 10, and 3 and 12 in M_3 and M_4 generations, respectively. The number of lines with significant within lines variance in M_3 and M_4 generations were found to be 1 and 4 for seed yield, 2 and 4 for biological yield, 0 and 4 for harvest index, zero and 1 for number of pods, and 2 each for number of primary branches. None of the lines showed significant variance for 100 seed weight.

Table 18. Estimates of line mean alongwith within line analysis of variance in M_3 and M_4 generations of macrosperma(HPL-4) variety of lentil under 15 kR

Progeny/ generation	Seed yield per plant(g)	Biological yield per plant (g)	Harvest index per plant (%)	Number of pods per plant	100-seed weight (g)	Number of primary branches/ plant	Plant height (cm)	Days to maturity
1.	2.	3.	4.	5.	6.	7.	8.	9.
M_3								
HPLM 425	0.83	3.28	23.59@	23.90	6.20	3.75	21.60*	199.35
426	0.81	3.54	22.50@	17.05	6.14	5.35*	21.22*	198.85
427	1.01	4.85	20.62	22.75	6.13	4.20	23.65*	198.65
428	1.28	6.09	21.36	26.00	5.87	4.90	23.82	200.00*
429	1.33*	6.29*	20.89	21.45	5.97	3.55	24.47*	201.70*
430	0.92	3.56*	25.47@	15.40	6.39	3.60*	21.95*	201.30*
M_4								
431	0.78	4.16	18.00	23.75	6.67	3.85	24.12	197.50
432	0.98	4.56	18.74	21.15	6.54	3.75	23.62	197.10
433	0.82	3.59	23.16@	19.60	6.02	3.45	23.90*	197.85
434	1.63*	7.45	17.95	31.40	6.53	4.95*	26.15	199.30
435	1.60*	6.88*	20.31	29.00	6.18	4.10	27.60	194.00@
436	2.41*@	9.80*	21.18	33.15*	6.61	5.45*	26.52*	198.85*
437	1.72*	9.58*	18.11	31.80	6.06	5.40	26.20*	198.80*
438	1.79	5.29	17.07*	21.50	6.10	3.95	24.80*	199.90*
439	0.94	3.23	24.93@	20.80	6.13	3.75	23.20@	199.50*
440	0.89	4.54*	22.09*	16.00	6.40	3.45	24.32*	199.10*
441	1.40	7.29	17.97	33.15	6.94	3.80	27.12*	198.10*
442	0.86	4.47	19.94	17.15	6.57	3.15	25.95	198.70*
443	0.92	4.01	21.23	19.35	6.29	4.00	24.67*	197.40*
444	1.11	4.99	22.05	19.40	6.73	4.10	22.82	195.55*@
445	1.10	4.98	19.79	25.10	6.54	4.15	23.85*	197.45*

Contd...

Table 18. Contd.

1.	2.	3.	4.	5.	6.	7.	8.	9.
446	1.19	4.89	25.89*@	25.45	6.43	3.95	24.10	197.15*
447	0.71	4.33	16.06	19.60	6.62	3.20	25.32	196.70*
448	0.95	4.22	20.57	17.90	6.21	3.00	25.95*	198.50
449	1.87	5.26	20.12*	18.50	6.07	3.80	25.67	198.40
450	1.76	7.26	22.80@	28.60	6.08	4.85	26.15	197.25
451	1.40	6.57	21.41	22.80	6.28	4.35	24.92	199.05
452	1.84	4.33	16.33	13.15	6.21	3.35	27.37*	199.35
HPL-4	1.27	6.85	17.28	25.70	6.62	5.60	25.80	198.65
Parental Line	SE± 0.10	0.48	1.31	3.58	0.13	0.33	0.48	0.51
mean	S.E.± 0.40	1.73	2.47	5.53	0.24	0.69	1.36	1.37
Pooled	S.E.± 0.35	1.55	2.66	6.42	0.26	0.72	1.29	1.32
Lines falling outside parental range	M_3 0	0	3	0	0	0	0	0
	M_4 1	0	4	0	0	0	0	2

* Indicates lines with significant within lines variance.
@ Indicates lines showing significant shift in desired direction.

4.4.4 Estimates of individual line mean and within line analysis of variance under 20 kR:

The variety wise results obtained on the estimates of line mean and within line analysis of variance under 20 kR are given in Table 19 and 20 and presented below:

Estimates of individual line mean and within line analysis of variance (Table19) under 20 kR for microsperma (HPL-5) lentil:

Individual line analysis for mean performance w.r.t. various polygenic traits revealed that none of the 7 and 20 lines studied in M_3 and M_4 generation showed a significant. shift in mean over control for seed yield, biological yield, harvest index, plant height and days to maturity. Line HPLM 305 in M_3 and HPLM 308 in M_4 showed a positive shift for number of pods. Two lines in M_3 and six lines in M_4 exhibited superior performance w.r.t. number of primary branches. For 100 seed weight, five lines in M_4 showed a desirable shift in mean.

Within lines analysis indicated that most of the 7 and 20 lines studied in M_3 and M_4 respectively, showed the presence of significant variance for biological yield and number of primary branches. The number of lines showing significant variance in both M_3 and M_4 generations were 1 and 3 for harvest index, 2 and zero for number of pods, 1 and zero for 100 seed weight and days to maturity. None of the lines showed significant variance either in M_3 or M_4 for seed yield and plant height.

Estimates of individual line mean and within line analysis of variance (Table 20) under 20 kR for macrosperma (HPL-4) lentil:

Estimates of line mean indicated that none of the lines in M_3 and M_4 generations showed superior mean performance for all the traits studied except 100 seed weight, where line HPLM 454 in M_3 and HPLM 462 and 464 in M_4 exhibited significantly positive shift in mean.

Table 19. Estimates of line mean alongwith within line analysis of variance in M_3 and M_4 generations of microsperma (HPL-5) variety of lentil under 20kR

Progeny/ generation	Seed yield per plant(g)	Biological yield per plant (g)	Harvest index per plant (%)	Number of pods per plant	100-seed weight (g)	Number of Primary branches/ plant	Plant height (cm)	Days to maturity
M_3								
HPLM299	1.42	5.55*	24.17	18.15	2.88	4.50*	20.17	173.85
300	1.39	5.64*	24.01	28.35	2.89	3.60*	20.45	171.40
301	1.58	6.02*	24.65	20.25	2.82	3.40*	19.07	170.70
302	1.24	4.34*	21.13*	23.55	2.97*	3.90*	19.52	173.80
303	1.17	5.80*	24.19	16.80	2.95	4.10	17.07	172.75
304	1.12	4.43*	24.00	37.85*	2.76	5.60*@	21.45	172.10
305	1.37	6.64*	21.25	49.55*@	2.93	5.15*@	21.55	171.35*
M_4								
306	1.18	4.49*	20.63	37.30	2.71	5.20*@	21.00	173.35
307	1.16	4.18*	26.22	23.60	2.67	3.95*	22.20	174.55
308	1.07	4.29*	25.14	42.35@	2.57	5.45*@	22.77	172.10
309	1.10	5.08*	23.41	25.25	2.81	3.75*	21.82	176.50
310	1.09	4.29*	22.98	30.10	2.85	4.10*	21.22	173.90
311	1.19	4.18*	26.03	27.10	2.74	3.95*	20.52	174.65
312	1.27	3.90*	21.30*	33.55	2.73	4.45*	19.77	174.80
313	1.21	4.18*	23.42*	32.75	2.83	5.05*@	20.92	174.70
314	1.14	3.85*	23.39	25.05	2.72	3.65*	21.90	175.95
315	1.12	3.71*	21.05	23.35	2.84	3.25*	21.82	175.65
316	1.97	2.87*	24.50	27.30	2.53	5.00*@	19.90	176.45
317	1.13	4.51*	24.37	31.70	2.61	4.50*	22.57	177.75
318	1.03	3.91*	18.28	28.10	2.73	4.00*	20.80	177.30
319	1.03	3.95*	17.10	28.40	2.62	4.35*	20.82	175.60

Table 19 Contd.

Table 19 Contd.

1.	2.	3.	4.	5.	6.	7.	8.	9.
320	1.08	4.04*	25.24*	20.95	2.82	3.65*	19.50	172.75
321	0.93	3.90*	18.47	24.70	2.65	3.10*	21.82	176.15
322	1.03	3.02*	22.28	24.60	2.71	4.30*	20.07	175.15
323	1.13	4.47*	22.35	37.75	2.93	4.70*	20.87	173.55
324	1.17	3.80*	24.75	32.05	2.74	5.00*@	21.42	175.80
325	1.05	4.47*	22.26	31.10	2.63	5.00*@	19.37	175.95
HPL-5 (Control)	1.98	7.01	25.11	24.70	2.84	3.55	24.52	173.20
Parental S.E±	0.12	0.02	1.09	2.93	0.05	0.29	0.08	0.88
Line mean S.E±	0.11	0.59	2.36	7.59	0.09	0.70	1.15	1.42
Pooled S.E.±	0.16	0.43	2.43	7.41	0.09	0.69	0.86	1.62
Lines falling outside parental range M_3	0	0	0	1	0	2	0	0
M_4	0	0	0	1	5	6	0	0

* Indicates lines with significant within line variance.

@ Indicates lines showing significant shift in desired direction.

Table 20. Estimates of line mean alongwith within line analysis of variance in M_3 and M_4 generations of macrosperma (HPL-4) variety of lentil under 20 kR

Progeny/ generation	Seed yield per plant(g)	Biological yield per plant (g)	Harvest index per plant (%)	Number of pods per plant	100-seed weight (g)	Number of primary branches/ plant	Plant height (cm)	Days to maturity
M_3								
HPLM 453	1.06	4.63	21.79*	20.30	5.98*	4.70	25.42	198.20
454	1.52	6.46*	22.29*	22.85	7.23*@	5.25	23.60*	200.60*
455	1.66*	7.67*	20.29	27.10	6.63	4.85	24.07	196.60
456	1.39*	5.88*	20.74	23.15	6.89*	4.50	25.25*	198.50
457	1.21*	4.71	20.08	22.75	5.88	4.65	25.30*	197.55
M_4								
458	1.19	3.84	25.23*	15.45	6.63	3.25	26.80*	196.75
459	1.11	3.83	25.06*	17.25	5.63	3.55	23.65*	196.80
460	1.36	6.32	22.90*	23.95	6.77	3.70	25.65*	196.40*
461	1.10	4.75	20.98	18.10	7.01*	3.20	28.20	198.00
462	1.17	4.73	23.97	18.50	7.36@	4.85	28.17*	197.25
463	0.94	3.96	23.30*	16.15	6.71*	3.60	27.85*	198.90
464	1.12	4.85	23.24	21.15	7.39*@	4.75	26.55	199.90*
HPL-4 (control)	1.27	6.85	17.28	25.50	6.16	4.75	25.80	198.40
Parental S.E.±	1.11	0.37	0.91	2.44	0.05	0.61	0.48	0.49
Line mean S.E.±	0.19	1.16	1.27	2.77	0.58	0.60	1.61	0.99
Pooled S.E.±	0.91	1.07	1.53	3.67	0.44	0.84	1.47	1.04
Lines falling outside parental range M_3	0	0	0	0	1	0	0	0
M_4	0	0	0	0	2	0	0	0

*Indicates lines with significant within line analysis of variance

©Indicates lines showing significant shift in desired direction.

Within lines analysis of variance indicated that in M_3, three lines exhibited the presence of significant variance for seed yield, biological yield 100 seed weight and plant height. For harvest index only two lines and for days to maturity only one line in M_3 showed significant variance within lines. In M_4 number of lines with significant variance were 2 for days to maturity, 3 for 100 seed weight, 4 for harvest index and 5 for plant height.

4.5 Estimates of population mean in M_2, M_3 and M_4 generations:

In order to understand the shift in mean in different generations under various radiation doses for different polygenic traits w.r.t both microsperma (HPL-5) and macrosperma (HPL-4) varieties of lentil in relation to parental varities (control), the population mean in each generation were estimated and same are incorporated in Tables 21 and 22. In the Tables 21 and 22 the mean values marked with star (*) indicate positive shift and the ones marked with '@' indicate negative shift at 5% level of significance. The variety wise and within a variety dose wise results obtained w.r.t shift in mean are given below in the following pages:

4.5.1 Estimates of mean in M_2, M_3 and M_4 generation under microsperma (HPL-5) lentil:

Estimates of mean in M_2, M_3 and M_4 generation of microsperma variety under 5, 10, 15 and 20 kR radiation doses for eight polygenic traits are given in Table 21. The estimated values revealed that under 5 kR dose the shift in mean following mutagenic treatment was positive and significant for many traits and persisted through various generations. The shift in mean for seed yield was positive and significant in M_2 and M_3. For biological yield, it was positively significant in all the generations. The shift in mean was positive and significant for number of pods in M_2 and M_3, for 100 seed weight in M_2, M_3 and M_4, for number of primary branches in M_2 and M_3 and for maturity days in all the

Table 21. Estimates of parental (M_0), M_2, M3 and M_4 populations mean with respect to various polygenic traits under different radiation doses in microsperma (HPL-5) variety of lentil

Dose/ generation		Seed yield per Plant(g)	Biological yield per plant (g)	Harvest index per plant (%)	Number of pods per plant	100-seed weight (g)	Number of primary branches/ plant	Plant height (cm)	Days to maturity
5kR	$\bar{M}_2$	1.58* ±0.04	4.86* ±0.07	27.36 ±0.38	34.84* ±0.60	2.94* ±0.01	4.18* ±0.07	21.59 ±0.14	174.55* ±0.19
	$\bar{M}_3$	1.39* ±0.02	4.39* ±0.05	26.54 ±0.14	29.68* ±0.27	2.87* ±0.01	3.95* ±0.04	20.50 ±0.52	176.11* ±0.08
	$\bar{M}_4$	1.11 ±0.02	4.16* ±0.06	21.56@ ±0.20	27.00 ±0.28	2.79* ±0.01	3.49@ ±0.04	20.51@ ±0.06	177.32* ±0.08
	$\bar{M}_0$	1.13 ±0.06	3.61 ±0.66	27.02 ±2.78	27.30 ±0.73	2.71 ±0.11	3.75 ±0.37	21.50 ±0.54	172.30 ±0.60
10kR	$\bar{M}_2$	1.63* ±0.05	6.38* ±0.15	23.70* ±0.36	48.14* ±1.30	2.81* ±0.02	6.13* ±0.13	25.59* ±0.18	176.96* ±0.15
	$\bar{M}_3$	1.73* ±0.04	7.24* ±0.12	22.48* ±0.21	44.24* ±0.71	2.77* ±0.01	6.07* ±0.08	24.64* ±0.11	177.13* ±0.07
	$\bar{M}_4$	1.05 ±0.03	5.08@ ±0.08	19.78@ ±0.24	39.49 ±0.67	2.60@ ±0.01	5.13 ±0.07	23.39 ±0.11	175.60* ± 0.09
	$\bar{M}_0$	0.01 ±0.09	5.31 ±0.34	21.47 ±1.60	39.50 ± 2.59	2.71 ±0.06	5.25 ±0.64	23.22 ±0.43	173.55 ± 0.66
15kR	$\bar{M}_2$	1.15@ ±0.04	5.602@ ±0.12	19.05@ ±0.34	41.54@ ±0.32	3.13* ±0.02	5.65@ ±0.08	24.59 ±0.14	178.11* ± 0.15
	$\bar{M}_3$	1.32@ ±0.03	5.54@ ±0.09	22.43@ ±0.33	44.03@ ±0.80	3.25* ±0.02	5.72@ ±0.07	23.18@ ±0.11	177.40 ±0.13
	$\bar{M}_4$	1.21@ ±0.02	5.59@ ±0.06	20.60@ ±0.20	41.24@ ±0.52	3.11* ±0.01	6.44@ ±0.09	23.24@ ±0.07	178.99* ±0.76
	$\bar{M}_0$	1.98 ±0.14	7.01 ±0.41	25.11 ±1.22	63.20 ±3.38	2.62 ±0.08	7.50 ±0.23	24.52 ±0.52	177.20 ±0.61
20kR	$\bar{M}_2$	1.27@ ±0.04	4.75@ ±0.15	24.13 ±0.61	35.40* ±1.30	2.75@ ±0.02	5.02* ±0.13	21.42@ ± 0.17	174.64* ±0.33
	$\bar{M}_3$	1.33@ ±0.05	5.49@ ±0.22	23.34@ ±0.55	27.78* ±1.13	2.86 ±0.02	4.32* ±0.13	19.90@ ± 0.23	172.28@ ±0.32
	$\bar{M}_4$	1.10@ ±0.02	4.06@ ±0.08	22.66@ ±0.33	29.35* ±0.58	2.72@ ±0.01	4.32* ±0.07	21.06@ ± 0.13	175.13* ±0.16
	$\bar{M}_0$	1.98 ±0.12	7.01 ±0.02	25.11 ±1.09	24.70 ±2.93	2.84 ±0.05	3.55 ±0.29	24.52 ± 0.08	173.20 ±0.88

* Significant + ve shift in mean @ significant -ve shift in mean.

generations studied. Harvest index and plant height exhibited a significantly negative shift in mean in M_4. A significant negative shift in mean was also noticed for number of primary branches in M_4.

Under 10 kR dose the shift in mean was positive and significant for all the traits under M_2 and M_3 generations and it was so also in M_4 for days to maturity. Biological yield per plant, harvest index and 100 seed weight showed a significantly negative shift in mean in M_4 generation.

Under 15 kR dose estimates of shift in mean indicated that generally the shift was negative and significant. It was so in all the generations for seed yield, biological yield, harvest index, number of pods and number of primary branches. For plant height,it was also significant but negative in M_3 and M_4. However, a significantly positive shift in mean was observed for 100 seed weight in all the generations and for days to maturity in M_2 and M_4.

Under 20 kR dose, seed yield, biological yield and plant height in all the generations, harvest index in M_3 and M_4, 100 seed weight in M_2 and M_4 and days to maturity in M_3 showed a significantly negative shift in mean. Positive and significant shift in mean was found for all the generations for number of pods and number of primary branches and for days to maturity in M_2 and M_4.

4.5.2 Estimates of mean in M_2, M_3 and M_4 generation under macrosperma (HPL-4) lentil:

Estimates of mean in M_2, M_3 and M_4 populations of macrosperma variety under 5, 10, 15 and 20 kR radiation doses for eight polygenic traits are given in Table 22.

Under 5 kR dose, shift in mean was positively significant for seed yield in M_3 and M_4, for biological yield and days to maturity in M_2, M_3 and M_4, and for number of primary branches in M_4. Harvest index and 100 seed weight exhibited a significantly negative shift in mean, whereas, it was so only in M_3 for number of pods and in M_2 for number of primary branches.

Table 22. Estimates of parental (M_0), M_2, M_3 and M_4 population mean with respect to various polygenic traits under different radiation doses in macrosperma (HPL-4) variety of lentil

Dose/ generation		Seed yield per plant (g)	Biological yield per plant(g)	Harvest index/ plant (%)	Number of pods per plant	100-seed weight (g)	Number of primary branches/ plant	Plant height (cm)	Days to maturity
5kR	$\bar{M}_2$	0.90 ±0.05	4.59* ±0.19	20.66@ ±0.63	17.38 ± 61	6.42@ ±0.04	3.79@ ±0.23	23.15* ±0.35	197.47* ± 0.30
	$\bar{M}_3$	1.14* ±0.05	4.96* ±0.15	22.29@ ±0.40	15.33@ ±0.45	6.37@ ±0.04	4.68 ±0.19	20.87 ±0.24	197.65* ± 0.22
	$\bar{M}_4$	0.96* ±0.02	4.46* ±0.07	22.21@ ±0.25	17.41 ±0.30	6.41@ ±0.03	4.83* ±0.11	22.55* ±0.14	197.07* ± 0.13
	$\bar{M}_0$	0.82 ±0.15	3.33 ±0.50	23.71 ±2.19	17.25 ±1.26	6.86 ±0.05	4.40 ±0.23	20.67 ±0.53	190.00 ± 0.91
10kR	$\bar{M}_2$	1.41* ±0.06	7.23* ±0.21	19.69@ ±0.56	25.09* ±0.80	6.53* ±0.04	4.09 ±0.14	28.40* ±0.30	197.08@ ± 0.23
	M3	1.08 ±0.04	4.89@ ±0.15	22.46 ±0.43	22.72* ±0.61	6.63* ±0.04	4.24* ±0.14	25.37* ±0.21	196.47@ ± 0.16
	$\bar{M}_4$	1.25* ±0.03	5.84 ±0.10	20.62@ ±0.30	23.92* ±0.48	6.38* ±0.02	4.28* ±0.10	26.06* ±0.15	196.90@ ± 0.12
	$\bar{M}_0$	1.10 ±0.09	5.75 ±0.41	22.39 ±1.36	17.40 ±2.01	6.29 ±0.08	3.85 ±0.19	24.77 ±0.48	199.80 ± 0.61
15kR	$\bar{M}_2$	1.02@ ±0.03	5.31@ ±0.11	18.79* ±0.37	21.46@ ±0.44	6.41@ ±0.03	3.65@ ±0.08	25.84 ±0.18	199.34* ± 0.16
	$\bar{M}_3$	1.03@ ±0.05	4.60@ ±0.20	22.41* ±0.62	21.09@ ±0.98	6.13@ ±0.06	4.19@ ±0.04	22.79@ ±0.36	199.97* ± 0.35
	$\bar{M}_4$	1.16@ ±0.03	5.53@ ±0.11	22.25* ±0.34	23.13@ ±0.50	6.37@ ±0.02	3.99@ ±0.08	25.20@ ±0.16	197.98@ ± 0.18
	$\bar{M}_0$	1.27 ±0.10	6.85 ±0.48	17.28 ±1.31	25.70 ± 3.58	6.62 ±0.13	5,60 ±0.33	25.80 ±0.48	198.65 ± 0.51
20kR	$\bar{M}_2$	1.34 ±0.06	6.32 ±0.26	21.02* ±0.57	20.27@ ±0.67	6.58* ±0.06	4.23 ±0.18	27.13* ±0.42	198.30 ± 0.27
	$\bar{M}_3$	1.35 ±0.07	5.87@ ±0.30	21.04* ± 0.63	22.23 ±0.91	6.50* ±0.04	4.66 ±0.18	24.73@ ±0.32	198.18 ± 0.28
	$\bar{M}_4$	1.14@ ±0.03	4.61@ ±0.15	23.53* ± 0.57	18.65@ ±0.57	6.79* ±0.05	3.84@ ±0.16	26.93* ±0.30	197.71@ ± 0.30
	$\bar{M}_0$	1.27 ±1.11	6.85 ±0.35	17.28 ± 0.91	25.50 ±2.44	6.16 ±0.05	4.75 ±0.61	25.80 ±0.48	198.40 ± 0.49

* Significant +ve shift in mean
@ Significant -ve shift in mean.

Under 10kR radiation dose, shift in mean was positive and significant for all the generations under study for number of pods, 100-seed weight and plant height and significantly negative for days to maturity. The shift in mean also tended to be significantly positive for seed yield in M_2 and M_4, for biological yield in M_2 and for number of primary branches in M_3 and M_4 and significantly negative for biological yield in M_3 and for harvest index in M_2 and M_4.

Under 15kR dose shift in mean was generally negative. Seed yield, biological yield, number of pods, 100-seed weight and number of primary branches in M_2, M_3 and M_4, plant height in M_3 and M_4 and days to maturity in M_4 exhibited significantly negative shift in mean. Shift in mean was significantly positive for harvest index in all the generations and for days to maturity in M_2 and M_3.

Under 20 kR dose the shift in mean was significantly positive for all the generations under study for harvest index and 100-seed weight and for plant height in M_2 and M_4. The shift was significantly negative for seed yield in M_4, for biological yield and plant height in M_3 and M_4, for number of pods in M_2 and M_4 and for number of primary branches and maturity days in M_4 generation.

4.6. Component analysis of radiation induced polygenic variation

Component analysis of induced polygenic variation was attempted by using the recent sophisticated biometrical techniques in order to understand the nature of induced genetic variation by partitioning the variation into additive and dominance genetic components and also to get the information on the role of non-allelic interaction in the induced genetic variation through

scaling test by testing the adequacy of additive dominance model. The results obtained on the adequacy of additive-dominance model and genetic component analysis with respect to induced polygenic variation for various traits studied under different radiation doses for both microsperma (HPL-5) and macrosperma (HPL-4) varieties of lentil are presented in the following pages.

4.6.1. Scaling test for the adequacy of additive-dominance model:

The results obtained on the scaling test with respect to both the varieties under different radiation doses are given in Table 23 and presented below variety wise. The values in the Table 23 marked with star(*) indicates the inadequacy of additive dominance model to account for the induced polygenic variation and establishes the presence of non-allelic interactions.

Adequacy of additive-dominance model in microsperma (HPL-5) lentil: The scaling test revealed that most of the values were significantly deviating from zero, indicating the inadequacy of the additive-dominance model. Under 5kR dose the values were significant for seed yield, harvest index, 100-seed weight, number of primary branches and days to maturity indicating the presence of non-allelic interactions, whereas, biological yield, number of pods and plant height showed that a simple additive-dominance model is adequate for induced variation. Under 10kR dose all the traits except number of pods exhibited inadequacy of additive dominance model. Under 15kR radiation dose all the traits except biological yield and number of pods had significant value of scaling test which indicated the presence of non-allelic interactions. Under 20kR dose of radiation all the traits except harvest index, 100 seed weight and number of primary branches showed the inadequacy of additive dominance model in explaining the variation induced.

Table 23. Estimated values in scaling test for additive-dominance model

Characters	Microsperma (HPL-5)				Macrosperma (HPL-4)			
	5kR	10kR	15kR	20kR	5 kR	10kR	15kR	20kR
Seed yield	-0.359* ±0.076	-1.45* ±0.139	-0.384* ±0.095	-0.502* .153	-0.600* ±0.159	0.668* ±0.149	0.259 ±0.164	-0.420 ± 0.220
Biological yield	0.009 ±0.008	-5.159* ±0.426	0.164 ±0.333	-3.604* ± 0.688	-1.371* ±0.485	4.250* ±0.536	2.556* ±0.890	-2.071* ±0.978
Harvest index	-9.142* ±0.707	-4.277* ±0.8818	-7.059* ±1.135	-0.570 ±1.865	-1.798 ±1.438	-6.438* ±1.531	-7.943* ±2.025	4.950* ±2.239
Number of pods	-0.208 ±2.052	-5.604 ±3.219	-0.054 ±2.749	5.374* ±1.908	6.185* ±2.424	4.778 ±2.875	4.442 ±3.147	-12.120* ± 3.336
100-seed weight	-0.087* ±0.014	-0.293* ±0.024	-0.399* ±0.069	-0.379* ±0.073	0.130 ±0.135	-0.604* ±0.131	0.756* ±0.194	0.643* ±0.195
Number of primary branches	-0.699* ±0.024	-1.816* ±0.307	1.353* ±0.292	0.702 ±0.435	-0.580 ± 0.655	-0.068 ±0.480	-0.946* ±0.213	-2.034* ±0.641
Plant height	1.097 ±1.586	-1.544* ±0.435	1.531* ±0.380	3.834* ±0.766	3.651* ±0.851	4.411* ±0.759	7.887* ±1.155	6.811* ±1.224
Days to maturity	0.858* ±0.209	-3.220* ±0.170	3.919* ±1.569	8.067* ±1.049	-1.338 ±0.773	1.466* ±0.586	-4.630* ±1.113	1.300 ±1.035

* Indicates inadequacy of additive dominance model at 5 per cent level.

Adequacy of additive-dominance model in macrosperma (HPL-4) lentil: The scaling test showed that under 5kR radiation dose, the additive dominance model was adequate for explaining the induced variation with respect to harvest index, 100 seed weight, number of primary branches and days to maturity. For seed yield, biological yield, number of pods and plant height, the scaling values were significant at 5kR dose, indicating the inadequacy of additive-dominance model and establishing the presence of non-allelic interactions. Under 10kR radiation dose, all the traits under study except number of pods and number of primary branches showed the inadequacy of additive-dominance model. Under 15kR radiation dose, the additive-dominance model was adequate for explaining induced variation only for seed yield and number of pods. Under 20kR dose, all the polygenic traits except seed yield and days to maturity exhibited the inadequacy of additive-dominance model.

4.6.2. Genetic component analysis of induced polygenic variation

In this genetic analysis both first and second degree statistics have been made use of for partitioning the induced variation into additive and dominance components. In the first degree statistics, population mean values of M_0 (parents), M_2 and M_3 generations in each dose were used. In this analysis as indicated earlier, M_2 was equated with F_2 and than the analysis was done by using Mather and Jinks (1971) approach as suggested and modified by Yonezawa (1979). In second degree statistics wherever the required statistics in the desired magnitude was available, the analysis was done as per Yonezawa (1979) approach. The results obtained on these estimates are presented below:

Genetic component analysis(first degree statistics approach)

Component analysis, using first degree statistics parameters was performed for both microsperma and macrosperma lentil for partitioning the

induced variation into additive and dominance effects and also to know the average degree of dominance. Results obtained are given below variety wise:

Estimates of induced additive(dm)dominance(hm) and (hm)/(dm) ratio in microsperma (HPL-5) lentil

The results obtained on the estimates of induced additive (dm), dominance(hm) and (hm)/(dm) ratio indicating average degree of dominance under various radiation doses for various polygenic traits in microsperma (HPL-5) are given in Table 24. For seed yield the additive effect was significant and negative under 10kR dose indicating that more increasing alleles have mutated to decreasing alleles or it may be more likely that either the increasing alleles are more radio-sensitive or the parent has more of decreasing alleles. However, under 15kR dose the seed yield exhibited a positive and significant additive effect for seed yield which showed that more increasing alleles are present. For seed yield the dominance effects were significant under 5 and 15kR dose of radiation, whereas, the average degree of dominance under 15kR exhibited incomplete or partial dominance. Additive effect was negative and significant under 10kR dose and significantly positive under 15kR dose for biological yield, whereas, dominance effects were significant under 5, 10 and 20 kR dose. Average degree of dominance for biological yield, under 10kR dose, where both additive and whereas, dominance effects were significant exhibibted partial dominance. For harvest index only dominance effects were found significant under 5, 10 and 15 kR radiation doses. Additive and dominance effects both, were significant under 5 and 15 kR dose of radiation for number of pods, whereas, only dominance effects were significant under 10 and 20kR dose. Average degree of dominance showed over-dominance under 5kR dose and incomplete dominance under 15kR dose. Hundred seed weight showed that both additive and dominance effects were significant under 5, 15 and 20kR

Table 24. Estimates of additive (d)m, dominance (h)m effects and average degree of dominance(h)m/(d)m for different polygenic traits under different radiation doses in microsperma(HPL-5) variety of lentil.

Dose/ estimate of effect		Seed yield (g)	Biological yield (g)	Harvest index (%)	Number of pods	100-seed weight (g)	Number of primary branches	Plant height (cm)	Days to maturity
5kR	(d)m	-0.04 ±0.04	-0.15 ±0.35	0.65 ±1.41	1.38* ±0.49	-0.05* ±0.01	0.01 ±0.01	1.04 ±0.59	-1.87* ± 0.34
	(h)m	0.38* ±0.08	0.94* ±0.15	1.64* ±0.82	10.34* ±1.32	0.13* ±0.03	0.47* ±0.16	21.70* ± 1.09	-0.34 ± 0.30
	Av.Dom.	-	-	-	7.44*	2.74	-	-	-
10kR	(d)m	-0.41* ±0.06	-1.39* ±0.26	0.10 ±0.84	-0.42 ±1.61	-0.01 ±0.03	-0.38 ±0.84	-0.23 ±0.26	-1.87* ±0.34
	(h)m	0.20 ±0.12	-1.72* ±0.38	2.47* ±0.83	7.80* ±2.97	0.09 ±0.03	0.13 ±0.30	1.90* ±0.41	-0.34 ±0.30
	Av.Dom.	-	1.23	-	-	-	-	-	-
15kR	(d)m	0.25* ±0.06	0.77* ±0.11	-0.36 ±0.72	8.34* ±1.95	-0.38* ±0.06	-0.85* ±0.19	1.38* ±0.13	0.26 ±0.34
	(h)m	-0.34* ±0.09	0.13 ±0.19	-6.77* ±0.96	-4.97* ±2.29	-0.25* ±0.05	-2.16 ±0.21	2.83* ±0.35	1.43 ±0.39
	Av.Dom.	1.36	-	-	0.59	0.65	-	2.05	-
20kR	(d)m	0.30 ±0.08	0.39 ±0.23	1.28 ±0.83	2.26 ±1.96	-0.06* ±0.01	0.03 ±0.21	3.07* ±0.25	1.64* ±0.56
	(h)m	-0.11 ±0.13	-1.47* ±0.53	1.58 ±1.63	15.23* ±3.44	-0.22* ±0.06	1.41* ±0.37	3.04* ±0.57	4.73 ±0.91
	Av.Dom.	-	-	-	-	3.41	-	0.99	-

*Significant at 5% level

doses of radiation, whereas, average degree of dominance indicated complete dominance under 5 and 20kR dose and partial dominance under 15kR dose of radiation. Dominance effects under 5 and 20 kR and positive additive effect under 15 kR dose was significant for number of primary branches. Plant height exhibited significant dominant effects under all the doses studied, whereas, the additive effects were positive and significant under 15 and 20kR. The average degree of dominance showed complete dominance under 15kR dose and incomplete dominance under 20kR dose. Additive effects were significantly negative for days to maturity under 5 and 10kR dose of radiation.

Estimates of induced additive(dm),dominance(hm) and (hm)/(dm) ratio in *macrosperma* (HPL-4) lentil

Results obtained on the estimates of induced additive (dm),dominance (hm) and average degree of dominance (hm)/(dm) under various radiation doses for eight different polygenic traits in macrosperma (HPL-4) are given in Table 25. Estimates indicated that both additive and dominance effects were significant for seed yield under 5 and 10kR dose except that of dominance effect under 5kR which was significantly negative. The average degree of dominance under 5 and 10kR dose exhibited complete dominance. For biological yield the additive effects were significantly positive under 10 and 15kR dose of radiation and significantly negative under 5kR dose, whereas, dominance effect was significant only under 10kR dose, with average degree of dominance exhibiting complete dominance under 10kR dose. Significantly negative effects were obtained for harvest index under 10, 15 and 20kR radiation dose,whereas, dominance effects were significant under 10 and 15kR doses of radiation. The average degree of dominance, under 10 and 15kR dose for harvest index,where both additive and dominance effects were significant, was complete dominance.

Table 25. Estimates of additive (d)m, dominance (h)m effects and average degree of dominance(h)m/(d)m for different polygenic traits under different radiation doses of macrosperma(HPL-4) variety of lentil

Dose/ estimate of effect		Seed yield (g)	Biological yield (g)	Harvest index (%)	Number of pods	100-seed weight (g)	Number of primary branches	Plant height (cm)	Days to maturity
5kR	(d)m	0.28* ±0.09	-1.00* ±0.31	-0.10 ±0.18	1.98* ±0.83	0.27* ±0.05	-0.58* ± 0.07	1.04* ±0.41	-8.91* ±0.49
	(h)m	-0 47* ±0.13	-0.73 ±0.48	-3.27* ±1.49	4.09* ±1.52	0.10 ±0.12	-1.77* ± 0.35	4.56* ±0.85	-0.35 ±0.75
	Av.Dom.	1.71	-	-	2.06	-	3.05	4.37	-
10kR	(d)m	0.17* ±0.07	1.60* ±0.22	-1.41* ±0.67	-1.47 ±1.42	-0.22* ±0.05	-0.27 ±0.18	1.22* ±0.27	1.97* ±0.52
	(h)m	0.65* ±0.12	4.68* ±0.51	-5.54* ±1.41	4.74 ±2.59	-0.20 ±0.11	-0.29 ±0.39	6.05* ±0.73	1.22* ±0.57
	Av.Dom.	3.82	2.92	3.91	-	-	-	4.98	0.62
15kR	(d)m	0.12 ±0.73	1.47* ±0.11	-4.37* ±0.79	2.49 ±2.05	0.38* ±0.10	0.43* ±0.19	3.03* ±0.45	-0.98* ±0.48
	(h)m	-0.01 ±0.11	0.13 ±0.30	-7.24* ±1.45	0.74 ±2.16	0.56* ±0.14	-1.09* ±0.18	6.11* ±0.81	-1.27* ±0.15
	Av.Dom.	-	-	1.65	-	1.46	2.52	2.01	1.29
20kR	(d)m	-0.04 ±0.09	0.71 ±0.37	-1.89* ±0.82	-0.34 ±1.56	-0.13 ±0.72	-0.17 ±0.36	1.73* ±0.46	0.17 ±0.40
	(h)m	0.01 ±0.18	0.89 ±0.79	-0.04 ±1.70	5.92* ±2.52	0.16 ±0.16	-0.86 ±0.50	4.80* ±0.58	-0.24 ±0.79
	Av.Dom.	-	-	-	-	-	-	2.77	-

* Significant at 5 per cent level.

For number of pods,additive effect was positive and significant only under 5kR dose of radiation, whereas, dominance was significant under 5 and 20 kR dose. Average degree of domiannce for number of pods under 5kR showed complete dominance. Significantly positive additive effects were revealed for 100-seed weight under 5 and 15 kR dose of radiation, whereas, it was significantly negative under 10kR. The dominance effect for 100 seed weight was significant under 15kR and the average degree of dominance exhibited complete dominance. For number of primary branches the additive effect was significant and negative under 5kR dose and significantly positive under 15kR dose of radiation, whereas,the dominance effects were significant under 5 and 15kR dose. The average degree of dominance showed complete dominance for number of primary branches under 5 and 15 kR dose of radiation. Positive and significant additive as well as dominance effects were obtained for plant height under all the doses of radiation studied, whereas, the average degree of dominance indicated complete dominance. For days to maturity, the additive effects were significantly negative under 5 and 15kR dose and significantly positive under 10 kR, whereas, the dominance effects were significant under 10 and 15kR doses. Average degree of dominance for days to maturity under 10 and 15kR doses exhibited partial and complete dominance, respectively.

Genetic component analysis (second degree statistics approach)

The second degree statistics required in appropriate magnitude as per Yonezawa (1979) for genetic component analysis were available in microsperma lentil with respect to number of pods under 5kR dose and plant height under 20kR dose and in macrosperma with respect to 100-seed weight under 20kR dose, hence the component analysis using second degree statistics was done with respect to above situations only. The results obtained on the estimates of additive (Dm), dominance (Hm), Fm, average degree of dominance, r_2/r_1 estimated

as $\frac{(h)m}{\sqrt{Hm}}$ $\frac{(d)m}{\sqrt{Dm}}$ measuring isodirectionality of dominance and degree of gene association and 'r_3' estimated as $\frac{Fm}{\sqrt{Dm \cdot Hm}}$ measuring the degree of gene association are incorporated in Table 26. All the variances i.e. Dm, Hm and Fm were found to be significant in microsperma under 5kR dose for number of pods whereas average degree of dominance exhibited overdominance. Value of 'r_2/r_1' ratio was more than one. As the value of (h)m for this was also more than one, hence, it indicated that about half of the parental genes have increasing effect compared to mutant genes, dominance being positively directed for most the genes concerned. Estimates of 'r_3' was also found to be more than one which indicated that all parental allele were dominant to mutant ones. For plant height in microsperma under 20kR dose, the Dm, Hm and Fm were significant, whereas, the average degree of dominance exhibited complete dominance. The value of 'r_2/r_1' ratio was less than one which indicated that parental genes lacked dominance as compared to mutant genes. Value of 'r_3' was more than one which indicated that all parental alleles were dominant to mutant ones. In macrosperma under 20kR dose for 100-seed weight, only Hm and Fm values were significant and average degree of dominance exhibited over dominance. The value of 'r_2/r_3' ratio for this trait was less than one but in negative direction, indicating that parental genes lack dominance in comparison to mutant genes, whereas 'r_3' value was again more than one indicating that all parental alleles were dominant to mutant ones.

Table 26. Estimates of different genetic components and probability estimates for obtaining potential mutants in M_2, M_3 and M_4 generations by using second degree statistics approach

Trait/ variety/ dose	Dm	Hm	Fm	$\sqrt{Hm/Dm}$	r_2/r_1	r_3	Normal probability estimates M_2	M_3	M_4
Microsperma									
Number of pods (5kR)	34.82*	423.53*	208.51	12.16*	2.14	1.72	0.102	0.184	0.480
	± 3.85	±12.11	± 9.49				(0.131)	(0.363)	(0.484)
Plant height (20kR)	3.82*	22.02*	15.09*	5.77	0.41	1.65	0.057	0.091	0.038
	±0.80	±3.33	±2.36				(0.059)	(0.099)	(0.041)
macrosperma									
100-seed weight (20kR)	0.09	0.49*	0.28*	5.02*	-0.53	1.26	0.090	0.140	0.022
	±0.93	±0.19	±0.07				(0.173)	(0.223)	(0.079)

* Significant at 5 per cent level

Probability values in parenthesis indicates the values obtained on the basis of both additive and environmental variance.

probability was highest for obtaining potential mutants for higher

4.7. Estimates of normal probability integrals for predicting the expected potential mutants excelling their parental values in the M_2,M_3 and M_4 generations

In order to predict the probability of isolating the potential mutants excelling their parental values for the desired traits under different doses with respect to both the varieties, the normal probability integrals corresponding to $\frac{P-m}{dm}$ and $\frac{P-m}{dm+e}$ values were estimated and the results obtained are given in Table 27 and 28 and are presented variety wise below:

4.7.1. Estimates of normal probability integrals in microsperma(HPL-5)lentil:

Results obtained on the estimates of normal probability integrals for predicting the number of potential mutant lines falling outside the parental range in M_2, M_3 and M_4 generations for various polygenic traits in microsperma are incorporated in Table 27. The estimates were obtained based on both induced additive effects as well as induced additive plus environmental effects, so as to know the precision of predictions. The estimated values obtained on the basis of combined induced additive and environmental effects (dm + e) were more as compared to one calculated mainly on the basis of induced additive effects (dm).

For higher seed yield, the highest probaility would be in M_4 generation under 10kR dose of radiation, where the value was 0.46 when calculated on the basis of dm and 0.472 when calculations were based on dm+e. For higher biological yield the highest probability of obtaining potential mutants would also be in M_4 generation under 10kR radiation dose, where the probability values were 0.43 and 0.456, respectively, for both type of probability estimates. In M_4 generation under 5kR dose of radiation the probability was highest for obtaining potential mutants for higher number of

Table 27. Estimates of probability values for obtaining true breeding lines in M_2, M_3 and M_4 falling outside the parental range under different radiation doses in microsperma(HPL-5) variety of lentil

Dose/ generation		Seed yield (g)	Biological yield (g)	Harvest index (%)	Number of pods	100-seed weight (g)	Number of primary branches	Plant height (cm)	Days to maturity
	M_2	-	-	-	0.0001 (0.165)	0.0001 (0.305)	-	-	0.110 (0.248)
5kR	M_3	-	-	-	0.043 (0.251)	0.003 (0.363)	-	-	0.022 (0.123)
	M_4	-	-	-	0.410 (0.468)	0.480 (0.428)	-	-	0.003 (0.630)
	M_2	0.064 (0.117)	0.220 (0.301)	-	-	-	-	-	0.034 (0.173)
10kR	M_3	0.038 (0.082)	0.084 (0.171)	-	-	-	-	-	0.028 (0.348)
	M_4	0.460 (0.472)	0.430 (0.456)	-	-	-	-	-	0.130 (0.333)
	M_2	0.0003 (0.085)	0.033 (0.238)	-	0.004 (0.105)	0.088 (0.151)	0.014 (0.095)	0.480 (0.492)	-
15kR	M_3	0.003 (0.137)	0.027 (0.229)	-	0.011 (0.133)	0.047 (0.102),	0.018 (0.088)	0.160 (0.312)	-
	M_4	0.0009 (0.100)	0.032 (0.235)	-	0.016 (0.149)	0.096 (0.161)	0.100 (0.208)	0.170 (0.319)	-
	M_2	-	-	-	-	0.080 (0.393)	-	0.150 (0.158)	0.190 (0.370)
20kR	M_3	-	-	-	-	0.380 (0.476)	-	0.066 (0.068)	0.280 (0.416)
	M_4	-	-	-	-	0.030 (0.355)	-	0.130 (0.131)	0.120 (0.326)

66

Note: Values in parenthesis are estimates obtained by taking environmental error also.

pods. For 100-seed weight, M_4 generation under 5kR dose and M_3 generation under 20kR dose exhibited high values of probability estimates, whereas, for more number of primary branches, M_4 generation under 15kR dose of radiation was found to be most suitable for isolating potential mutant lines. For plant height best estimates were observed under 15kR dose in M_2 generation where probability of isolating mutants with desirable shift would be 0.48, when estimated on the basis of dm alone and 0.492 when estimated on the basis of dm+e. For early maturity, the best generation would be M_3 under 20kR dose of radiation on the basis of dm alone and in M_4 generation under 5kR dose on the basis of dm+e.

4.7.2. Estimates of normal probability integrals in macrosperma (HPL-4)lentil

Estimates of normal probability values for predicting the number of potential mutnats falling outside the parental range in M_2, M_3 and M_4 generation for eight different types of polygenic traits were obtained for macrosperma and are given in Table 28. Here again the probability values obtained on the basis of dm alone were less than the ones obtained on the basis of dm+e. For higher seed yield, the highest probability would be in M_3 generation under 10kR dose, whereas, for biological yield, M_4 generation under 10kR would give the maximum probability of isolating desirable potential mutants. For harvest index, M_3 generation under 10kR dose was found to have maximum probability of isolating desired mutants. For number of pods M_4 generation under 5kR radiation dose was found to have maximum probability value. The normal probability value for isolating potential mutants for hundred seed weight was maximum under 10 kR dose in M_4 generation, whereas, for number of primary branches, the maximum probability would be in M_3

Table 28. Estimates of probability values for obtaining true breeding lines in M_2, M_3, M_4 falling outside the parental range under different radiation doses in macrosperma (HPL-4) lentil

Dose/ generation		Seed yield (g)	Biological yield (g)	Harvest index (%)	Number of pods	100-seed weight (g)	Number of primary branches	Plant height (cm)	Days to maturity
5kR	M_2	0.389 (0.464)	0.100 (0.305)	-	0.260 (0.492)	0.054 (0.146)	0.140 (0.298)	0.086 (0.173)	0.200 (0.223)
	M_3	0.120 (0.352)	0.051 (0.251)	-	0.160 (0.374)	0.036 (0.21)	0.310 (0.405)	0.420 (0.472)	0.190 (0.217)
	M_4	0.310 (0.436)	0.130 (0.322)	-	0.460 (0.492)	0.049 (0.140)	0.230 (0.335)	0.035 (0.238)	0.210 (0.235
10kR	M_2	0.034 (0.261)	0.180 (0.270)	0.028 (0.333)	-	0.140 (0.267)	-	0.001 (0.070)	0.083 (0.211)
	M_3	0.450 (0.484)	0.300 (0.363)	0.480 (0.496)	-	0.061 (0.189)	-	0.310 (0.405)	0.045 (0.163)
	M_4	0.190 (0.378)	0.480 (0.488)	0.100 (0.389)	-	0.340 (0.409)	-	0.160 (0.301)	0.070 (0.194)
15kR	M_2	-	0.150 (0.280)	0.360 (0.420)	-	0.290 (0.378)	0.000003 (0.103)	0.490 (0.496)	0.240 (0.393)
	M_3	-	0.064 (0.192)	0.120 (0.241)	-	0.100 (0.242)	0.0005 (0.181)	0.160 (0.208)	0.090 (0.298)
	M_4	-	0.180 (0.301)	0.250 (0.344)	-	0.250 (0.355)	0.0009 (0.149)	0.420 (0.440)	0.240 (0.393)
20kR	M_2	-	-	0.023 (0.203)	-	-	-	0.220 (0.319)	-
	M_3	-	-	0.023 (0.203)	-	-	-	0.270 (0.351)	-
	M_4	-	-	0.0005 (0.082)	-	-	-	0.250 (0.344)	-

Note: Values in parenthesis are estimates obtained after tak ing environmental error also.

generation under 5kR dose. For plant height and early maturity the maximum probability of isolating potential mutants of macrosperma would be under 15 kR radiation dose in M_2 generation.

5. DISCUSSION

DISCUSSION

The objectives of the present investigation in microsperma and macrosperma varieties of lentils (Lens culinaris Medik.) were, firstly, to understand the pattern of segregation and persistance of induced variation over generations under different radiation doses for seed yield and other polygenic traits, secondly, to understand the genetic architecture of induced polygenic variations through sophisticated biometrical genetic models and thirdly, to understnad the relationship of different radiation doses with various parameters of induced variability and varieties used. It was also considered apt to establish the appropriate stage of selection in lentil mutation breeding programme on the basis of segregation pattern of induced variation and probability estimates of obtaining potential mutants excelling parents and to identify the potential mutants with desirable attributes. Results obtained on the above mentioned aspects have also been discussed for formulating an effective mutation breeding programme for the genetic amelioration of lentil crop.

Mutation breeding is a valuable supplementary approach in plant breeding under the situation as is prevailing in food legumes, specifically in lentil where the variability existing in natural gene pools is not meeting the requirements of present genetic transformation and also because of tedious crossing procedure owing to small, delicate flowers and non-synchrony in flowering between microsperma and macrosperma types. Under such situations, it is imperative to create the desired variation artificially through mutagenesis. Among the various mutagens, ionizing radiations have been used most effectively for induction of mutations in the past and have resulted in the development of new varieties (Micke, 1976).

They are preferred primarily because of their effectiveness, the ease of treating material and its handling immediately after treatment. Data on chemically induced polygenic variation are very limited (Ramel, 1983). Among ionizing radiations, gamma rays are considered to be the most effective on account of their shorter wave length possessing more energy per photon and mono-energetic radiations and hence the same have been used in present study for induction of polygenic mutations.

The importance of genotypes used for polygenic mutation as well as the intensity of radiation applied, are factors of prime consideration specially in the initial stage of an effective mutation breeding programme. From a resume of work on the induction of polygenic variation in various crops, it can be clearly seen that low doses of radiation are more effective for inducing polygenic mutations. Therefore, in the present study low doses ranging from 5 to 20 kR have been used, which are either below or around the LD 50 for lentil (Sharma, 1977). It has been speculated that best adapted and high yielding lines should be favoured for induction of polygenic mutants so that it is possible to accumulate in one genotype the most favourable alleles and at the same time eliminate the deleterious ones (Rawlings et al., 1958). In the present material, HPL-5, a microsperma type of lentil is this kind of genotype which is high yielding, resistant to blight and rust and adapted to wide range of environments in H.P. State. Another variety used in the present study is HPL-4, a very bold seeded, having resistance to blight and rust but it is specifically adapted to sub-temperate climate of mid-hill zone and the purpose of including this variety is its genetic diversity and also to improve its adaptation by identifying high yielding mutants with bold seeds along with desired maturity.

Micro-mutations are of importance for their adaptive evolution unlike macro-mutations with deleterious pleiotropic effects. Thus, the polygenic variations are of paramount importance for achieving desirable and directed evolution. The high rate of micro-mutations coupled with their much greater probability of improving adaptation explains why evolution in natural populations usually proceeds in the classical Darwinian mode, trekking its way through a series of small steps. Numerous studies of natural populations have demonstrated that phenotypic differences between individuals within populations, as well as differences between populations, race and species are generally influenced by multiple genetic factors with relatively small effects (Wright, 1968; Falconer, 1981; Lande, 1981;and Coyne, 1983). The optimum phenotype can be more nearly achieved by most individuals in the populations based on micro-mutations, while avoiding the segregation load produced by polymorphism of macro-mutations. Thus, in the present study, emphasis has been on the polygenic mutations induced by different radiation doses and to carry out their genetic analysis in order to know the nature and magnitude of induced variability by using sophisticated biometerical genetic models of Yonezawa (1979) and Virk et al., (1978), which have considerably removed difficulties in applying a mutagenicity screening technology to polygenes.

The results obtained on the induction of variation under different doses over generation (Table 1-4) indicate that sufficient polygenic mutations have been induced for most of the traits studied, namely seed yield, biological yield, number of pods, 100-seed weight, number of primary branches, plant height and days to maturity in both microsperma and macrosperma varieties of lentil. The exception is only the harvest index, for which the

induction of polygenic mutation is dose and variety specific. As the dose increases from 10kR onwards in both the varieties, there is a considerable induction of polygenic muations for this trait also. On the other hand traits like seed yield and number of primary branches exhibit absence of induction of polygenic mutations in both the varieties at higher doses. Under higher dose, number of pods exhibit absence of induction of polygenic mutations in macrosperma type. It is worth mentioning that in all the doses , the induction of mutation for polygenic traits are showing their persistance from M_2 to M_4, indicating thereby that in the material studied, sufficient genetic variability has been induced in comparison to environmental variance (parental variance). Earlier workers have also reported induction of genetic variation in the irradiated material. Such induction of polygenic variation through mutation in microsperma lentil have also been reported earlier by Abo Hegazi (1973), Shaikh (1975), Tirdea (1978), Sharma and Sharma (1978,1979), Ravi et al.,(1979), Shaikh et al.,(1979), Sen (1982), Kalia (1982) and Sharma and Sharma (1982). In macrosperma lentil, the report on the induction of polygenic variation is limited (Tomozei and Tirdea, 1975 and Kalia, 1982). Induction of polygenic mutations in other economic crop plants have also been reported by numerous workers (Koo, 1962 in oats; Gaul, 1963 and Bansal,1969 in barley; Verma, 1973 in Brassica juncea; Rao and Joshi, 1976 in triticale; Raja Ram, 1973, Bhatti et al., 1970 and Mandal, 1974 in gram; Rao,1974 in pigeon pea; Rajput, 1974 and Malik et al., 1979 in mungbean). Segregation pattern in M_2, M_3 and M_4 generations resulting from heterozygous gene loci following mutation in the two pure line varieties studied has further revealed the presence of appreciable amount of genetic variability present both between lines and within lines for most of the polygenic traits.

With respect to variances due to lines, the magnitude appears to be changing from generation to generation being, in general, at peak in M_4 for most of the polygenic traits in both varieties under different radiation doses with minor exceptions. However, in some of the traits under certain doses, variance due to lines is higher in M_3 generation. Variance within lines, is in general, higher in M_3 in comparison to M_2 and M_4 generations, specifically under medium to higher doses of radiation. Individual within line analyses (Table 13 to 20) also further establish the fact that the number of lines exhibiting significant within line variance is higher in majority of the doses in M_3 as compared to M_4 in both the varieties. The importance of within line variance in M_3 and later generations has also been emphasised earlier in lentil (Ravi et al., 1979; Sharma and Sharma, 1978 ; and Kalia, 1982). Presence of sufficient genetic variation within lines in later generations is understandable from the fact that polygenes which are numerous for a quantitative trait like seed yield have high mutation frequency as compared to major genes, as reported by Ramel (1983). Higher polygenic mutations lead to retention of more induced genetic variation in later generations. Probably, in the present material too, the presence of considerable amount of induced genetic variation even in M_4 generation, for many of the polygenic traits studied under majority of the doses, specifically under higher ones, might be due to high mutation rate of polygenes for the traits under study. Presence of such segregation as recorded in the present material has also been documented by Dumanovic et al.,(1970) in wheat and by Hussain and Abdalla (1979) in Vicia faba.

Another important point to note in Tables 1 to 4, is the presence of considerable amount of line x block interaction. In some cases this

interaction, under certain doses in both the varieties for different traits, happens to be considerably high when compared to within line variances in different generations, indicating the importance of genotype x micro-environment interaction, however, line x block interaction does also contain some amount of genetic variability due to heterogenity of M_3 and M_4 lines. Probably, this interaction is responsible for rendering variance due to lines non-significant when tested against parental or within line variances for some of the traits in some radiation doses in different generations. In M_3 and M_4 generations, ineffectiveness of mutagens is apparently due to high amount of genotype x micro-environment interaction, which is normally taken as error variance for testing the variance due to lines in the analysis of variance. Such conclusions are erroneous, because in such cases, there is induction of polygenic mutations but as usual the effect of such individual genes is so small that it is too much influenced by environment and gets confounded into line x block interaction. Present findings, suggest that to conclude whether the induction of mutations in the polygenes is there or not, variances due to lines, line x block and within lines must be tested against the parental variance and if any one of the above three variances is significant within the limit of sampling error then one can safely say that induction of polygenic mutations has occured. This point also needs consideration while deriving conclusion about the effectiveness and efficiency of various doses of a mutagen.

In order to compare the extent and magnitude of variability over traits over generations and doses, estimates of coefficient of variability is considered to be the most potential and reliable parameter. In the present study the estimates of C.V.(Tables 5 to 8) again confirm the induction of large amount of variability for all the polygenic traits as in most of the

cases C.V. in different generations over different doses is higher than the parental C.V., in both due to lines and within lines. The value of C.V. due to lines is, in general, higher as compared to within lines in all the generations for all the traits except for seed yield where C.V. due to within lines in general is higher in both microsperma and macrosperma varieties. It is worth mentioning that the variances due to within lines are in general higher in M_3 than in M_4 but C.V. in both M_3 and M_4 generations is more or less of equal magnitude at least in microsperma. However, in macrosperma within line C.V. is slightly reduced in M_4 as compared to M_3. High estimates of C.V. have been observed with respect to seed yield, biological yield, harvest index, number of pods and number of primary branches in all the generations over different doses. For 100-seed weight and plant height, the estimates of C.V. are moderate but low for days to maturity. Over doses, coefficient of variation reveals that in microsperma the estimates increase from 5 to 15kR but get reduced under high dose of 20kR, whereas, in macrosperma, C.V. is maximum under 5kR and starts showing progressive decline with increasing radiation doses. This confirms the differential radiosensitiveness of microsperma and macrosperma types in lentil (Sinha and Godward, 1972 and Kalia, 1982). High C.V. following mutation, has also been reported in lentil by Abo-Hegazi (1973), Nandan and Pandya (1980), Sharma and Sharma (1982) and Kalia (1982). In the present material, the seed yield under 5kR in microsperma has the highest C.V. due to lines which is more than four times of parental C.V. whereas, the lowest C.V. has been with respect to days to maturity.

Another important parameter of variability which needs consideration for the induced polygenic variation is the heritability which is estimated as ratio between genetic variance and total phenotypic variance observed in a

particular population. In any crop improvement programme may be through hybridisation or mutation, response to selection would depend upon the magnitude of heritability i.e. on the magnitude of genetic variance generated or induced, besides, other factors. In the present study, estimates of heritability due to lines ignoring genotype x micro-environment interaction (line x block interaction) and due to within lines (Tables9 to 12) are considerably higher as compared to heritability due to lines eleminating line x block interaction for most of the traits under different radiation doses in M_2, M_3 and M_4 generations. In lentil moderate to high heritability estimates in M_3 has also been reported earlier by Chowdhry et al.,(1978), Ravi et al.,(1979), Haddad,(1980), Nandan and Pandya (1980) and Kalia (1982). High heritability estimates following mutation has also been observed in various other crop species by Rawlings et al.,(1958), Papa et al.,(1961) and Williams and Hanway (1961) in soybean, Krull and Frey (1961) and Koo (1962) in oats, Gill et al.,(1974) in barley; Sarma (1975) in peanut, Borojevic (1965), Goud (1967) and Ibrahim and Sharaan (1974) in wheat and Jana and Roy (1973) in rice. It is worth noting that elimination of genotype x micro-environment interaction has considerably reduced the heritability estimates due to lines and the extent of reduction has been to the tune of 75 per cent. In case of days to maturity under 5kR dose in M_3 generation with respect to microsperma, it is reduced from 91 per cent to 4 per cent. Heritability, due to lines eliminating genotype x micro-environment interaction has remained more or less constant over generations with the exceptions of seed yield under 5kR dose of radiation, whereas, in microsperma variety heritability estimates have reduced in M_3 and M_4 as compared to M_2. In macrosperma these estimates are higher in M_3 as compared to M_2 and M_4. In general, the heritability estimates

are higher under lower doses as compared to higher ones. Present findings reveal that the presence of genotype x micro-environment interaction leads to over-estimation of heritability in induced polygenic variation. Therefore, it is suggested that while evaluating the induced polygenic variation, presence of genotype x micro-environment interaction must be considered, as it is well established that presence of this interaction creates hindrance in realising the expected gain through selection in a population (Sprague, 1966). High heritability estimates in M_3 and M_4 generations within lines also indicate that selection would be more effective in later generations, as late as in M_4 for seed yield and other yield contributing traits.

Another important parameter to detect the induction of new variation caused by mutagenic agents is the shift in mean of the irradiated population in relation to parental control. The mean values for polygenic traits in irradiated population are in most cases lower than the unirradiated material indicating negative shift in mean (Scossiroli, 1965; Gregory, 1968 and Gaul, 1965). This effect of radiation on mean has been attributed to deleterious mutations which are supposed to occur in higher frequency than the favourable ones. In the present material, the shift in mean appears to be variety-trait-generation-dose specific (Tables 21 and 22). In microsperma, under 5 and 10kR doses the shift in mean in M_2 and M_3 generations as compared to parent is mostly positive or neutral and in M_4 generation, all trends, negative, neutral and positive shifts have been observed for different traits, however, for seed yield and number of pods, it is neutral, but for days to maturity, shift is towards lateness. Such a positive, neutral shift in mean under low doses has also been documented in M_3 generation by Kalia (1982). Under higher doses in microsperma, the shift in mean is negative for most of the

traits in different generations as has been earlier observed by various workers (Scossiroli, 1965; Sinha and Godward, 1972; Sharma and Sharma, 1978; Tirdea 1978; and Kalia, 1982). The trend in shift in mean with respect to macrosperma is somewhat different from that in microsperma. In this case for important traits like seed yield, the positive shift in mean has been observed in M_3 and M_4 generations and neutral in M_2 under 5 kR dose and positive shift in M_2 and M_4 and neutral in M_3 under 10kR. Under higher doses as observed in microsperma, the shift is negative for most of the traits in macrosperma. The important trait under consideration in macrosperma has also been early maturity and for this the desired shift in mean has been noticed under 10kR in all the three generations and under 15 and 20kR dose in M_4 generation only. For 100-seed weight, consistent positive shift in mean over generations has been recorded under 10 and 20kR doses, whereas, under 5 and 15kR doses, the shift in mean has been towards negative side. In general, for majority of the traits in most of the generations under different doses, the shift is towards negative side. These results on the shift in mean are not following exactly the Brock's hypothesis and the present study reveals that such shift in mean of irradiated population are generally unpredictable and are dependent upon specific genotypic-trait-dose-generation combination. Shift in mean has also been reported to be genotypic-trait specific by Frey (1968) in oats and Kalia (1982) in lentil. A disharmonious and deleterious effect of higher doses of gamma rays for seed yield has also been reported by Oka et al.,(1958), Rawlings et al.,(1958) and Kao et al.,(1960). Aastveit (1966) also concluded that Brock's hypothesis can not be universally valid and the direction of micro-mutational variability is independent of genotype, but associated with vitality.

Beside considering the shift in irradiated population mean, it will also be worthwhile to consider the shift in mean on the basis of individual line mean in M_3 and M_4 generations in both varieties studied under different doses (Tables 13 to 20). It is interesting to note that irrespective of past selection history of traits under consideration in both varieties, the shift in line mean in both M_3 and M_4 generation for all the traits studied in both the varieties is either unidirectional or there is no shift in mean from parental variety. Bateman (1959) has also stated that in a population mutations can occur in one direction only as has been the case in the present study. Even on the basis of line mean analysis, the present findings do not follow the Brock's hypothesis. Wherever there has been a shift, it has been mainly towards positive side. Therefore, according to present results, past history of selection has nothing to do with the pattern of shift in mean of irradiated material.

It is now well recognised that effectiveness of radiation dose and efficiency of dose are distinct phenomenon. While effectiveness of all the doses have been observed in both the varieties for most of the traits studied, it will be desirable to identify the most efficient one by looking at relationship of various doses with different parameters of variability like, shift in mean, coefficient of variability and heritability. As discussed earlier, the shift in mean is dose-trait-variety specific and lower doses appear to be more efficient for most of the yield traits. In microsperma also on the basis of line mean analysis in M_3 and M_4 generations excelling their parental control are higher under 5 and 10kR for seed yield, biological yield, pods per plant, branches per plant and tallness, however, for 100-seed weight, 15kR dose appears to be the most efficient for having unidirectional

positive shift. Beyond 10kR, except for 100-seed weight, there is not much shift in mean for majority of the lines studied in M_3 and M_4 generations. In macrosperma for seed yield, biological yield, branches and height, 5kR appears to be the most efficient dose, for 100-seed weight, 10kR appears to be the most efficient, and for days to maturity, 15kR appears to be the good one. In general, on the basis of both population and individual mean, it can be safely concluded that in microsperma 5 and 10kR doses and in macrosperma 5kR or below would be more efficient for seed yield and some of its components, whereas, for 100-seed weight, 15kR in microsperma and 10kR in macrosperma and for days to maturity, 10 and 15kR doses in macrosperma would be most efficient for inducing desirable mutations. On the basis of M_3, Kalia (1982) has also reported lower doses to be the most efficient for yield and yield components in lentil. Negative shift in mean at population level in irradiated material in comparison to control at higher doses as recorded in present material has also been documented earlier (Scossiroli, 1965; Sinha and Godward, 1972; Sharma and Sharma, 1978; Tirdea, 1978; and Kalia, 1982).

Looking at the relationship of various doses with phenotypic coefficient of variability, it appears that C.V. due to lines in some instances appears to be linearly related with the radiation doses administered, but in others, it is lacking as reported earlier (Scossiroli, 1965). Only the intermediate doses have induced maximum increase in variation and there is a strong decline with increasing doses. The lack of linearity may be due to elimination of non-reproductive mutants in earlier generations as actually practised in the present material. The increase in variation upto 15kR has been with respect to M_2 generation, however in M_3 and M_4 generations, there is a slight reduction from 5 to 10kR and sometimes there

is slight increase but beyond 10kR there is general reduction in induced variability in both the varieties. Results on the coefficient of variability, reveal that 5 and 10kR doses are the most efficient for most of the yield components for inducing variation between lines and for days to maturity, higher doses i.e. 15 and 20kR appear to be better. Within line, coefficient of variance in M_3 and M_4 generations further indicates that for seed yield within lines genetic variance under different radiation doses remains more or less same in both the varieties. However, on the basis of the highest coefficient of variance due to within lines in M_3 and M_4 generations, 10kR dose of gamma radiation appears to be the best for both the varieties. It is worth mentioning that though in most of the traits, under low doses shift in mean has been unidirectional, still high amount of induced genetic variation has been documented in the present study.

Relationship of heritability estimates with different doses of radiation indicates that heritability due to lines eliminating genotype x micro-environmental interaction, in general, decreases with increasing dose of radiation in microsperma, whereas, in macrosperma it increases with increasing dose, being highest under 20kR. With respect to heritability within lines, it is highest at lower doses and negligible at higher doses with respect to microsperma variety, whereas, with respect to macrosperma variety, the situation is reverse specifically for seed yield. It appears that at higher doses, there has been random mutation specifically in microsperma type leading to little shift in mean but such random mutations normally leads to high magnitude of variation as has been mentioned by Brock (1965).

On the basis of shift in mean, estimates of coefficient of variance, heritability, pattern of variation and segregation within and between lines, it is emerging out that present results confirm the earlier views that macrosperma is more radio-sensitive than microsperma. On the basis of desirable mutant lines in M_3 and M_4 generations, it also appears that number of lines thrown under 5 and 10kR doses are much higher for microsperma as compared to macrosperma for seed yield. This further confirms difference in radiosensitivity of the two varieties under study. Sinha and Godward (1972) and Kalia (1982) have also reported that variety macrosperma is more radio-sensitive than microsperma.

Another most important aspect of the present investigation is to know the genetic architecture of induced variation with respect to yield and its components. Importance of such an analysis in purposeful management of induced genetic variability is obvious. Rational choice of most suitable breeding method among several available, would depend to a large extent on the nature of gene action involved in control of a trait or traits of interest to the breeder with respect to induced variation. Meaningful genetic analysis of polygenic traits can be said to have been initiated with the work of (Fisher, 1918), when he showed that continously varying traits are also governed by genes which obey Meandelian laws and suggested partitioning the hereditary variance into additive, dominance and epistatic components. After this, there has been a prolific development in biometrical genetical models for partitioning the genetic variability generated through hybridisation. However, such developments in partitioning the induced genetic variation into its various components has received little attention. While many experiments

have been conducted to assess the amount of induced genetic variation in self fertilising plants, the genetical interpretation of variation has more or less been neglected. Like created variation through hybridisation, genetic architecture of induced variation is of paramount importance in deciding appropriate breeding methodology to achieve the desired breeding goal. Recently, there has been some developments in genetic analysis of induced polygenic variation by deriving some biometrical genetical expectations of different generations of irradiated material by treating M_1 as F_1 and M_2 as F_2 and so on. Kao et al.,(1960) took the first step in this direction and based their genetic analysis on the assumption that allele 'A' mutates to 'a' at the rate 'p' when an individual AA is subjected to mutagenesis. Aastveit and Gaul (1967) suggested the use of genetic variances and covariances of M_2, M_3 and M_4 populations by growing them simultaneously in the same year to avoid biasness due to genotype x environment interaction for partitioning the induced variation into genetic components. Noticing the inconvenience of growing three generations in one year, Virk et al., (1978) proposed another method which requires single generation of a population with an hierarchical pedigree system by considering each M_1 plant as F_1 and M_2 as F_2. They used Mather and Jinks (1971) approach. Though this approach appears to be a novel one, specificially for detection of non-allelic interaction in induced variation, however, due to its few shortcomings as being not applicable before the M_4 generation, not providing the estimate of multiplicating component of additive-dominance gene affect and leading to genetic drift because of hierarchical pedigree structure, Yonezawa (1979) proposed another method for predicting the additive and dominance components of induced variation

which are practicable upto M_3 generations since M_3 is regarded as being the best generation to start selection for breeding. Present study also indicates that M_3 is the best stage for starting selection both within and between lines, however, selection in M_4 generation between lines for most of the traits and within line for few traits is also equally effective. Virk and Gupta (1980) also suggested a simple equation to test the adequacy of additive-dominance model by using M_0, M_2 and M_3 population mean but this equation appears to be incorrect as per Mather and Jinks (1971) expectations, however, in the present study, the equation has been modified by correcting the same as per Mather and Jinks (1971). In the present study, the novel approach of Yonezawa (1979) for partitioning the induced variation into genetic components and the modified equation of Gupta and Virk (1980) for testing the adequacy of additive-dominance model for detecting the presence of non-allelic interaction in induced polygenic variation under different radiation doses in both microsperma and macrosperma varieties have been made use of.

Scaling test reveals that for seed yield under all doses of microsperma and under 5 and 10kR doses in macrosperma, there is a inadequacy of additive-dominance model indicating, thereby the presence of non-allelic interaction in radiation generated variability. With respect to microsperma non-allelic interaction has been detected under 10 and 20kR for biological yield, under 5, 10 and 15kR for harvest index, and number of primary branches, under 20kR for number of pods, under 10,15 and 20kR for plant height, and under all the doses for hundred seed weight and days to maturity. With respect to macrosperma, presence of non-allelic interaction has been noticed under all the doses for biological yield and plant height, under 10,15 and 20kR

doses for harvest index and hundred seed weight, under 15 and 20kR for number of primary branches, and under 10 and 15kR for days to maturity. It is further interesting to note that it is only under 5 and 10kR, where non-allelic interaction has been noticed for seed yield, that high yielding mutants excelling parents have been noticed in both the varieties indicating thereby, non-allelic interaction of additive x additive nature, because only such interactions are fixable in advanced generations and can lead to transgressive segregants in M_3 and M_4 generations following mutagenesis of a pure line variety. Other traits where additive x additive type of interaction appears to be present, are biological yield under 10kR, hundred seed weight under all doses, number of primary branches under 5 and 10kR, plant height under 10kR in microsperma, whereas, in macrosperma it is existing for biological yield under 10kR, harvest index under 15kR, hundred seed weight under 10 and 20kR, plant height under 5 and 10kR and for days to maturity under 15kR, as indicated by the presence of transgressive segregants in M_3 and M_4 generations (Table 29). Presence of such non-allelic interaction for induced polygenic variation in lentil is being reported for the first time. Such studies on non-allelic interaction with respect to induced polygenic variation in other crops too, is as good as nil.

Presence of non-allelic interaction in quantitative traits as a major portion of total genetic variance has been confirmed by Cockerham (1959). Ketata et al.,(1976) have reported in wheat that genetic models neglecting epistasis may result in biased information. Non-allelic interaction of additive x additive type has also been documented recently in lentil by Haddad et al.,(1982) for several polygenic traits following diallel technique. Presence of non-allelic interaction following hybridisation have

Table 29. Estimates of the mutant progenies under different doses and generations in both microsperma and macrosperma varieties of lentil, surpassing significantly the control in desirable direction for different polygenic traits.

Characters/ generation		microsperma				macrosperma			
		5kR	10kR	15kR	20kR	5kR	10kR	15kR	20kR
Seed yield (g)	M_3	1	19	0	0	3	1	0	0
	M_4	0	2	0	0	9	4	1	0
Biological yield (g)	M_3	5	12	0	0	7	0	0	0
	M_4	7	0	0	0	6	2	0	0
Harvest index(%)	M_3	0	1	0	0	0	0	3	0
	M_4	0	0	0	0	0	0	4	0
Number of pods	M_3	15	3	0	1	0	6	0	0
	M_4	4	1	0	1	3	9	0	0
100-seed weight(g)	M_3	8	3	19	0	0	6	0	1
	M_4	4	0	40	5	0	2	0	2
Number of primary branches	M_3	3	3	0	2	0	1	0	0
	M_4	0	0	0	6	8	6	0	0
Plant height (cm)	M_3	0	8	1	0	0	1	0	0
	M_4	0	0	0	0	6	2	0	0
Days to maturity	M_3	0	0	0	0	0	0	0	0
	M_4	0	0	0	0	0	0	2	0

been found to be a non-trivial factor in the inheritance of agronomically important traits in various crops by Bauman (1959), Gorsline (1961), Sprague et al.,(1962) and Stuber and Moll (1969) in corn, by Hanson and Weber (1961) in soybean, by Burton (1968) in pearl millet, and Yermanos and Allard (1961) in flax. However, such information with respect to induced polygenic variation has not been taken up in any crop so far.

Component analysis (Tables 24 and 25) reveals that mutagenically induced additive effects are present for number of pods, hundred seed weight and days to maturity under 5 kR, for seed yield, biological yield and days to maturity under 10kR, for all the traits except harvest index and days to maturity under 15kR and for hundred seed weight, plant height and days to maturity under 20kR in microsperma variety of lentil. It is interesting to note (Table 24) that at 15 kR dose the induction of additive effects is universal for all the traits studied, whereas, at lower or higher doses it is trait specific. Moreover, at 15kR dose, most of the estimated induced additive effects are positive. Under 5kR for hundred seed weight and days to maturity, under 10 kR for seed yield, biological yield and days to maturity, and under 15 and 20kR for hundred seed weight, the negative induced additive effects indicate that the net direction of polygenic mutation is from increasing alleles to decreasing alleles. The positive additive effects,under 5kR dose for number of pods, under 15kR for all the traits except harvest index, and days to maturity, and under 20kR for plant height and days to maturity, indicate that the net direction of induced mutation is from decreasing allele to increasing allele as per Virk et al.,(1978). This establishes that either the decreasing alleles have a high mutation rate or the parents contain more of increasing than decreasing alleles for the traits

exhibiting positive additive effects. It is interesting to note that induced positive dominance effects are present for all the traits except days to maturity under low doses of 5kR, for harvest index, number of pods and plant height under 10kR, for plant height under 15k^{R} , and for number of pods, number of primary branches and plant height under 20k^{R}, indicating, thereby, that more increasing alleles are dominant than decreasing alleles. Negative induced dominant effects are present for biological yield under 10kR, for seed yield, harvest index, number of pods and hundred seed weight under 15kR and for biological yield and hundred seed weight under 20kR, indicating that more decreasing alleles are dominant than increasing alleles. Relationship of doses with genetic components indicates that at lower doses, more positive dominance effects have been induced through mutation and under medium radiation doses, more of positive additive effects have been induced. Induction of mutation for induced additive effect is universal for all traits under 15kR and for dominance under 5kR in microsperma. Therefore, in microsperma, 5kR for induction of dominance and 15kR for induction of additive effects are most efficient doses for all polygenic traits except days to maturity. Average degree of dominance, wherever both additive and dominance effects are significant, reveals overdominance for number of pods under 5kR and complete dominance is present for hundred seed weight under 5kR, biological yield under 10kR, number of pods, hundred seed weight, plant height and seed yield under 15kR, and hundred seed weight and plant height under 20kR. The genetic components estimated on the basis of second degree statistics for microsperma (Table 26) variety indicate that for number of pods under 5kR additive and dominant variances are significant and average degree of dominance is over-dominance. This finding is exactly in line with the one

based on first degree statistics for this trait under similar radiation dose. Plant height under 20kR dose in microsperma exhibits both additive and dominance variances to be significant with complete dominance and these estimates are again exactly similar to the one based on first degree statistics (Table 24).

In macrosperma, the net direction is mutation of decreasing alleles to increasing alleles with respect to seed yield under 5 and 10kR, biological yield under 10 and 15kR, number of pods and hundred seed weight under 5 and 15kR, number of primary barnches under 15kR, plant height under all doses and days to maturity under 10kR, whereas, net direction is mutation of increasing alleles to decreasing alleles with respect to biological yield under 5kR, harvest index under 10,15 and 20kR, hundred seed weight under 10kR, number of primary branches under 5kR and days to maturity under 5 and 15kR doses. Estimates of induced dominance effects indicate that net direction of dominance is that increasing alleles are dominant to decreasing alleles in case of seed yield, biological yield and days to maturity under 10kR, number of pods under 5kR, hundred seed weight under 15kR and for plant height under all doses, whereas, in case of seed yield under 5kR, harvest index under 5, 10 and 15kR, number of pods under 20kR, number of primary branches under 5 and 15kR, and days to maturity under 15kR, more decreasing alleles are dominant than increasing alleles. In this variety,no specific trend is emerging out with respect to genetic components and radiation doses as has been observed in microsperma. However, for seed yield, 5 and 10kR are the most efficient doses for induction of additive and dominance effect. Complete dominance has been observed for seed yield under 5 and 10kR, for biological yield under 10kR, for harvest index under 10 and 15kR, for number

of pods under 5kR, for hundred seed weight under 15kR, for number of primary branches under 5 and 15kR, for plant height under all doses, and for days to maturity under 10 and 15kR. In macrosperma, hundred seed weight under 20kR dose exhibits absence of additive variance on the basis of second degree statistics (Table 26), which is not in line with the information obtained from first degree statistics for this trait. However, the dominance variance is significant in positive direction indicating that increasing alleles are dominant over decreasing alleles.

The estimates of 'r_2/r_1' ratio and 'r_3' values measuring the isodirectionality of dominance and degree of gene association indicate that in microsperma under 5kR for number of pods, about half of the parental genes have increasing effect compared to mutant genes, dominance being positively directed for most of the genes concerned and all the parental alleles are dominant to mutated ones. For plant height, under 20kR dose in microsperma, the parental genes are lacking dominance as compared to mutant genes. Parental genes lack dominance in comparison to mutant genes for 100-seed weight under 20kR dose in macrosperma variety of lentil. Average degree of dominance on the basis of second degree statistics is over dominance for number of pods under 5 kR in microsperma and 100 seed weight under 20kR in macrosperma, whereas, complete dominance is present for plant height under 20kR in microsperma.

Following mutagenesis, reports available on the investigation of gene action for polygenic traits in any crop including lentil are as good as nil. However, there are some reports regarding the gene action of various traits in lentil estimated through hybridisation studies. Singh and Jain (1971) have observed heterosis for number of branches, number of pods and seed yield indicating non-additive genetic variance for these traits.

Malhotra et al.,(1973) have shown GCA effects to be important for maturity, seed yield, number of pods and plant height and have reported partial dominance for days to maturity and complete dominance for plant height as observed in the present study. Singh et al.,(1975) have observed dominance for seed yield and number of pods. Goyal et al.,(1976 and 1977) have observed significant GCA and SCA effects for seed yield, number of primary branches and seed size. Haddad et al.(1982)have obtained additive genetic variance for days to maturity in one cross and dominance variance for seed weight, plant height and days to maturity in another cross.

On the basis of above information obtained on the genetic architecture of induced polygenic variations, it is very difficult to recommend a suitable breeding technology for handling the induced variability under all the doses, because type of gene action and component of gene effects vary not only from dose to dose but also from variety to variety. Differences in genetic variances from treatment to treatment, generation to generation for different traits are not unusual since as stated by Brim and Cockerham (1960), different populations and different traits need not to exhibit the same type of gene action.

In lentil breeding as with other crops, knowledge of the additive component is important because it assists in defining appropriate breeding method. With a significant additive component, all methods of breeding and selection are appropriate and should be effective. For traits, where dominance variance is equally important, improvement will require the proper combination of mass, family and progeny test selection (Cockerham, 1961). In the present study with respect to important traits like seed yield, it appears on the basis of genetic component analysis under 10kR dose that pedigree method following mutagenesis in M_3 generation would be profitable.

Under 15kR dose, probably modified bulk methods like stratified bulk breeding method or single seed descent which also makes use of some portion of non-additive variation besides exploiting additive would be profitable in microsperma variety. In macrosperma, for seed yield, where both additive and dominance variance have shown their appearance under 5 and 10kR doses in irradiated material, it is suggested that stratified bulk breeding method or any other form of bulk breeding or family selection method may be used. Recently, Saini (1983) while comparing different breeding methods in soybean has shown that stratified bulk method is comparable to pedigree method under a situation where additive genetic variance is present and has advantage over other methods under a situation where both additive and dominance variance are present. Stratification in lentil can be done easily on the basis of seed size, maturity, plant type, seed colour etc. etc. For handling the irradiated material following mutagenesis, single seed descent method as proposed by Goulden (1939) and modified by Grafius (1965) and Brim (1966) and also further advocated by Haddad (1980) and Muehlbauer et al.,(1981) in lentil, would also be an efficient mean of advancing irradiated population without selection while preserving genetic variance for selection at later stages. Single seed descent method has been shown to be an efficient cost saving procedure for advancing lentil population by Haddad (1980). A high amount of within line variance present both in M_3 and M_4 generations (Table 29) besides significant variance due to lines in the present study further goes in favour of adopting single seed descent method in mutation breeding programme too, as it has been shown by Haddad (1980) and Muehlbauer et al.,(1981), that the breakdown of additive genetic variance is different between single seed descent method and pedigree method. In the single seed descend method all the additive genetic

variance is in between lines while in bulk population method the additive genetic variance is a combination of between lines and within lines variance. The substantial amount of within lines variance component in the bulk population breeding, indicate the presence of closely related plants and therefore reducing the potential for selection and increasing probability of selecting closely related genotypes. It may be mentioned that in the present study each line in M_3 and M_4 generation which are showing high amount of within line variance, has descended from individual normal looking M_1 plants following bulk method without making selection at any generation. So, therefore, in lentil mutation breeding programme, stratified single seed descent method or bulk method would be advantageous in handling the irradiated population in early generations, specifically under situation where additive or both additive and dominance alongwith complimentary type of gene action are present for the trait under genetic improvement.

Under the situation where dominance or non-allelic interaction or both are present as it is the case under 5kR for seed yield, the best would be to launch an hybrid breeding programme, but due to floral morphology of lentil and non-availability of male sterility mechanisms for efficient and economically viable hybrid breeding programme, it would be advisable to defer the selection so that natural selection plays its part and through evolution, non-additive gene effects gets converted into fixable effects as suggested by Fasoulas (1980), whereby, he has emphasised that role of various recombinational mechanisms following hybridisation/mutation, is not to merely reshuffle the genes into random recombinations, but to reorganise the structure of genetic material and change its function, and that all heterotic effects are constantly converted through recombination into additive and fixable effects

and vice versa. This happens because the genetic material carries built-in-forces for adaptive and progressive conversions reflected in the extra-ordinary properties of self organisation, self regulation and self replication. Recent findings of Schimke (1980) and Chambon (1981) in biochemical genetics of higher organisms concerning the phenomenon of gene amplification and of split genes coroborate this theory on the evolution of gene action.

Prediction about the potentiality of irradiated material following mutagenesis under a particular dose for throwing lines excelling its parental unirradiated material is another most important area in dealing with polygenic traits like seed yield, seed size etc. in mutation breeding programme. Such predictions related to crosses following hybridization between two diverse parents for their potentiality in throwing transgressive segregants have been made recently by Jinks and Pooni(1976) on the basis of additive genetic component and differences between parental and hybrid or mutated line mean. Effectiveness of such predictions as suggested by these workers depends mainly on the accuracy of the estimation of various genetic components. The above approach has been found satisfactory by Jinks and Pooni (1980) in Nicotiana and Saini (1983) in soybean. Till today, the use of above approach has not been made in mutation breeding programme, probably because of non-availability of efficient biometrical genetic models for estimating various genetic components precisely. In the present study by using sophisticated biometrical genetic models, genetic components of induced polygenic variation have been estimated and by using the approach of Jinks and Pooni (1976), predictions have also been made (Table 27 and 28) about the potentiality of irradiated material for throwing potentially desirable mutants excelling its parents (unirradiated material), it would be interesting to

Table 30. Estimates of actual number of lines obtained excelling parental control and expected number of lines on the basis of prediction values for various polygenic traits in microsperma and macrosperma varieties of lentil in M_3 and M_4.

Characters/ generation		microsperma(HPL-5)				macrosperma (HPL-4)			
		5kR	10kR	15kR	20kR	5kR	10kR	15kR	20kR
Seed yield (g)	M_3	-	3.61 (19) 1.67	3.84 (0) 0.08	-	5.98 (3) 2.04	8.71 (1) 8.10	-	-
	M_4	-	12.74 (2) 12.42	4.9 (0) 0.04	-	16.57 (9) 11.78	9.83 (1) 4.94	-	-
Biological yield (g)	M_3	-	7.52 (12) 3.69	6.41 (0) 0.75	-	4.27 (7) 0.87	6.53 (0) 5.40	1.15 (0) 3.38	-
	M_4	-	12.31 (0) 11.61	11.51 (0) 1.57	-	12.24 (6) 4.94	12.69 (2) 12.48	6.62 (0) 3.96	-
Harvest index (%)	M_3	-	-	-	-	-	8.93 (0) 8.64	1.45 (3) 0.72	1.01 (0) 0.11
	M_4	-	-	-	-	-	10.11 (0) 2.60	7.57 (4) 5.50	0.57 (0) 0.01
Number of pods	M_3	22.33 (15) 3.83	-	3.72 (0) 0.31	-	6.36 (0) 2.72	-	-	-
	M_4	28.55 (4) 25.01	-	7.30 (0) 0.78	-	18.70 (3) 17.48	-	-	-
100-seed weight(g)	M_3	32.31 (8) 0.27	-	2.85 (19) 1.32	3.33 (0) 2.66	2.06 (0) 0.61	3.40 (6) 1.09	1.39 (0) 0.60	-
	M_4	26.11 (4) 29.28	-	7.89 (40) 4.70	7.10 (5) 0.60	3.64 (0) 1.86	10.63 (2) 8.84	7.81 (0) 5.50	-
Number of primary branches	M_3	-	-	2.46 (0) 0.50	-	6.88 (0) 5.27	-	1.07 (0) 0.01	-
	M_4	-	-	10.19 (0) 4.90	-	13.49 (8) 8.74	-	3.23 (0) 0.02	

Contd...

Table 30 Contd.

Characters/ generation		microsperma(HPL-5)				macrosperma(HPL-4)			
		5kR	10kR	15kR	20kR	5kR	10kR	15kR	20kr
Plant height (cm)	M_3	-	-	8.73 (1) 4.48	0.47 (0) 0.46	8.02 (0) 7.14	7.29 (1) 5.58	1.25 (0) 0.96	1.75 (0) 1.35
	M_4	-	-	15.63 (0) 8.33	2.62 (0) 2.60	9.04 (6) 1.33	7.83 (2) 4.16	9.68 (0) 9.24	2.41 (0) 1.75
Days to maturity	M_3	10.95 (0) 1.96	15.31 (0) 1.23	-	2.91 (0) 1.96	3.69 (0) 3.23	2.93 (0) 0.81	1.79 (0) 0.54	-
	M_4	38.43 (0) 0.18	8.99 (0) 3.51	-	6.52 (0) 2.40	8.93 (0) 7.98	5.04 (0) 1.82	8.64 (0) 5.28	-

Note: The values in parenthesis indicate actual number of mutant lines obtained. The values above and below parenthesis indicate expected number of mutant lines on the basis of both additive and environmental variance and additive variance alone, respectively.

examine whether predictions are holding true with the expected one on the basis of predictions made. It can be seen from the Table 30 that the prediction is holding true for some of the traits under certain doses which indicates that there is certain co-linearity between predicated and expected values. For a plant breeder, seed yield is the most important polygenic trait and for this the present prediction approach is fitting very well specifically under 5 and 10 kR doses in both microsperma and macrosperma varieties of lentil. It is further interesting to note that this prediction is holding true where additive component is important and there is absence of non-allelic interaction as indicated by scaling test. However, this prediction is not universally fitting under all the doses for all the traits and therefore this aspect of prediction in mutation breeding programme, warrants further in-depth studies by utilising these biometrical genetic models which at present in literature are as good as nil in all the crops and probably the present one is the first attempt in this direction.

Besides, above in mutation breeding, plant breeder is also generally posed with a question regarding the appropriate stage to start selection for efficient genetic gains. This aspect in mutation breeding has also recieved very little attention by workers engaged with polygenic mutations. However, Scossiroli (1965) has reported that both M_2 and M_3 generations are good for effective selections, whereas, Palenzona (1966) and Yonezawa (1979) have suggested M_3 to be the best generation to start selection in mutation breeding. The study by Sharma (1977) reveals that the stage at which selection is to be made varies from trait to trait. In the present study, it is apparent that besides high amount of induced variance due to lines, there is a sufficiently equally high magnitude of variance due to within lines for seed yield and other traits in M_3 generation, whereas, in M_4 generation, though some amount of

within line variance is present but variance due to lines is comporatively more in microsperma (Table 1 to 4). However, in macrosperma, the situation appears to be little different. Individual line analysis (Table 31) further reveals that in microsperma specifically under low dose, the number of lines exhibiting significant within line variance for seed yield and its components are higher in M_3 generation as compared to M_4 and in macrosperma under 5 kR dose, the frequency of lines exhibiting significant within lines variance are higher in M_3 generation but such lines under 10 and 15 kR are more in M_4 generation.

In general, the coefficient of variation and heritability estimates due to within lines in M_3 generation are comparatively higher as compared to due to lines in M_3 generation, whereas, these genetic parameters are having higher magnitude due to lines in M_4 generation with some exceptions. On the basis of all these informations, it is self-evident that in lentil mutation breeding programme, M_3 generation would be most appropriate stage for starting selection both between and within lines and in M_4 generation, one can upto some extent restrict the selection between lines depending upon trait under improvement. However, under higher doses, it would be appropriate to start selection both within and between lines in M_4 generation and this holds more true in macrosperma variety of lentil. Prediction studies based on the additive component have also further revealed that the selection between lines in M_4 generation would be more effective as the prediction approach for identifying the potential mutant lines is holding more true in M_4 generation than in M_3. Therefore, present findings are in favour of starting effective selection, both within and between lines in M_3 and between lines in M_4 and supports the earlier views of Palenzona (1966), Dumanovic et al., (1970),

Table 31. Number of lines exhibiting significant within line variance for different polygenic traits under different radiation doses in M_3 and M_4 generations for microsperma and macrosperma varieties of lentil

Characters/ generation		Microsperma				Macrosperma			
		5kR	10kR	15kR	20kR	5kR	10kR	15kR	20kR
Seed Yield (g)	M_3	70	39	2	0	5	9	1	3
	M_4	22	11	3	0	2	10	4	0
Biological Yield(g)	M_3	5	32	4	7	2	11	2	3
	M_4	6	2	8	20	2	3	4	0
Harvest index (%)	M_3	8	3	13	1	0	4	0	2
	M_4	0	0	9	3	0	1	4	4
Number of pods	M_3	85	34	5	2	6	4	0	0
	M_4	57	7	5	0	9	5	1	0
100-seed weight(g)	M_3	0	2	5	1	17	14	0	3
	M_4	0	1	2	0	36	10	0	3
Number of primary branches	M_3	10	2	23	6	17	18	2	0
	M_4	2	0	19	19	35	24	2	0
Plant height(cm)	M_3	7	27	3	0	15	15	5	3
	M_4	2	9	0	0	26	14	10	5
Days to maturity	M_3	14	2	6	1	8	2	3	1
	M_4	7	0	9	0	16	1	12	2

Hussain and Abdalla (1979), and Yonezawa (1979).

Though last, yet the most important aspect is to look at the induced polygenic variation in order to identify potential mutants for desirable traits. The number of potential desirable mutants under each radiation dose for both the varities with respect to different traits studied are given in Table 29. It can be seed that in microsperma, such desirable mutants are available for seed yield, biological yield, number of pods, 100 seed weight, number of primary branches and plant height under different doses. For seed yield, the frequency of desired mutants is more under 10 kR dose, whereas, for 100 seed weight, it is more under 15 kR in microsperma. In macrosperma, for seed yield and other desired traits like number of pods, number of primary branches, plant height and biological yield, such desirable mutants are more under 5 kR, which appears to be most effective dose for isolating desired mutants. However, for bold seed size which is a unique speciality of macrosperma, 10 kR dose appears to be most efficient for inducing still bolder seed size mutants. As, in macrosperma, earliness is the most desired trait in order to widen its adaptability, 15 kR dose happens to be one which has thrown two mutants which are significantly earlier in maturity than parent. These two mutants namely HPLM 435 and HPLM 444 (Table 18) are 3 and 4 days earlier than the parental control and have good seed yield and seed size. In both the varities 20 kR dose appears to be inefficient dose with regard to isolation of desirable mutants. Some of the most promising mutants for seed yield in microsperma are HPLM 74 (280.5 % increase over parent) under 5 kR dose, HPLM 189 (211.8% increase), and HPLM 196 (105.9% increase) under 10 kR. In macrosperma, the maximum number of mutants for seed yield are under 5 kR dose and these are HPLM 326 (128 % increase), HPLM 328 (98.8% increase), HPLM 348 (117% increase), HPLM 349 and HPLM 350 (136% increase),

HPLM 354 (123% increase), HPLM 355 (126% increase), HPLM 364 (134% increase), HPLM 365 (140% increase), HPLM 366 (138% increase) and HPLM 380 (118% increase). Under 10 kR in macrosperma, HPLM 391 and HPLM 423 and under 15 kR dose HPLM 436 are the best yielding mutant. Some mutants having still bolder seed size in macrosperma, are HPLM 381, 382, 385, 386, 393 and 397 under 10 kR (Table 16) and HPLM 454, 462 and 464 (Table 20) under 20 kR dose of radiation, the maximum increase in seed size being under 20 kR where mutant HPLM 464 had a 100 seed weight of 7.39 gm. Earlier workers have also isolated useful mutants for improving yield in lentil (Moursi, et al. 1974; Shaikh, 1975; Uhlik and Urban, 1976; Ravi et al., 1979 and Kalia, 1982).

It is concluded from the above discussion that gamma radiations are effective in the induction of polygenic variation over generations and lower to medium doses are efficient. Persistance of variation over generations indicates that the induced variation is of genetic nature. Line and withinline analysis of variance in M_3 and M_4 generations indicate that M_3 is the most appropriate stage for starting selection both within and between lines. Coefficient of variation (C.V.) in microsperma increases from 5 to 15 kR dose but in macrosperma, it is highest under 5 kR dose. Heritability is more under low doses and genotype x micro-environment interaction inflates the estimates of heritability. The shift in mean is variety-trait-generation and dose specific, with positive and neutral shift under lower doses and negative shift under higher doses. Additive, dominance and non-allelic interaction have been detected in the induced polygenic variation and these are dose and trait specific. In microsperma, dominance is mainly present under 5 kR, and additive effects are predominant under 15 kR dose. First degree and second degree statistics are giving more or less similar information. Macrosperma is more radiosensitive than microsperma.

6. SUMMARY

SUMMARY

The objectives of the present investigation entitled "Genetic analysis of induced polygenic variation in microsperma and macrosperma varieties of lentils (Lens culinaris Medik), were, to understand the pattern of segregation and persistance of induced variation over generations under different rediation doses, to understand the genetic architecture of induced polygenic variation, and to understand the relationship of different radiation doses with various parameters of induced variability and varieties used with respect to various polygenic traits. Establishing the appropriate stage of selection and breeding method in lentil mutation breeding programme and to isolate mutants with desirable traits, were also of prime interest.

The material consisted of M_2, M_3 and M_4 generations of microsperma (HPL-5) and macrosperma (HPL-4) varities of lentil under 5, 10, 15 and 20 kR doses of gamma radiations. Polygenic traits studied were, seed yield, biological yield, harvest index, number of pods, hundred seed weight, number of primary branches, plant height and days to maturity. Genetic analysis of induced polygenic variation was done as per Virk et al., (1978), Yonezawa, (1979) and Virk and Gupta (1980).

Results obtained on the induction of variation under different doses over generations indicated that sufficient polygenic variation has been induced for most of the traits studied, in both microsperma and macrosperma varieties of lentils in all the generations. However, with respect to harvest index, the variation induced was not significant and was dose and variety specific. Induction of polygenic mutation under all the doses showed their persistance from M_2 to M_4 for most of the traits. Segregation pattern of induced polygenic mutants in M_2, M_3 and M_4 generations revealed the presence of significant amount of genetic variability both between lines and within lines for most of the traits. Magnitude of variance due to lines appeared to be changing from

generation to generation, being highest in M_4 for most of the traits under different doses in all the generations with few exceptions, whereas, variance due to within lines was higher in M_3 generation specifically under medium to higher radiation doses. Individual line analysis of variance in M_3 and M_4 revealed that the frequency of lines exhibiting significant within line variance was highest in M_3 in both the varieties for most of the traits. Considerable amount of line x block interaction was also observed which in some cases was even higher than the within lines variance in different generations, signifying the presence of genotype x micro-environment interaction.

Coefficients of variation (C.V.) due to line and within lines in both the varieties of lentil over generations and doses were higher than parental C.V. In general, C.V. due to line was higher as compared to corresponding C.V. within lines except for seed yield, where this relation was reverse. Magnitude of C.V. was constant in M_3 and M_4 of microsperma. High estimates of C.V. were observed for seed yield, biological yield, harvest index, number of pods and number of primary branches in all the generations under different doses, whereas, these estimates were moderate for 100-seed weight and plant height and low for days to maturity. In microsperma, C.V. increased from 5 to 15kR, whereas, for macrosperma it was maximum under 5kR dose only.

Heritability (broad sense) estimates, in general, were higher under low radiation doses. Presence of genotype x micro-environment interaction (line x block interaction) inflated the heritability estimates for most of the traits under different doses in M_2, M_3 and M_4 generations. Heritability in M_3 and M_4 was higher in both the varieties.

The shift in mean of irradiated population for various polygenic traits appeared to be variety-trait-generation-dose specific. The shift was positive or neutral under low doses of radiation and it became negative at higher doses of radiation in both the varieties, however, the positive, neutral shift was observed under M_2 and M_3 generations in microsperma and in later generations like M_4 in macrosperma. Desired shift in mean for days to maturity in macrosperma was observed in all the generations under 10kR dose and in M_4 only under 15 and 20kR. Study of shift in mean at individual line mean level revealed that either the shift was unidirectional or neutral for most of the traits. In microsperma, 5 and 10kR doses and in macrosperma, 5kR were more efficient for producing desired shift for seed yield and its components.

Relationship of various doses with various parameters of variability indicated that intermediate doses induced the largest increase of variation and there was a strong decline with highest dose. Heritability estimates obtained by eliminating genotype x micro-environment interaction decreased with increasing dose in microsperma, whereas, in macrosperma, it increased with increasing dose, being highest at 20kR. Macrosperma variety of lentil was more radio-sensitive than microsperma. A larger number of potential mutants with desired traits under 5 and 10kR in microsperma as compared to macrosperma, further confirmed the differential radio-sensitivity.

Scaling test in microsperma variety revealed the presence of non-allelic interaction for seed yield, hundred seed weight and days to maturity under all the radiation doses used, for biological yield under 10 and 20kR, for harvest index and number of primary branches under 5, 10, and 15 kR, for number of pods under 20kR, and for plant height under 10, 15, and 20kR doses

of gamma rays. With respect to macrosperma, detection of non-allelic interaction was noticed under all radiation doses for biological yield and plant height, under 10, 15 and 20kR for harvest index and hundred seed weight, under 15 and 20kR for number of primary branches, and under 10 and 15 kR for days to maturity. The nature of non-allelic interaction was additive x additive for seed yield under 5 and 10kR in both microsperma and macrosperma, for biological yield under 10kR, for hundred seed weight under all doses, for number of primary branches under 5 and 10kR, and for plant height under 10kR in microsperma. In macrosperma, the additive x additive nature of non-allelic interaction was under 10 kR for biological yield, under 15kR for harvest index, under 10 and 20kR for hundred seed weight, under 5 and 10kR for plant height, and under 15kR dose for days to maturity.

Component analysis in microsperma revealed that mutagenically induced additive effects were significantly positive for number of pods, hundred seed weight and days to maturity under 5kR, for seed yield, biological yield and and days to maturity under 10kR, for all traits except harvest index and days to maturity under 15kR, for hundred seed weight, plant height and days to maturity under 20kR. The additive effects induced were significantly negative for hundred seed weight and days to maturity under 5kR, under 10kR for seed yield, biological yield, and days to maturity and under 15 and 20kR for hundred seed weight. Under 15kR dose induction of positive additive effects for all the traits was universal, whereas, at lower or higher doses, it was trait specific . Significant positive dominance effects were reported for all the traits except days to maturity under 5kR, for harvest index, number of pods and plant height under 10kR, for plant height under 15kR, and for number of pods, number of primary branches and plant height under 20kR radiation dose. Significant negati

dominance effects were present for biological yield under 10kR, for seed yield, harvest index, number of pods and hundred seed weight under 15kR, and for biological yield and hundred seed weight under 20kR. Induction of mutation for induced dominance effects was universal for all the traits under 5kR dose. Average degree of dominance exhibited over-dominance for number of pods under 5kR. Complete dominance was exhibited for 100-seed weight under 5kR, biological yield under 10kR, number of pods, hundred seed weight, plant height and seed yield under 15kR, and hundred seed weight and plant height under 20kR. The genetic components estimated on the basis of second degree statistics for microsperma indicated that both additive and dominance variance were significant for number of pods under 5kR and plant height under 20kR, with former showing over-dominance and later one exhibiting complete dominance.

In microsperma significant positive additive effects indicated that the net direction was mutation of decreasing alleles to increasing alleles with respect to seed yield under 5 and 10kR, biological yield under 10 and 15kR, number of pods and 100-seed weight under 5 and 15 kR, number of primary branches under 15kR, plant height under all the doses and days to maturity under 10kR, whereas, net direction was mutation of increasing alleles to decreasing alleles with respect to biological yield under 5kR, harvest index under 10,15, and 20kR, hundred seed weight under 10kR, number of primary branches under 5 kR and days to maturity under 5 and 15 kR doses. Estimates of induced dominance effects indicated that net direction of dominance was that increasing alleles were dominant/to decreasing alleles in case of seed yield, biological yield and days to maturity under 10kR, number of pods under 5kR, hundred seed weight under 15kR and for plant height under all the doses, whereas, in case of seed yield under 5kR, harvest index under 5, 10 and 15kR,

number of pods under 20kR, number of primary branches under 5 and 15kR, and days to maturity under 15kR, more decreasing alleles were dominant than increasing alleles. Out of all the doses, 5 and 10kR doses of radiation appeared to be the most efficient for induction of additive and dominance effects. Complete dominance was found for seed yield under 5 and 10kR, for biological yield under 10kR, for harvest index under 10 and 15kR, for number of pods under 5kR, for hundred seed weight under 15kR, for number of primary branches under 5 and 15kR, for plant height under all the doses, and for days to maturity under 10 and 15kR. Over dominance was exhibited for hundred seed weight under 20kR on the basis of second degree statistics.

Estimates of 'r_2/r_1' and 'r_3' measuring the isodirectionality of dominance and degree of gene association revealed that for number of pods in microsperma under 5kR dose about half of the parental genes have increasing effect as compared to mutant genes, dominance being positively directed for most of the genes concerned with parental alleles being dominant to mutant ones. For plant height under 20kR in microsperma, parental genes lack dominance as compared to mutant ones. Parental genes also lacked dominance as compared to mutant genes for 100-seed weight in macrosperma under 20kR dose of radiation.

Estimates of normal probability integrals for predicting the number of potential mutant lines falling outside the parental range obtained on the basis of both induced additive genetic and environmental components were more as compared to one estimated on the basis of additive genetic component alone. In microsperma variety of lentil, the highest probability for isolating potential mutants would be in M_4 under 10kR for seed yield, biological yield, in M_4 under 5kR for number of pods, in M_4 under 15kR for number of primary branches, and in M_2 under 15kR for plant height. These probability estimates

were found to be maximum in M_4 under 5kR and in M_3 under 20kR for 100-seed weight and in M_3 under 20kR and in M_4 under 5kR for days to maturity, respectively, when the values were obtained on the basis of additive variance alone and additive plus environment variance.

In macrosperma variety, the probability of obtaining highest number of potential mutants would be maximum in M_3 under 10kR for seed yield and harvest index, in M_4 under 10kR for biological yield and 100 seed weight, in M_4 under 5kR for number of pods, in M_3 under 5kR for number of primary branches and in M_2 under 15kR for plant height and early maturity. Comparison of the actual mutant lines excelling their parents with the expected number of lines on the basis of these predictions indicated that the prediction approach based on additive component alone was fitting well for some of the traits under certain doses. For seed yield, the predictions were holding true under 5 and 10kR doses in both the varieties. It was interesting to note that the predictions were holding more true where additive component was predominant and non-allelic interaction was absent.

Line and within lines analysis of variance, estimates of parameters of genetic variability, genetic component analysis and prediction approach further revealed that in lentil mutation breeding programme, M_3 generation would be most appropriate stage to start selection both between and within lines and in M_4 generation the selection could be restricted to between lines.

It was further suggested that stratified single seed descent method or stratified bulk breeding method would be advantageous in handling the irradiated population in early generations, specifically under situations where additive or both additive and dominance variance alongwith complimentary

type of gene action were present. Under the situation where dominance or non-allelic interaction or both were present, it would be advisable to defer the selection at later stage.

In general, it was concluded that sufficient polygenic variation was induced for most of the traits studied over generations and radiation doses. The variation induced was dose-variety-trait specific. Variability induced persisted in later generations and segregation pattern revealed that within lines variance was more in M_3, whereas, between lines variance was more in M_4. Sufficient amount of genotype x micro-environment interaction was found for various traits. Coefficient of variation increased from 5 to 15kR in microsperma, whereas, in macrosperma it was maximum under 5kR. Heritability estimates were high under low doses and were biased upwardly due to the presence of genotype x micro-environment interaction. The shift in mean of irradiated population both at individual and population level was variety-trait-generation-dose specific, with positive or neutral shift under low doses and negative shift under higher doses. Non-allelic type of gene action was found for various polygenic traits which in some cases was of additive x additive nature. Component analysis revealed all type of gene action i.e. additive, dominance and over-dominance for different traits, and was dose and trait specific. Prediction values for obtaining potential mutants were generally satisfactory when obtained on the basis of additive genetic component alone and were holding true in M_4 generation. Selection would be more effective both between and within lines in M_3 and between lines in M_4 generation. Some desirable mutants with respect to seed yield, seed size and maturity were isolated in both the varieties. The results obtained were also discussed for formulating an appropriate breeding methodology for handling the irradiated material for genetic amelioration of lentil crop.

BIBLIOGRAPHY

BIBLIOGRAPHY

Aastveit, K. 1966. Induced mutations in polygenic systems. Hereditas. 56: 20-26.

Aastveit,K. and H. Gaul, 1967. Variation and selection of micromutants. Rad.Bot. 7: 353-361.

Abo-Hegazi,A.M. 1973. Studies on the possibility of enlarging variation in certain characters in M_1 plants in five legume crops grown in Egypt after gamma-ray seed irradiation. Int.Symp. on use of Isotopes in Agriculture and Animal husbandry Research NRL, IARI, New Delhi : 175-183.

Anonymous, 1981. FAO Statistics. LENS, 1981.

Bansal,H.C. 1969. Studies on the induction of mutations with special reference to biochemical traits in Chilli and Polygenic characters in wheat and barley. Ph.D Thesis, Sardar Patel University, Vallabh Vidyanagar.

Bateman, A.J. 1959. Induced polygenic variation in rice. Int. J. Rad. Biol. 1 : 425-427.

Bauman, L.F. 1959. Evidence of nonallelic gene interaction in determining yield, ear height and kernel row number in corn. Agron. J. 51 : 531-534.

Baur, E. 1924. Untersuchugen über das wesen die Entestehung und die vererbung von unterscheidon bei. Antirrhinum majus. Biblio. Genet. 4 : 1-170.

Bhatia, C.R. and M.S.Swaminathan. 1962. Induced polygenic variability in bread wheat and its bearing on selection procedures. Z.Pflanzenzüchtg. 48: 317-328.

Bhatti, I.M., M.A. Rajput, and M.A.Awan. 1970. Variability of quantitative characters in gram as affected by gamma-irradiation. J.Agric. Res.(Punjab). 8: 269-273.

Borojevic, K. 1965. The effect of irradiation and selection after irradiation on the number of kernels per spike in wheat. In 'The use of induced mutations in plant breeding'. Rad. Bot. 5(Suppl.) : 505-513.

Brim, C.A. 1966. A modified pedigree method of selection in soybeans. Crop Sci. 6: 220.

Brim, C.A. and C.C. Cockerham. 1960. Inheritance of quantitative characters in soybeans. Proc. of Annual Meeting of American Society of Agronomy. Ohio : 54.

Brock, R.D. 1965. Induced mutations affecting quantitative characters. In 'The use of induced mutations in plant breeding'. Rad. Bot.(Suppl.) 5: 451-464.

Brock, R.D. and B.D.H.Latter. 1961. Radiation induced quantitative variation in clover. In. Proc.Third Australian Conf. on Radiation Biol.: 205-215.

Burton, G.W. 1968. Epistasis in pearl millet forage yields. Crop Sci. 8: 365-368.

Chambon, P. 1981. Split genes. Scientific American, May : 60-71.

Chowdhry, S.K., P.B.Jha, V.K. Shahi, and V.K.Chaudhry. 1978. Genetic variability for yield components in lentil. Ind. J. Agric. Sci. 48(12): 711-712.

Cockerham, C.C. 1959. Partitions of hereditary variance for various genetic models. Genetics. 44: 1141-1148.

Cockerham, C.C. 1961. Implications of genetic variances in a hybrid breeding programme. Crop Sci. 1 : 47-52.

Conger, B.V., L.W.Skinner, and L.N.Skold. 1976. Variability for components of yield induced in soybeans by seed treatment with gamma radiations, Fission neutrons and EMS. Crop Sci. 16: 233-236.

Coyne, J.A. 1983. Genetic basis of differences in genetical morphology among three sibling species of Drosophila Evolution (in press).

Daly, K. 1960. The induction of quantitative variability by gamma-radiation in Arbidopsis thaliana. Genetics. 45: 983.

Dickinson, A.G. and J.L.Jinks. 1956. A generalised analysis of diallel crosses. Genetics. 41 :65 - 77.

Dumanovic,J., L. Ehrenberg and M.Denic. 1970."Induced variation of protein content and composition in hexaploid wheat" Improving Plant Protein by Nuclear Techniques (Proc.Symp. Vienna 1970), IAEA, VIENNA : 219.

East, E.M. 1935. Genetic reaction in Nicotiana, III. Dominance, Genetics. 20 : 443-451.

Falconer, D.S. 1981. Introduction to Quantitative genetics. 2nd ed. Longman, London and New York.

Fasoulas, A. 1980. "Principles and methods of plant Breeding" Department of Genetics and Plant Breeding. Aristotelian University of Thessaloniki - GREECE.

Fisher, R.A. 1918. The correlation between relatives on the supposition of Mendelian inheritance. Trans. Roy.Soc. Edinburgh. 52: 399-433.

Fisher, R.A. and F. Yates 1938. Statistical Tables for Biological, Agricultural and Medical Research, 5 Auff.Oliver and Boyd. Edinburgh.

Gaul, H. 1961. Use of induced mutation in seed propaged species. Mutation and plant breeding NAS-NRC, 891 : 206-251.

Gaul, H. 1963. Mutationem in der Pflanzenzüchtung. Z. Pflanzenzüchtung. 50: 194-307.

Gaul, H. 1964. Mutations in Plant Breeding. Rad. Bot. 4(3): 155-232.

Gaul, H. 1965. The concept of macro and micromutations and results on induced micromutations in barley. Rad.Bot.(Suppl.) 5: 407-428.

Gaul, H. 1967. " Studies on populations of micro-mutants in barley and wheat without and with selection". Induced Mutations and their utilization. Proc. Symp. Erwin-Bauer-Gedachtnisvorlesungen IV, Gatersleben, Akademie-verlag, Berlin : 269-281.

Gill, K.S., G.S. Nanda, and Karam Chand. 1974. Induced polygenic variation in M_3 and M_4 generations of barley cultivar C 164 for plant height, spike length and number of spikelets per spike. Genet. Agr. 28 : 232 - 241.

Gorsline, G.W. 1961. Phenotypic epistasis for ten quantitative characters in maize. Crop Sci. 1: 55-58.

Goud, J.V. 1967. Induced polygenic mutations in hexaploid wheats. Rad. Bot. 7 : 321-331.

Goulden, C.H. 1939. Problems in Plant Selections. (In) 7th Int. Genetic Cong. Proc. (Edinburgh) (ed. by R.C.Burnett). Cambridge University Press.: 132-133.

Goyal, S.N., S.N. Jaimini, and S.B. Tikka. 1976. Heterosis in lentil. Lens 3: 1-5.

Goyal, S.N., S.N.Jaimini, and S.B. Tikka. 1977. Combining ability analysis for seed yield and some other biometeric characters in lentil. Lens. 4: 10-13.

Grafius, J.E. 1965. A geometry of plant breeding. Res. Bull. Mich. Agric. Exp. Sta. 1965. No. 7: 59.

Gregory, W.C. 1955. X-ray breeding of peanuts (Arachis hypogea L.). Agron.J. 47: 396-399.

Gregory,W.C. 1956. Induction of useful mutations in the peanuts.Brook Haven Symp. Biol., 9 : 177-190.

* Frey K.J. 1965. Mutation Breeding for quantitative attributes. In' The Use of induced mutation in Plant Breeding" Rad. Bot. 5(Suppl.) 465 - 47

Gregory, W.C. 1957. Progress in establishing the effectiveness of radiation in breeding peanuts. Radiation in Plant Breeding. Proc. 9th Oak Ridge Regional Symp. : 36-48.

Gregory, W.C. 1961. The efficiency of mutation breeding. Mutation in plant breeding. NAS-NRC 891: 81-148.

Gregory, W.C. 1968. A radiation breeding experiment with peanuts. Brook Haven Symp. Biol. 9: 177-190.

Gupta, A.K. and M.S. Swaminathan. 1967. Induced variability and selection advance for branching in autotetraploids of Brassica compestris Var. toria. Rad. Bot. 7 : 512-527.

Haddad, N.I. 1980. Breeding methods, breeding behaviour and estimation of genetic parameters in three lentil (Lens culinaris Medik.) hybrids. Ph.D Dissertation. Wash.State University, Pullman, USA.

Haddad, N.I., T.P. Bogyo, and F.J. Muehlbauer. 1982. Genetic variance of six agronomic characters in three lentil (Lens culinaris Medic.) crosses. Euphytica. 31(1): 113-120.

Hanson, W.D. and C.R. Weber. 1961. Resolution of genetic variability in self pollinated species with an application to the soybeans. Genetics. 46: 1425-1434.

Hayman, B.I. 1954. The analysis of variance of diallel tables, Biometrics. 10 : 235-244.

Hayman, B.I. 1958. The theory and analysis of diallel crosses. II. Genetics. 43: 63-85.

Hayman, B.I. 1960. The separation of epistatic from additive and dominance variation in generation means : II, Genetica, 31: 133-146.

Hussain, H.A.S. and M.M.F. Abdalla 1979. Gamma ray and EMS induced mutations in Vicia faba L.(In) Seed Protein improvement in cereals and grain legumes. IAEA, Vienna : 23-31.

Ibrahim, A.F. and A.N.Sharaan. 1974. Studies on certain early barley mutants in M_3 and M_4 generations after seed irradiations with gamma rays. Z. Pflanzenzüchtg. 73: 44-57.

Jana, M.K. and K. Roy. 1973. Induced quantitative mutations in rice. Rad. Bot. 13: 245-247.

Jeswani, L.M. and R.S. Saini. 1981. Pulses : striving for adequacy. Pulse Crops. News Letter. 1(2): 6-8.

Jinks, J.L. 1954. The analysis of continuous variation in a diallel cross of Nicotiana rustica varieties. Genetics. 39: 767-788.

Jinks, J.L. and Pooni, H.S. 1976. Predicting the properties of recombinant inbred lines derived by single seed descent. Heredity. 36 : 253-266.

Jinks, J.L. and Pooni,H.S. 1980. Comparing predictions of mean performance and environmental sensitivity of recombinant inbred lines based upon F_3 and triple test cross families, Heredity. 45 : 305 - 312.

Johannsen, W. 1913. Elements der exakten Erblichkeitslehre, Gustav Fischer Verlag, Jena.

Kalia, N.R. 1982. Studies on induced polygenic variation in microsperma and macrosperma lentils (Lens culinaris Medik.) Ph.D Thesis,HPKVV Palampur.

Kao, K.N.,C.H.Hu, W.T.Chung and H.I.Oka. 1960. A biochemical genetic study of irradiated population in rice - Genetic variance due to different doses of x-rays. Bot.Bull Acad.Sinica, N.S.I.: 101-108.

Kay, D.E. 1979. Food legumes, Crop and Production Digest No.3. London; Tropical Products Institute.

Ketata, H., E.L.Smith, L.H. Edwards, and R.W.McNew. 1976. Detection of epistatic, additive and dominance variation in winter wheat. Crop Sci. 16 : 1-4.

Koo, F.K.S. 1962. Polygenic variability induced by thermal neutron irradiation. Radiation Res. 16 : 591.

Krull, C.F. and K.J.Frey. 1961. Genetic variability in oats following hybridization and irradiation. Crop Sci. I : 141-146.

Ladizinsky, G. 1979. The origin of lentil and its wild gene pool. Euphytica. 28: 179-187.

Lande, R. 1981. The minimum number of genes contributing to quantitative variation between and within populations. Genetics. 99: 541-553.

Lawrence, C.W. 1965. Radiation induced polygenic mutation. 'The Use of Induced Mutations in Plant Breeding'. Pergamon Press, Oxford : 491-496.

Lerner, I.M. 1958. The genetic basis of selection. John Wiley, New York: 298.

Malhotra, R.S., K.B. Singh, and J.S.Sodhi. 1973. Selection criteria in Lens culinaris Medic. Madras Agric. J. 60(9/12) : 1605 -1609.

Malik, I.A., M.T.Nadeem, G. Sarwar, and S. Ali. 1979. Evaluation of radiation induced mutant lines of mungbean (Vigna radiata (L.)Wilczek) for grain yield and protein content. (In) Protein Improvement in cereals and grain legumes. IAEA,Vienna : 445.

Mandal, N. 1974. Induction of variability for nutritional and agronomic characters in Bengal gram (Cicer arietinum L.) Ph.D Thesis IARI,New Delhi.

Mather, K. 1941. Variation and Selection of polygenic characters. J.Genet. 41 : 159-193.

Mather, K. 1943. Polygenic inheritence and natural selection. Biol. Revs. 18: 32-64.

Mather,K. 1949. The genetical theory of continuous variation. Proc. 8th Int. Cong. Genetics. Hereditas.(Suppl) : 376-401.

Mather, K. 1954. The genetical units of continuous variation. Proc. XIth Int. Cong.Genetics, Caryologia (Suppl.) : 106-123.

Mather,K. and J.L. Jinks. 1971. Biometrical Genetics - The study of continuous variation. 2nd Ed. Chapman and Hall, London, New York.

Mather, K. and J.L.Jinks. 1982. Biometrical Genetics - The study of continuous variation. 3rd revised Ed. Chapman and Hall, London,New York.

Micke, 1976. "Introduction" (In) Induced mutations in cross breeding (Proc. Advisory Group, Vienna,) IAEA, Vienna : 1-4.

Moes, A. 1958. Les mutations induites par les rayous x chez lorge distique. Bul. Inst.Agr. Gembloux. XXVI; 335-361.

Moursi, M.A., K.A. Shouny, and H.A. Yada. 1974. Gamma rays induced mutations in lentil. Egyption J.Genetics and Cytology. 3(2): 302-303.

Muehlbauer, F.J., D.G.Burnell, T.P. Bogyo, and M.T. Bogyo. 1981. Simulated comparisons of single seed descent and bulk breeding methods. Crop Sci. 21(4): 572-577.

Muller, H.J. 1927. The production of mutation. Heredity. 38 : 259-270.

Nandan, R. and B.P.Pandya. 1980. Correlation, path coefficient and selection indices in lentil. Ind. J. Genet. 40(2): 399-404.

Oka, H.I., J.Hayashi, and I. Shijoiri. 1958. Induced mutations of polygenes for quantitative characters in rice. Heredity, 49: 11-14.

Palenzona, D.L. 1964. Confronto tra gli effetti delle radiazioni ionizzanti sulla variabilita genetica e ambientale del frumento esaploide e tetraploide.Genet.Agr. 18: 195-202.

Palenzona, D.L. 1965. Stima della varianza dovuta all effetto ambientale nell'anolis di tipo gerarchico.Genet. Agr.19: 338-350.

Palenzona,D.L. 1966. The progress of selection for quantitative traits under different pressures after x-irradiation of seeds in Triticum aestivum SSp vulgare.Proc.5th Yugoslav Symp. on Res. in wheat : 255-261.

Panse,V.G. and P.V.Sukhatme. 1978. Statistical methods for agricultural workers. ICAR Publication.

Papa, K.E., J.H.Williams, and D.G. Hanway.1961. Effectiveness of selection for quantitative characters in the third generation following irradiation of soybean seeds with x-rays and thermal neutrons. Crop Sci. 1: 87-90.

Papp,E. 1980. Drawing of Lens culinaris ssp macrosperma and Lens culinaris ssp microsperma. LENS . 7: 1-3.

Pate, J.B. and E.N.Duncan. 1963. Mutations in cotton induced by gamma-irradiation of pollen. Crop Sci. 3: 136-138.

Rajput, M.A. 1974. Increased variability in the M_2 of gamma - irradiated mungbeans. Radiation Bot. 14: 85-89.

Raja Ram. 1973. Irradiation studies in diploid and tetraploid varieties of Gram (Cicer arietinum L.) Ph.D Thesis. H.A.U.,Hissar.

Rao, C.H. 1974. Studies on induced variability in pigeonpea and chickpea. Ph.D Thesis, IARI,New Delhi.

Rao,V.R. and Joshi,M.G. 1976. Induced quantitative variation in hexaploid triticale. Mutation Res. 36: 85-92.

Ramel,C. 1983. Polygenic effects and genetic changes affecting quantitative traits. Mutation Research. 114 : 107-116.

Ravi, J.L. Minocha, and Avatar Singh. 1979. Induced mutations for quantitative traits in lentil. Proceedings of the symposium on the role of induced mutations in crop improvement. Osmania University, Hyderabad. : 414-419.

Rawlings, J.O., D.G. Hanway, and C.O. Gardner. 1958. Variation in quantitative characters of soybean after seed irradiation. Agron.J. 50: 524.

Saini, G.C. 1983. Studies on gene action and response to different selection methods in early generations of a soybean (Glycine max(L) Merrill) cross. Ph.D.Thesis, H.P.K.V.V. Palampur.

Sarma, V.S. 1975. Studies on induced mutagenesis in cultivated varieties of groundnut (Arachis hypogea L.) with special reference to the improvement of oil content and yield. Ph.D Thesis,IARI,New Delhi.

Sarvella,P., R.A.Nilan, and C.F.Konzak. 1962. Relation of embryo structure node position, tillering and depth of planting to the effects of x-rays in barley. Rad.Bot. 2: 89-108.

Schimke,R.T. 1980. Gene amplification and drug resistance. Scientific American. November : 50-59.

Schuler, J.F. and G.F. Sprague. 1956. Natural mutations in inbred lines of maize and their heterotic effect. II. Comparison of mother line vs mutant when outcrossed to unrelated hybrids. Genetics. 41: 281-291.

Scossiroli, R.E. 1960. Caratteri quantitativic mutabilita proligenica, Atti Ass.Genet. Ital.,Padua, 5: 9-38.

Scossiroli,R.E. 1962. Effects of ionizing radiation on variability in corn. Strahlewwithung und Milliou,Urdan and Schwarzenberg,München und Berlin, 51: 156-159.

Scossiroli,R.E. 1965. Value of induced mutations for quantitative characters in plant breeding. In "The use of induced mutations in plant breeding".Rad. Bot.(Suppl.) : 443-460.

Scossiroli, R.E. 1966. Wheat mutagenesis in quantitative traits (Wheat Genetics Symp.,Lund),Hereditas.(Suppl.) 2: 85-101.

Scossiroli, R.E., D.L. Palenzona and S. Scossiroli-Pellegrini. 1966."Studies on the induction of new genetic variability for quantitative traits by seed irradiation and its use for wheat improvement" Mutations in Plant Breeding. IAEA : 197-229.

Sen, S.N. 1982. New Lentil mutant variety in West Bengal. Mutation Breeding Newsletter 20: 3-4.

Seyffert,W. 1962. Uber Geninteraktionen bei der Ausbildung von Bliitenfarben Rep. XVI. Int.Hort.Congr.Brussels : 1-11.

Seyffert,W. 1963. Die wirkung nichtalleler Interaktionen auf die Acylierung der Glykosi dierung aus Anthocyan molekiiulen,Ber.Dtsch.Bot.Ges. 76 : 414-415.

Shaikh, M.A.Q. 1975. Grain legumes in Bangladesh (In) Induced mutations for the improvement of grain legumes in South East Asia. IAEA,Vienna, Austria : 61-70.

Shaikh,M.A.Q. ,A.K.Kaul, M.M.Mia, M.H.Chaudhry and A.D.Bhuiya.1979. Screening of natural variants and induced mutants of some legumes for protein content and yielding potential. Plant Genet.Div.Inst. Nuclear Agric. MymenSingh Bangladesh.

Sharma, A.K. and A.K.Chatterji. 1962. An investigation of the genomic influence on radio-sensitivity. Proc.Nat. Inst. Sci. India. 28: 478-484.

Sharma, K.D. and J.W.Boyes. 1962. Some effects of radiation on buck wheat. Canad. J. Bot. 40 : 213-237.

Sharma, S.K. 1977. Induction of mutations for qualitative and quantitative characters in lentil. Ph.D Thesis. Division of Genetics, IARI, New Delhi.

Sharma, S.K. and B.Sharma. 1978. Induced variability for pod and seed size in lentil (Lens culinaris Medik.) Curr.Sci. 47 : 806-807.

Sharma, S.K. and B. Sharma. 1979. Pattern of induced mutability in different genotypes of lentil (Lens culinaris Medik.). Z. Pflanzenzücht. 83 : 315-320.

Sharma, S.K. and B.Sharma. 1981. Effect of mutagens on the growth association in lentil. Indian J.Agric.Sci. 51(9): 619-622.

Sharma, S.K. and B.Sharma. 1982. Induced polygenic variability in lentil(Lens culinaris Medik). Genet. Agraria. 36: 9-18.

Singh, K.B. and R.P.Jain. 1971. Heterosis in lentil (Lens culinaris Medic.). Ind.J.Agric.Sci. 41(8): 678-681.

Sinha, S.S.N. and M.B.E.Godward. 1972a. Radiation studies in Lens culinaris. Ind.J.Genet. 32: 331-339.

Sinha, S.S.N. and M.B.E. Godward. 1972b. Radiation induced chromosomal abnormalities and its consequences in lentil. Cytologia. 37: 685.

Sprague, G.F. 1966. Quantitative genetics in plant improvement. Plant Breeding (K.J.Frey ed.) A symposium held at Iowa State University : 315-354.

Sprague, G.F., W.A.Russell, L.H. Penny, T.W.Horner and W.D.Hanson. 1962. Effect of epistasis on grain yield in maize. Crop Sci. 2 : 205-208.

Stadler, J. 1928. Mutation in barley induced by x-ray and radium. Science, 68: 186.

Stubbe, H. 1934. Ennige Kleinmutationen von Anthirrinum majus L., Zuechter 6 : 299-303.

Stuber, C.W. and R.H.Moll. 1969. Epistasis in maize (Zea mays L.).I. F_1 hybrids and their S_1 progeny. Crop Sci. 9: 124-127.

Swaminathan, M.S. 1965. A comparison of mutation induction in diploids and polyploids. Uses of induced mutation in plant breeding(Suppl.) Rad. Bot. 5 : 619-643.

Tirdea, G. 1978. The effect of gamma rays upon some lentil sorts in the M_1 generation. Agronomic, 10 M Lonesev de La.Brad.Agronomy Lasi Romania.: 89-90.

Tomozei, I. and G. Tirdea. 1975. Study of some quantitative characters in some lentil varieties. Romania International Agronomic : 37-38.

Uhlik, J. 1972. The cytogenetic effect of Thermal Neutrons in Lens esculenta (Moench). Biologia Plantarum. 14(2): 97-102.

Uhlik, K. and J. Urban. 1976. Evaluation of the effect of thermal neutrons, fast neutrons and NEU on M_3 and M_4 generations of Lens culinaris (Medicus). Genetika a Slechteni. 12(3): 129-138.

Verma, P.K. 1973. Studies on the improvement of Brassica juncea Coss and Czern. through mutagenesis. Ph.D Thesis. IARI, New Delhi.

Virk, D.S., J.L.Jinks, and H.S. Pooni. 1978. The assessment of induced continuous variation in pure-breeding lines following selfing. 40(2): 255-268.

Virk, D.S. and V.P.Gupta. 1980. Genetical assessment of induced quantitative variation following hierarchical selfing. Env. and Exp. Botany. 20 : 445-454.

Vries, H. de. 1901. Die-Mutations-Theorie. I.Von Veit, Leipzig : 648.

Webb, C. and G. Hawtin (ed.) 1981. Lentils. Commonwealth Agricultural Bureaux ICARDA, ALEPPO, Syria.

Williams,J.H. and D.G.Hanway. 1961. Genetic variation in oil and protein content of soybeans induced by seed irradiation. Crop Sci. 1: 34-36.

Williams, J.T., A.M.C.Sanchez, and M.T. Jackson. 1974. Studies on lentil and their variation. I. The taxonomy of the species. Sabras J., 6 : 133-145.

Wittemer,G. 1960. Influenza di tratmenti con raggi x applicati al semegulla veriabilita di alcuni caratori fiorali in Nicotiana tabacum. Genet. Agraria. 13: 157-169.

Wright,S. 1968. Evolution and genetics of populations. Vol.I. Biometrical foundations. University of Chicago. Press, Chicago.

Yermanos, D.M. and R.W. Allard. 1961. The detection of epistatic gene action in flax. Crop Sci. 1: 307-310.

Yonezawa, K. 1975. Method and efficiency of mutation breeding for quantitative traits. Gamma Field Symposia. 14 : 39 - 58.

Yonezawa, K. 1979. Some additional considerations on the method of genetical analysis for induced continuous variation of self fertilizing plants. Heredity. 43(2) : 191-204.

Yonezawa, K. and H. Yamagata. 1977. Comparison of the scoring methods for mutation frequency in self pollinating disomic plants. Rad.Bot. 15 : 241-256.

Youngman, V.E. 1968. Lentils - a pulse of the Palouse. Econ. Bot. 22: 135-139.

Zohari, D. 1972. The wild progenator and place of origin of cultivated lentil (Lens culinaris medik). Econ.Bot. 26 : 236-332.