



Variability Analysis and Correlation in Mutant Genotypes of Pea (*Pisum sativum* L.)

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Abstract

The experimental material comprised of three pea genotypes viz; Arkel, Kashi Nandini and PSM-3. Mature and well filled seeds of these genotypes were irradiated with 150 and 200 Gy doses of gamma rays, six treatments with three controls were laid into randomized block design at Research Farm, Krishi Vigyan Kendra during Rabi 2018-19. In this investigation, the highest frequency of chlorophyll mutation was recorded in PSM-3 at 150Gy and the lowest in Kashi Nandini at 200Gy. The widest spectrum of chlorophyll mutation with seven different mutants were recorded in PSM-3 variety at 150 Gy dose. With an increase in the dose of gamma rays there was decrease in the mutation frequency in all the varieties. It is concluded that 150 Gy dose of gamma rays was the best for increasing the mutation frequency and it can be used for induction of desirable mutations in pea. The obtained results confirms that the high potency of the selected mutagenic doses induced a high phenotypic diversity in the treated population and the isolated distinct mutants were of great economic as well as academic interest for future breeding on pea. The seeds derived from control and treated population should be advanced to further generations, to release more variability for quantitative traits which will favor better selection.

Key words : Structural mutants, gamma irradiation, mutation spectrum, mutagenic efficiency

Introduction

A large number of legume species possess great potential for contributing to not only protein-rich food for humans but also excellent quality forage for animals. Green pea is an important dietary component because they are fairly low in calories and contain several vitamins, minerals and antioxidants. Among such novel legumes the pea (*Pisum sativum* L.) is quite notable and belongs to family Leguminosae. Mutation breeding is relatively a quicker method improvement the crops. Crop improvement can be easily achieved by irradiating the genotypes with the help of Gamma radiations Mutations are the tools and being used to study the nature and basis of plant growth and development thereby producing raw materials for genetic improvement of crops Adekola *et al.*, (2012).

Due to its heritable nature mutation breeding is widely used in breeding program to develop the new and varieties which are better adaptive to the changing environment and an important source of variation creation in plants. Gamma irradiation has been used extensively as a potent physical mutagenic agent Aguilar-Meléndez *A et al.*, (2009). Physical mutagens provide handy tools to enhance natural mutation rate, thereby enlarging the genetic variability and increasing the scope of obtaining desired mutants. Induced mutations can rapidly create variability in quantitatively and qualitatively inherited traits in crops Ajala *A et al.*, (2019). In plant breeding programs the irradiation of seeds causes genetic variability that may

allow plant breeders to select novel genotypes with improved characteristics such as earliness, salinity tolerance, yield and quality (Ashraf *et al.*, 2003; Dobariya *et al.*, 2022). Improvement in the frequency and spectrum of mutations in a predictable manner and thereby direct or indirect exploitation in the breeding programme is an important goal of mutation research. Morphological mutation affecting plant parts can be utilized practically and can be released directly as crop varieties Aremu *C et al.*, (2018), Aremu *CO et al.*, (2020).

Selection of effective and efficient mutagen is very essential to recover high frequency of the desirable mutations in a mutation breeding studies. Hence previous knowledge of effectiveness and efficiency of used to the gamma radiations in a number of varieties is indispensable to classify the range of doses of useful mutagens in a number of breeding programmes. So, the present investigation was undertaken to study the frequency and spectrum of macro mutations along with the mutagenic effectiveness and efficiency of different doses of gamma rays in M3 generation.

Materials and Methods

The present experiment was conducted to assess the genetic diversity and correlation, investigated at the research farm, College of Agriculture, Gwalior (M.P.). Out of 28 varieties of green pea, 3 improved varieties viz., Arkel, Kashi Nandini and PSM-3 were irradiated with gamma radiation derived from Co⁶⁰ source at 3 doses i.e.,

Table-1 : Analysis of variance for yield and different attributing traits.

Source	DF	Days to first flowering	Days to 50% Flowering	Days to Maturity	Plant Height	Pods per plant	100 Seed Weight	No. of seeds/pod	Primary Branch	Pod Length	Yield per plant
Rep	2	2.31	0.57	18.67**	44.96**	8.00**	0.02	0.07	0.08	0.00	4.90
Varieties	27	339.71**	224.24	375.21**	294.63**	16.54**	13.97**	1.30**	0.24**	1.81**	29.56**
Error	54	1.68	447.83	2.72	3.44	2.44	0.13	0.03	0.04	0.03	2.31

Table-2 : Parameters of genetic variability for yield traits.

Parameters	DTFF	DT50%F	DM	PH	P/P	100SW	NS/P	PB	PL	Y/P
Genotypic variance	23.91	22.38	29.19	13.69	4.82	8.58	1.97	1.15	0.80	7.77
Phenotypic variance	24.01	18.35	11.34	10.92	18.69	17.11	12.32	6.52	17.69	25.05
Environmental variance	2.25	2.05	1.41	3.89	12.05	0.92	2.44	1.80	9.23	11.19
Heritability (%)	99.12	98.75	98.45	87.34	58.44	99.71	96.08	92.38	72.79	80.04
Genetic Advance	21.71	22.24	22.71	19.94	3.63	4.36	1.30	1.55	0.41	5.54
Genetic Advance % Mean	47.65	40.84	20.89	34.26	26.74	22.46	19.57	20.52	21.29	36.92

Days to first flowering (DTFF), days to 50% flowering (DT50%F), days to maturity (DM), plant height (PH), number of branches per plant (NB/P), number of pods per plant (NP/P), pod length (PL), number of seeds per pod (NS/P), hundred seed weight (100SW) and seed yield per plant (Y/P).

0 Gy (Control), 150Gy and 200Gy which were used to create variability for morphological characters in M₂ generation at Bhabha Atomic Research Centre, Mumbai, India. Treated seeds of each dose along with the dry and wet control were sown during *Rabi* (2018-19) for M1 generation and *Rabi* (2019-20) for M2 generation was raised on M1 and M2 plant basis following plant to progeny methods in a Randomized Block Design All the recommended cultural measures namely, irrigation, weeding and plant protection methods were carried out during the growth period of the crop.

The frequency and spectrum of different types of viable mutants were scored at various developmental stages of M2 plants particularly from flowering to maturity period. Sampling of random plants were used to take the data on days to first flowering, days to 50% flowering, days to maturity, plant height, number of branches per plant, number of pods per plant, pod length, number of seeds per pod, seeds per plant, hundred seed weight and seed yield per plant from each plot of each replication. All cultural operations were carried out following standard procedures as described by Mondalet *et al.*, (2019).

Results and Discussion

Analysis of variance : Analysis of variance (ANOVA) in respect of ten characters was carried out and the mean sum of squares for 28 genotypes used is presented in Table-1 Analysis of variance revealed significant differences among the treatments for all the characters.

Analysis of Genetic parameters : The genetic variability is the raw material of plant breeding on which selection acts to evolve superior genotypes. Thus, higher the amount of variation present for a concerned character in the breeding materials, greater is the scope for its

improvement through selection. The phenotypic coefficient of variation was higher in magnitude than that of genotypic coefficient of variation for all the characters under study (Table-2).

Phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were categorized as low (<10%), moderate (10-20%) and high (> 20%) as suggested by Sivasubramanian and Madhavamenon (1973). Days to maturity recorded the highest PCV and GCV content (128.58, 126.59) followed by days to first flowering (85.68, 84.93), days to 50% flowering (75.38, 74.43), plant height (31.87, 27.84) moderate PCV and GCV for 100 seed weight (10.97, 10.94) and grain yield per plant (11.21, 8.98) low PCV and GCV for pods per plant (5.90, 3.45), number of seeds per pod (0.60, 0.58) and number of primary branches per plant (0.21, 0.20) and pod length (0.13, 0.09).

Correlation among the traits : It is evident from Table-3 that the genotypic correlation coefficients were larger in values as compared to their respective phenotypic correlation coefficient. This indicates greater contribution of genetic factor in the development of the association. Significant positive genotypic and phenotypic correlations were found between days to first flowering, days to 50% flowering, days to maturity, plant height, number of branches per plant and pod length. Seed yield per plant showed highest significant positive correlations with number of pods per plant height followed by primary branches per plant, number of seeds per pod and pod length. Similar results were recorded by Ghodrati *et al.*, (2013).

Such results indicated that the increase of one character will increase in the correlated character. For example, plant height was positively and significantly

Table-3 : Pearson Correlation Matrix of 28 genotypes.

	DTFF	DT50%F	DM	PH	P/P	100SW	NS/P	PB	PL	Y/P
DTFF	1	0.996**	0.765**	0.270NS	-0.119NS	0.041NS	0.249NS	-0.320NS	0.595**	0.105NS
DT50%F	0.996**	1	0.765**	0.254NS	-0.106NS	0.034NS	0.232NS	-0.318NS	0.595**	0.118NS
DM	0.765**	0.765**	1	0.473*	0.111NS	0.363NS	0.531**	-0.041NS	0.628**	0.344NS
PH	0.270NS	0.254NS	0.473*	1	0.095NS	0.061NS	0.630**	-0.196NS	0.628**	0.204NS
P/P	-0.119NS	-0.106NS	0.111NS	0.095NS	1	-0.049NS	0.108NS	0.708**	0.065NS	0.917**
100SW	0.041NS	0.034NS	0.363NS	0.061NS	-0.049NS	1	0.549**	0.192NS	0.224NS	0.154NS
NS/P	0.249NS	0.232NS	0.531**	0.630**	0.108NS	0.549**	1	0.048NS	0.663**	0.298NS
PB	-0.320NS	-0.318NS	-0.041NS	-0.196NS	0.708**	0.192NS	0.048NS	1	-0.198NS	0.622**
PL	0.595**	0.595**	0.628**	0.628**	0.065NS	0.224NS	0.663**	-0.198NS	1	0.243NS
Y/P	0.105NS	0.118NS	0.344NS	0.204NS	0.917**	0.154NS	0.298NS	0.622**	0.243NS	1

Days to first flowering (DTFF), days to 50% flowering (DT50%F), days to maturity (DM), plant height (PH), number of branches per plant (NB/P), number of pods per plant (NP/P), pod length (PL), number of seeds per pod (NS/P), hundred seed weight (100SW) and seed yield per plant (Y/P).

correlated with number of pods per plant, hence taller plants are more likely to produce greater number of branches and number of pods per plant. Chand *et al.*, (1999) and Rajanna *et al.*, (2000) reported similar results and showed positive and significant correlations of plant height with number of pods and number of branches. Therefore, to improve yield of soybean, emphasis should be given on the correlated traits (pod length, number of seeds per pod, number of pods per plant, hundred seed weight, branches per plant, plant height and number of seeds per plant) based on the strength of their correlation. On the other side, hundred seed weight showed significant negative genotypic and phenotypic correlation with number of pods per plant, similarly number of primary branches shows negative correlation with plant height. It means that increase of plant height reduces number of primary branches and pods per plant decreased the seed weight. Khanghah and Sohani(1999), Rajanna *et al.*, (2000), Singh and Yadava (2000) and Arshed *et al.*, (2014) also reported similar findings for different parameters in soybean.

Conclusions

The results of present investigation conclude that the morphological characters viz. days to first flowering, days to 50% flowering, days to maturity, plant height, number of branches per plant, number of pods per plant, pod length, number of seeds per pod, seeds per plant, hundred seed weight and seed yield per plant had sufficient amount of variability. High heritability coupled with high genetic advance as percent of mean recorded for Days to maturity, days to first flowering, days to 50% flowering, plant height and 100 seed weight. Seed yield per plant found moderate. These conditions indicate that there is good opportunity to improve these characters using the tested genotypes. Therefore, emphasis should be given on correlated characters with yield contributing characters and inter genotypic distance with these traits

during selection in breeding program in order to increase soybean production.

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