

Variability, heritability and scope of selection for some quantitative traits in induced mutant lines of grass pea (*Lathyrus sativus* L.)

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SUMMARY

Nature and amount of induced genetic variability for 10 quantitative characters were studied in different mutant lines (M_3) of grass pea cv. Bio R-231. Considerable amount of genetic variability was exhibited in plant height, number of primary branches, pods per plant, 100 seed weight, seed yield/plant, biological yield/plant and harvest index (%). Barring days to flower, smaller magnitudinal differences between GCV and PCV in rest of the 9 traits indicated greater influence of genotypes rather than environment. High heritability coupled with high genetic advance (as percentage of means) estimated for important yield components offer scope for selection.

Key words : Induced mutation, Genetic variability, Heritability, Genetic advance, Grass pea.

Breeding strategy of grass pea (*Lathyrus sativus* L.) is mainly based on developing high yielding and low seed neurotoxin ODAP containing lines. Low genetic variability for the major characters becomes a limiting factor for its improvement (Waghmare and Mehra, 2000; Tadesse and Bekele, 2001). In the present years induced mutation has been used as an effective tool to create additional genetic variability for improvement of grass pea as an ideal pulse crop by increasing grain yield and reducing seed ODAP content and hence knowledge of genetic variations of important yield attributes, their heritability, genetic advance and response to selection assumes significance (Kumari *et al.*, 1995; Kumar and Dubey, 2001 and Biswas, 2007). The present authors were able to induce genetic variations in different qualitative as well as quantitative traits in grass pea through gamma ray irradiation and several mutant lines have been recovered (Talukdar *et al.*, 2001a, 2001b; Talukdar and Biswas, 2002, 2005, 2006 and 2007). In the present study attempt has been made to estimate the magnitude of genetic variability, heritability and scope of selection of different yield components in different mutant (M_3) population of grass pea.

MATERIALS AND METHODS

During the ongoing investigations on induced mutagenesis in grass pea cultivar Bio R-231 following treatment with different doses (50, 100, 150, 200, 250, 300, 350 and 400Gy) of gamma ray, a number of macromutants were isolated at M_2 generation. Selfed seeds of individual M_2 viable mutants along with control variety BioR-231 were sown at experimental garden,

university of Kalyani, in R.B.D. with three replications keeping a uniform distance of 20cm. and 30 cm. between plants and rows, respectively to raise M_3 generation. Observations were recorded on 10 characters, namely, plant height, days to flowering, days to maturity, number of primary branches, pods per plant, seeds per pod, 100 seed weight, seed yield/plant and biological yield per plant. Harvest index (HI %) was calculated by using the formula-

$$H.I \% = \frac{\text{Economic yield (seed yield/plant)}}{\text{Biological yield/plant}} \times 100$$

Extent of variations between control plants and mutant lines under uniform environmental conditions were studied by analysis of variance. The coefficients of variation, heritability (%) in broad sense and genetic advance (G.A as percentage of means) for these traits were estimated following standard methods (Burton and Devane, 1953; Lush, 1949).

RESULTS AND DISCUSSION

Analysis of variance revealed significant differences among the mutant lines as well as from control for each of the yield influencing traits (Table1). The estimates of mean, phenotypic and genotypic co-efficient of variability, heritability and genetic advance for all the characters are presented in the Table2. The magnitude of genotypic co-efficient of variability (G.C.V) and phenotypic co-efficient of variability (P.C.V) was highest in case of seed yield/plant and was followed by harvest index, pods/plant indicating presence of high amount of variation in these

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