

RESEARCH ARTICLE

Studies on induced genetic variability in m₁ generation for quantitative traits in chickpea (*Cicer arietinum* L.)

■ Induri Anusha and Gaibriyal Lal

SUMMARY

Mutations were induced in three chickpea genotypes, ICC-15936, BRC-1104-127 and C-108 using sodium azide (SA) as a mutagen. The immediate effects of mutagenic treatments were measured in terms of biological damage caused in M₁ generation. All the mutagenic treatments brought reduction in seed germination, seedling length and plant survival. Such reduction, with an exception of plant survival, were found to be depended upon the dosage of the concentration. High GCV and PCV in chickpea germplasm were observed for number of effective pods per plant, number of secondary branches per plant, number of pods per plant, seed yield per plant, plant height, number of primary branches per plant, seed index, harvest index, biological yield per plant. High estimate of heritability coupled with high genetic advance as per cent of mean was recorded for number of effective pods per plant, number of secondary branches, number of pods per plant and seed yield per plant. High values for heritability indicates that it maybe due to higher contribution of genotypic components. Traits exhibiting high heritability coupled with genetic advance as percent of mean suggest that the traits are governed by additive gene action, equal contribution of additive and non-additive gene action, respectively.

Key Words: Chickpea, Genetic variability, M, generation, Sodium azide

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hickpea (*Cicer arietinum* L.) is highly self pollinated diploid annual leguminous plant. It is the third most important pulse crop in the world,

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Gaibriyal Lal, Department of Genetics and Plant Breeding, Naini Agricultural Institute, Sam Higginbottom University of Agriculture Technology and Sciences, Prayagraj (U.P.) India (Singh *et al.*,2018) being widely grown in many subtropical and warm-temperate regions. Globally chickpea mean annual production is over 11.60 million tones which is cultivated in an area of 13.20 million hectares with an average productivity of 880 kg/ha (FAOSTAT, 2020). In India, chickpea was grown on 9.93 million hectares area and production contributed 9.53 million ones with the productivity of 960 kg/ha in 2020 (Directorate of Economics and Statistics, 2020). In U.P., Chickpea production was 577 thousand tones with yield of 824 kg/ha from an area of 475 thousands ha in year 2020. Major chickpea producing states are Madhya

Pradesh (40%), Uttar Pradesh (16%), Rajasthan (14%), Karnataka (10%) and Andhra Pradesh (10%). Low genetic variability for major characters becomes a limiting factor for its improvement. Induced mutations can provide additional source of variability for quantitative inherited traits in number of crop plants (Brock, 1971). Sodium azide (NaN₃) is well known for its high mutagenic effect in several crops. It is an toxicity to biological materials as compared with alkylating compounds that are usually used for mutation induction in plants (Ando and Neto, 1996). In the present study, attempt has been made to ascertain the magnitude of induced genetic variability following mutagenesis with sodium azide and also magnitude of associations between quantitative characters in M₁ generation.

MATERIAL AND METHODS

The present investigation was carried out at the Field Experimentation Centre of Department of Genetics and Plant Breeding, Naini Agricultural Institute, Sam Higginbottom University of Agriculture, Technology and Sciences, Prayagraj, U.P. during *Rabi* 2020 – 2021. Seeds of three chickpea (*Cicer arietinum* L.) genotypes, *viz.*, ICC-15936, BRC-1104-127 and C-108 were presoaked in distilled water for 8 hours and then treated with 0.01%, 0.02%, 0.04%, 0.06%, 0.08% concentrations

of sodium azide for 8 hours, seeds soaked in distilled water were used as controlfor comparison with mutagen treated population and then washed with running water before sowing to initiate the reaction mutagen and to leach out residual chemical. The experimental material for present investigation comprised of three genotypes with five treatments (0.01%, 0.02%, 0.04%, 0.06%, 0.08% concentrations of sodium azide) and control (parental variety), were grown in Randomized Block Design with three replications with spacing of 30 cm x 30 cm to study in the M_1 generation. The seeds of all plants from each treatment in M_1 generation were harvested separately. The treated as well as control plant populations were screened to study the induced genetic variability for quantitative characters.

RESULTS AND DISCUSSION

The data on seed germination parameters and seedling length in first mutant (M_1) generation for sodium azide (SA) treatments in *Cicer arietinum* L. are given in Table 1. It had shown an evidence that increase in the mutagenic concentration or dose of the sodium azide, the germination percentage had gone down. As compared to the control (100%), the germination percentage was lower in 46.66% in ICC-15936 (0.08% SA), BRC-1104-127 (0.04% SA) and C-108 (0.06% SA),40.00% in BRC-

Table 1: Effect of different c	oncentrations of soc						er arietinum L.
Genotypes	Germination percentage (%)	Root length (cm)	Shoot length (cm)	Seedling length (cm)	Seed dry weight (g)	Seed moisture weight (g)	Seed vigour index
ICC-15936 (Control)	100%	2.4	3.8	6.2	2.145	3.93	620
ICC-15936 (0.01% SA)	86.66%	2.2	3.6	5.8	2.145	3.93	502.62
ICC-15936 (0.02% SA)	80%	2	3.5	5.5	2.145	3.93	440
ICC-15936 (0.04% SA)	66.66%	1.6	3.1	4.7	2.145	3.93	313.3
ICC-15936 (0.06% SA)	53.33%	1.2	2.8	4	2.145	3.93	213.32
ICC-15936 (0.08% SA)	46.66%	0.8	2.1	2.9	2.145	3.93	135.31
BRC-1104-127 (Control)	100%	2.2	3.6	5.8	2.73	4.935	580
BRC-1104-127 (0.01% SA)	80%	2	3.2	5.2	2.73	4.935	416
BRC-1104-127 (0.02% SA)	66.66%	1.9	3	4.9	2.73	4.935	326.63
BRC-1104-127 (0.04% SA)	46.66%	1.6	2.6	4.2	2.73	4.935	195.97
BRC-1104-127 (0.06% SA)	40.00%	0.8	2.2	3	2.73	4.935	120
BRC-1104-127 (0.08% SA)	33.33%	0.6	1.7	2.3	2.73	4.935	76.659
C-108 (Control)	100%	2.6	3.5	6.1	1.62	3.36	610
C-108 (0.01% SA)	80%	2.1	3.1	5.2	1.62	3.36	416
C-108 (0.02% SA)	73.33%	2	2.9	4.9	1.62	3.36	359.31
C-108 (0.04% SA)	60%	1.5	2.4	3.9	1.62	3.36	234
C-108 (0.06% SA)	46.66%	1.1	2.1	3.2	1.62	3.36	149.31
C-108 (0.08% SA)	33.33%	0.5	1.6	2.1	1.62	3.36	69.99

1104-127 (0.06% SA), 33.33% in BRC-1104-127 (0.08% SA) and C-108 (0.08% SA). The lowest laboratory germination of 33% with lowest seedling height 2.1 cm in C-108 (0.08% SA).

The present experiment is on genetic variability studies in mutated population of chickpea genotypes which were treated with chemical mutagen (SA) was conducted mainly to evaluate the extent of genetic variability, which will be useful for further improvement by selection and genetic advancement. The extent of variability as measured by GCV and PCV also gives information regarding the relative amount of variation in different mutated populations. So the present study was conducted to analyze variability parameters (Table 2) (Fig. 1).

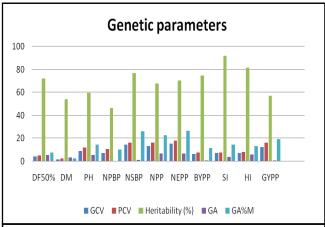


Fig. 1: Bar graph representation to relationship among the GCV, PCV, heritability, genetic advance and genetic advance % mean

In sodium azide (SA) treated population, high values of GCV were observed for no. of effective pods per plant, no. of secondary branches, no. of pods per plant and seed yield per plant. Other trait recorded low estimates of GCV. High values of PCV were observed for no. of effective pods per plant, no. of secondary branches, no. of pods per plant, seed yield per plant, plant height andno. of primary branches.

High estimates of heritability (broad sense) was recorded for characters seed index, harvest index, no. of secondary branches, biological yield, days to 50% flowering, no. of effective pods per plant, no. of pods per plant. Moderate heritability (broad sense) was recorded for plant height, seed yield per plant, days to maturity and no. of primary branches.

High estimates of genetic advance was observed for character no. of effective pods per plant followed by no. of pods per plant, harvest index, days to 50% flowering and plant height. However high genetic advance as per cent of mean was recorded for no. of effective pods per plant, no. of secondary branches, biological yield, no. of pods per plant and seed index.

However, heritability does not alone does not provide any indication of the amount of genetic improvement that would result from the selection of individual genotypes. Thus, to arrive at more reliable conclusion high heritability should be accompanied by high genetic advance (Johnson *et al.*, 1955). Thus, knowledge of heritability and genetic advance of the character indicate the scope for the improvement through selection.

Table 2 : Genetic parameters for 11 characters of 3 chickpea genotypes								
	GCV	PCV	h ² (Board sense)	Genetic advancement 5%	Genetic advancement as % of mean 5%			
DF50%	4.35	5.126	72.033	5.547	7.606			
DM	1.834	2.492	54.154	3.38	2.78			
PH	9.218	11.948	59.521	5.375	14.65			
NPBP	7.381	10.863	46.173	0.254	10.332			
NSBP	14.464	16.48	77.033	1.133	26.152			
NPP	13.44	16.42	67.89	6.623	22.662			
NEPP	15.29	18.203	70.55	6.917	26.456			
BYPP	6.551	7.582	74.635	0.842	11.658			
SI	7.304	7.619	91.889	3.531	14.422			
HI	7.224	8.003	81.473	5.77	13.432			
SYPP	12.32	16.337	56.869	0.606	19.139			

DF50%: Days to 50% flowering, NSB: No. of secondary branches per plant, BYPP: Biological yield per plant, DM: Days to maturity, NPP: No. of pods per plant, SI: Seed index, PH: Plant height, NPB: No. of primary branches per plant, NEPP: No. of effective pods per pod, HI: Harvest index, SYLD: Seed yield per plant

Conclusion:

In this experiment high heritability coupled with high genetic advance as per cent of mean was recorded for the traits *viz.*, number of effective pods per plant, number of secondary branches per plant, number of pods per plant and seed yield per plant by induced mutagenic treatments. Based on high heritability and high genetic advance as per cent mean indicating predominance of additive gene component. Thus, there is further scope for these characters through direct selection in conventional breeding.

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