



REGULAR ARTICLE

GENETIC IMPROVEMENT OF CHICKPEA THROUGH INDUCED MUTATION

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SUMMARY

Following seed treatment by two mutagens (HZ and MMS), four chickpea mutant lines were evaluated to find out selection response in M₃ generation. Estimates of variability for yield and yield components were recorded higher. In comparison with the control plants, nitrate reductase activity (NRA) in leaf tissues of all the mutant lines was increased. The early maturity mutant lines showed the highest seed protein content and NRA.

Keywords: Chickpea mutants, Quantitative traits, Protein content, Nitrate reductase activity (NRA).

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1. Introduction

The application of mutagenesis has given an aided impetus to plant breeding efforts in evolving improved varieties with better agronomic characteristics leading to higher production. It is preferably suited for diploid and amphidiploid self fertilizing species (2). Chickpea (*Cicer arietinum* L.) is an autogamous crop with natural cross pollination ranging between 0–1 % (6). Due to lack of sufficient natural variability, conventional methods of plant breeding had a limited scope in the improvement of chickpea.

The present study deals with mutagenically induced genetic variability in chickpea mutants with regards to quantitative traits, particularly yield and yield contributing traits. Induced mutation in protein contents and nitrate reductase activity (NRA) has also been studied.

2. Materials and methods

A field experiment was conducted during winter (rabi) season of 2005, 2006 and 2007 at the Agricultural Farm, Aligarh Muslim University, Aligarh, India. Uniform and healthy seeds of chickpea variety Pusa-212 (desi), presoaked in distilled water for 9 hours, were treated with chemical mutagens, 0.02% and 0.03% of HZ (hydrazine hydrate) and 0.01 % and 0.02% MMS (methyl methane sulphonate) for 6 hours. For each treatment 300 seeds were used. Treated seeds were sown in the field with three replications in a complete randomized block design (CRBD), with each replication consisting of 100 seeds. The distance between the seeds in a row and between the rows was kept as 30 and 60 cm, respectively. Seeds soaked in distilled water were used as control. Seeds of M₁ plants and control plants were harvested separately and sown in plant progeny rows to raise M₂

generation. Certain mutants such as early maturity, bold seed, dwarf and gigas were isolated in M₂ and grown in progeny rows in M₃ generation and were evaluated not only for the seed yield but also for total seed protein contents and NRA from leaf samples at flowering stage. Phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability in broad sense (h²) and genetic advance (GA) were estimated for yield and yield contributing traits of M₃ mutant lines by the formulae suggested by Singh and Chaudhary (7) and Johnson *et al.* (4). Seed protein content was estimated following the method of Lowry *et al.* (5) and NRA from leaf samples of the mutants was estimated by the method suggested by Jaworski (3).

3. Results and Discussion

Increase in mean values and variability for yield and its component traits of the four M₃ mutant lines of chickpea var. Pusa-212 is an indicative of the wider scope for genetic improvement of this crop in breeding programme (Tables 1 & 3).

Table 1. Mean performance for yield and yield contributing traits among selected M₃ mutant lines of chickpea var. Pusa 212

Control/Mutant	Treatment	No. of pods bearing branches	Pods/plant	100 seed weight(g)	Total plant yield(g)
Control	-	9.54	50.23	22.56	27.17
Early maturity	0.02% HZ	15.16	60.43	23.70	34.33
Bold seed	0.02% MMS	14.15	58.66	24.46	34.36
Dwarf	0.03% HZ	14.26	59.96	24.43	33.43
Gigas	0.01% MMS	13.93	58.66	24.08	32.43
SD		2.47	5.12	2.23	4.07
CV (%)		18.43	8.90	9.37	12.58
SE±		0.64	1.32	0.57	1.05
CD(p=0.01)		1.67	3.43	1.48	2.20

The mean days to maturity reduced significantly by eleven days with the treatment of 0.02% HZ (control mean=116.33, treatment mean=105.40). The estimates of phenotypic variability were higher than the genotypic coefficient of variation (GCV) indicating that

the environmental variation was also significant (Table 3).

Table 2. Mean performance of selected M₃ mutant lines for days to maturity, protein content and nitrate reductase activity (NRA) of chickpea var. Pusa-212

Control/Mutant	Days to maturity	Protein content (%)	NRA (nM/g FW/h)
Control	116.33	221.89	130.20
Early maturity	105.40	22.72	147.10
Bold seed	115.20	22.34	146.00
Dwarf	114.90	22.31	138.00
Gigas	116.10	22.43	134.20
Total mean	113.58	22.33	139.10
SD	6.22	1.43	6.11
CV(%)	5.47	6.40	4.39
SE±	1.6	0.37	1.98
CD (p=0.05)	3.2	0.74	3.96

SD; Standard deviation, SE: Standard error, CV: Co-efficient of variation, CD: Critical difference

Highest estimates of GCV was recorded for days to maturity followed by total yield (g), pods/plant, pods bearing branches and 100 seed weight (g). High heritability (h²) along with high genetic advance (GA) were recorded for all quantitative traits. This indicated that these traits are governed by additive gene action and continued selection in subsequent generations will be highly responsive. The increase in heritability is an indication of effective selection and more useful when coupled with high genetic advance (4).

Table 3. Estimates of variability components for quantitative traits of chickpea mutants in M₃ generation

Trait	PCV (%)	GCV (%)	h ² (%)	GA(% of X)
Days to maturity	16.43	14.29	70.51	33.34
Pods bearing branches	15.95	13.20	68.65	28.35
Pods/plant	15.60	13.30	69.80	30.50
100 seed weight (g)	15.46	12.94	66.31	28.92
Total plant yield (g)	16.80	14.22	67.33	32.09

PCV: Phenotypic coefficient of variation, GCV: Genotypic coefficient of variation, h₂: Heritability, GA: genetic advance.

The studies on protein content and NRA aided more impetus on the selection criteria. Seed protein content was increased over control in all the mutant lines. However, the increase was insignificant except for early

maturity mutants. NRA provides good estimates of the nitrogen status of plants and is correlated with growth and plant yield (8). The highest NRA (147.10 nM/g FW/h) was observed in early mutants followed by bold seeded mutants (146.00 nM/g FW/h). The lowest value was recorded in gigas mutants (134.20 nM/g FW/h) (Table 2). The early maturity mutants showed the highest seed protein content and NRA (Table 3). The NRA could be used as a tool to correlate with seed protein content and overall productivity of mutants in early stage (1).

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