# Biotechnological Study of Comparative Mutagenicity on Morphological and Phenological Traits in Wild Chickpea

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## ABSTRACT-

The chickpea is one of important leguminous cereal crop and India, largest producer of the crop The major concern of breeding is, therefore to increase the genetic potential for yield. The genetic diversity within the genus and characterization of interspecific relationship are crucial for a better exploitation of the genetic resources available for crop improvement. Mutation induction offers the possibility to induce the desired attribute that cannot be found in nature or have been lost during the evolution The crossability barriers might be eliminated from the wild chickpea species through the mutation breeding making it suitable candidates for introgression towards the improvement programme.. The chemical and physical mutagen showed the potential to cause the mutation in the wild chickpea. The variation was observed between control and its induced mutants. The induced mutants with suitable qualitative and quantitative traits which may be utilized in to the improvement breeding programme.

**Key words:-** wild chickpea, Phenology, Physical Mutagen, Chemical Mutagen, ANOVA.

## Introduction

Chickpea is a one of the most important grain legumes of Indian Subcontinent (Wani and Anis, 2008). Chickpea is third most important cool season pulse crop of the world (FAO, 1994; 2004). It is important food legume of dry lands and tropics in the world and production worldwide (Toker and Canci, 2003). Chickpea genotype adapted to these condition by acquiring bushy, spreading and indeterminate growth habit and photo-thermo-sensitivity (Bahl *et al.,* 1979).Asia is most important chickpea producer and India is largest single producer of the crop (Gebisa *et al.,* 2000). Chickpea became principle pulse crop and a dietary mainstay in the Indian subcontinent (Muehlbauer, 1993).

The available genetic variability has been exploited in the breeding programme narrowed the genetic base (Wani and Anis, 2008). A few undesirable characters constraints the use of wild *Cicer* in chickpea breeding programs (Jaiswal *et al.,* 1986). The mutagenesis could create many different mutants alleles with varied and different degree of great modification (Brown, 2003). Mutation

breeding could be used towards the induction and improvement of economically important traits and characters as well as elimination of undesirable gene from the elites lines (Lippart *et al.*, 1964).

## Material and Method

The germplasm of wild chickpea (*Cicer reticulatum* L.) Accession No. ICC 17164 JM 2106 and ICC 17121 JM 2100 was obtained from ICRISAT, Patancheru (AP) India for the present investigation.

**Figure 1:Seeds of *Cicer reticulatum* L.**

The seeds were divided into three sets. The seeds of 1st set treated with three different concentration viz. 0.1%, 0.2%, 0.3%,of Sodium azide (SA) and encoded as $T_2$, $T_3$, $T_4$ respectively. The seeds of 2nd set were treated with combination treatment of SA and X-rays radiation viz. 0.1% SA+5KR, 0.2% SA+10KR, 0.3% and SA +15KR and encoded as $T_5$, $T_6$, $T_7$ respectively. The healthy seeds were first treated with 0.1% to 0.3% SA thereafter washed thoroughly and soaked with blotting paper to remove any residual effect of treating solution then the pre-treated seeds were irradiated with 5KR to 15 KR X rays. The seeds of 3rd set were treated with different doses 5 KR, 10 KR, 15 KR of X-ray radiation and encoded as $T_8$, $T_9$, and $T_{10}$ respectively while $T_1$ as the untreated control. All the treated seeds alongwith the untreated control $T_1$ seeds were sown to raise M1 generation in triplicate. The 10 seeds of each treatments were presoaked in distilled water for overnight placed in Petri plates lined with 2-3 layers of moist filter paper and sterile distilled water was added to keep the moisture level proper. The germination percentage and time required for germination were observed (ISTA, 1993). The phenotypic data such as shoot length height, number of branches, number of flower per plant, pod per plants, pod length, grain per pod were recorded at regular interval and presented in **Table 1**. The data subjected to the statistical analysis and computation of various quantitative and qualitative data was executed as per standard statistical procedure and ANOVA such as standard error (SE), standard deviation (SD) and coefficient of variability (CV) etc. (Sukhatme and Amble, 1995).

## Result and Discussion

The seed germination percentage has been observed decreased at higher doses. The inhibition of seed germination at higher doses of mutagen independently and in combination radiation might have resulted due damage to chromosome (Al- Safadi and Simon, 1996). However, $T_2$, $T_3$ and $T_5$ treatments showed 80% germinability The delayed germination has been observed in all the treatments. Similar observation has been reported with increasing concentration of mutagenic treatment (Alka *et al*., 2007).

The plant height were higher in $T_5$, $T_7$, $T_{10}$ with maximum mean plant height 22.94 cm in $T_{10}$ The maximum height induced in combination mutagenic treatments has been reported in chickpea (Wani and Anis, 2008). The significant higher plant height has been reported in grasspea (Waghmare and Mehra, 2000). No dose dependant relation has been observed.

The number of primary branches was observed higher as compared to control and maximum mean 5.74 in $T_8$ treatment and the number of secondary branches were also recorded as maximum in $T_8$ treatment 5.14. The similar observation has been reported followed by the mutagenic treatment in grasspea (Waghmare and Mehra, 2000) in wild chickpea (Kamble and Petkar, 2015).

The increase in number of flower except $T_7$ and $T_{10}$ has been observed in present study as compared to the control treatments. The number of pods was recorded maximum 8.83 in $T_8$ treatment. Wani and Anis (2008) have reported the significant quantitative increase in pod in chickpea induced by lower dose of mutagen. The higher number of pod per plants has been reported followed by mutagenic treatment as compared to control in grasspea (Waghmare and Mehra, 2000). The increase in variability for number of pods per plants following mutagenic treatment has been reported in khesari (Singh and Chaturvedi, 1990).

The mutation inducing many traits could be attributed to the mutation of pleiotropic gene or mutation of gene cluster or chromosomal arrangement as has been reported in chickpea (Wani and Anis, 2008). The observations in present investigation revealed the conformity as reported in chickpea (Wani and Anis, 2008).

## Conclusion

The overall comparative study with respect to phenological parameter the $T_8$ treatment appeared the fairly good treatment over all other treatments as it shows maximum qualitative traits and characteristics over all other treatments.

ANOVA for all the treatments were observed significant for all phenotypic characters ($p<0.05$). The treatment with desirable character could be used in breeding programme. Similarly, ANOVA for genotypes were significant for all the characters t ($p<0.05$). The genotypes possessed desirable characters that could be directly produced after release and they could used indirectly in breeding programme. The comparative result on overall variability was observed significant except in present investigation.

**Figure 2: $T_1$ Treatment**

**Figure 3:$T_8$Treatment**

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**Table 1: Effect of SA and radiation on Phenotypic characters in $M_1$ Generation**

| Sr. No | Treatment | Days Required to Germinate Mean (Days) | Germination Percentage | Mean Plant Length (in cm) 30 DAS Mean | Number of Primary Branches 60 DAS Mean | Length of Primary Branches Mean (In cm) | Number of Secondary Branches Mean 70 DAS Mean | Length of Secondary Branches Mean (In cm) | Number Of Flowers 100DAS Mean | Number of Pods 110 DAS Mean |
|---|---|---|---|---|---|---|---|---|---|---|
| 1 | $T_{1.}$ | 3.3 | 100% | 21.94 | 3.36 | 29.7 | 4.34 | 11.8 | 5.95 | 8.65 |
| 2 | $T_2$ | 7.5 | 80% | 21.55 | 4.26 | 28.23 | 4.66 | 12.24 | 6.77 | 5.92 |
| 3 | $T_3$ | 7.9 | 80% | 20.95 | 3.50 | 27.95 | 5.42 | 9.76 | 6.45 | 6.74 |
| 4 | $T_4$ | 8.5 | 70% | 21.37 | 4.16 | 29.4 | 4.08 | 10.45 | 7.01 | 6.79 |
| 5 | $T_5$ | 9.3 | 80% | 22.12 | 5.18 | 29.82 | 4.24 | 13.67 | 6.21 | 6.47 |
| 6 | $T_6$ | 7.2 | 70% | 20.14 | 5.11 | 27.34 | 4.21 | 14.1 | 6.34 | 6.95 |
| 7 | $T_7$ | 9.6 | 60% | 22.94 | 4.95 | 26.92 | 4.92 | 12.1 | 5.56 | 7.23 |
| 8 | $T_8$ | 9.4 | 70% | 21.85 | 5.74 | 27.64 | 5.14 | 9.34 | 7.84 | 8.83 |
| 9 | $T_9$ | 9.5 | 70% | 20.85 | 4.96 | 27.84 | 4.12 | 9.20 | 7.62 | 7.21 |
| 10 | $T_{10}$ | 8.7 | 60% | 22.42 | 5.28 | 26.75 | 4.5 | 8.95 | 5.64 | 8.62 |
| F-test | | | | Sig | Sig | Sig | Sig | Sig | Sig | Sig |
| SE(m±) | | | | 0.03 | 0.26 | 0.43 | 0.54 | 0.72 | 0.77 | 0.84 |
| CD at 5% | | | | 0.12 | 0.34 | 0.59 | 0.76 | 1.48 | 1,27 | 2.44 |