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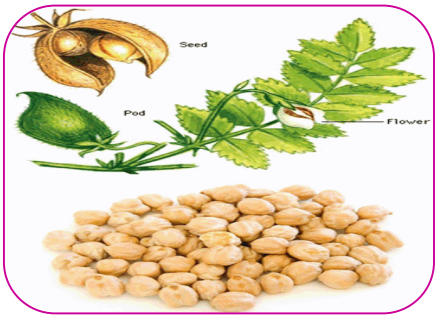
"MORPHOLOGICAL ASSESSMENT STUDY IN WILD CHICKPEA TREATED WITH MUTAGENIC AGENTS"



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ABSTRACT

The chickpea is the third global important legume crop. The wild species of Cicer offer genetic variation for cultigens breeding programme as a natural valuable resource. Some of the undesirable traits and characters the wild species constraint its utilization in improvement breeding programme and the crossability barriers in interspecific crossbreeding as well. One of the techniques, mutation breeding is an important and useful to bring the desirable traits in the genome and elimination of undesirable traits. The suitable and desirable induced mutants could be used in the breeding programme. The numbers of chemical and physical mutagenic agent are used in the mutagenesis.

KEYWORDS: *Wild chickpea, Morphological traits, EMS, Gamma rays, Mutagenic agent.*

INTRODUCTION:

Chickpea (*Cicer arietium*) field pea (*Pisum sativum*) lentil (*Len culineris*) fababean (*Vicia faba*) grasspea (*Lathyrus sativus*) are identified as cool season food legume (Muehlbauer, 1993). Chickpea is the third important pulses crop with worldwide cultivation and India as single largest producer (Gebisa *et al.,* 2000).The rotational cropping pattern with legume crop could not only offer a basis to break disease cycle but improve the soil fertility also (Davies *et al.,*1985). The genetic variation in chickpea has been largely exploited in the conventional plant breeding programme which narrowed the genetic variation base for this crop (Wani and Anis, 2008). Therefore, the breeding programs have limited themselves to a small range of cultivated genotypes with sources of biotic stress resistance and abiotic stress tolerance (Singh *et al.,* 1994). Mutagenesis could be used for induction and improvement of the economically important traits and elimination of the undesirable gene from the elites lines (Lippert *et al.,*1964).It is a useful and significant method to broaden the genetic variation spectrum of a species and the development of many crop varieties in short time-span (Micke,. 1988)Breeding value of mutants can be improved by uniting different mutant genes in the same genome (Gottschalk, 1986). The mutants with desirable characters could be utilized in the hybridization programme to transfer specific gene into the genome of the cultivar variety. Mutation breeding was used to develop cultivars having good stability for exogenous factors with increased productivity (Mlihov and Mehandjiv, 1982). The success rate of crossing between cultivated and wild species of chickpea has been reported as more than 75% when wild chickpea used as female parent (Singh

and Ocampo, 1997).The mutagenesis could create many different mutants alleles with various degree of considerable modification (Brown, 2003). The EMS and gamma radiation have been reported as important mutagenic agents applied to enhance mutation frequency in plants (Borkar and More, 2010). Wild germplasm contains important sources of novel genetic variation for improvement of cultigen traits (Croser *et al.,* 2003). A few undesirable characters constraints the use of wild Cicer in chickpea breeding programs (Jaiswal *et al.,* 1986). *C. echinospermum* and *C. reticulatum* are commonly used in chickpea improvement programs (Berger *et al.,* 2004).

MATERIAL AND METHOD

The germplasm of wild chickpea *Cicer reticulatum* were procured from the ICRISAT, Patancheru, India. The different sets of healthy seeds were treated independently and in combination with chemical and physical mutagenic agents viz. various concentration of EMS 0.1%, 0.2%, 0.3%, 0.4%, combined treatment 0.1% EMS +5KR, 0.2% EMS +10KR, 0.3% EMS +15KR, 0.4% EMS +20KR, various doses of radiation 5KR, 10KR, 15KR, 20KR, 25KR and 30KR and encoded as T_2, T_3, T_4, T_5, T_6, T_7, T_8, T_9, T_{10}, T_{11}, T_{12}, T_{13}, T_{14} and T_{15} respectively while untreated formed T_1.

The pretreated Cicer seeds were sown to raise the M_1 generation and M_1 seed yield was collected and were sown to raise the M_2 generation. The treated seeds alongwith the control were sown in the field following randomized block design (RBD) to raise M_2 generation in 3 replicates (Cochran and Cox, 1992). The seed-to-seed and row-to-row distance was maintained at 15 cm and 50 cm, respectively. Data for various phenological quantitative and qualitative traits were recorded to analyze and deduce mean, standard error (SE), standard deviation (SD) and coefficient of variability (CV) using standard statistical procedure and ANOVA (Sukhatme and Amble, 1995).

RESULT AND DISCUSSION

The effect of mutagenic agents independently in combination on stem length and plant length of M_2 generation are depicted in Table 1.

The stem length and plant length were observed at regular interval of 20 days after sowing (DAS).

The maximum mean plant length 23.06 cm was observed in T_4 treatment and minimum 9.93 cm in T_{15} treatment of M_2 generation at 20 DAS, found to be significant at 0.05%. The mean maximum stem length 3.26 cm was observed in T_{14} and minimum 2.86 cm was observed in T_{15} treatment in M_2 generation at 40 DAS and was observed significant.

The mutagenic effect on the primary and secondary branching pattern was observed and represented in the Table 2 and Table 3 for M_2 generation.

The delayed primary branching was observed in the treatments T_4,T_5,T7,T8,T9,T13,T14,T15 over the control as reported previously in chickpea (Kamble and Petkar,2015) while the primary branches were observed in T_1,T_2,T_3,T_6,T_{10},T_{11},T_{12} treatment at 20 DAS for M_2 generation . The maximum number of primary branches i. e. 4.93 in T_{11} treatment 40 DAS , 6.73 in T_{13} treatment at 40 and 80 DAS , while minimum 2.93 in T_5 treatment at 40 DAS, 3.93 in T_7 at 60 DAS and 4.6 in T_{15} at 80 DAS were observed in the M_2 generation. The variation in length of primary branches were observed in present study at different time interval viz.25.26 cm maximum length in T_8 and 16.03 cm minimum length in T_{15} at 40 DAS; 34.03 cm maximum length in T_{13} and 24.43 cm minimum in T_5 treatment at 60DAS; 34.03 cm maximum length in T_{13} and 26.2 cm minimum length in T_5 treatment at 80 DAS were found to be significant at 0.05 % in present study and represented in the Table 2.

The number and length of secondary branches revealed the variation in M_2 generation. The maximum number of secondary branches 6.13 in T_{13} treatment at 60 and 80 DAS while minimum 2.6 in T_5 treatment at 60 DAS and 4.13 in T_4 and T_8 at 80 DAS were observed in M_2 generation and found to be significant at 0.05%. The maximum length of secondary branches 12.9 cm was observed in T_{11} and minimum 6.03 cm in T_{15} at 40 DAS. The minimum length 6.26 and 6.9 cm in T_7 and maximum length 16.46 cm in T_{13} at 60 and 80 DAS respectively. The data are depicted in the Table 3 for M_2 generation.

The plant heights were significantly higher in T_2 to T_4 and T_8 in M_2 generation and maximum mean plant height 23.06 cm in T_4. The maximum height has been reported in chickpea treated with EMS and gamma rays in combination (Wani and Anis, 2008). The plant height has been reported as significantly higher in M_1 generation of grasspea treated with 10KR, 15KR, 20KR and 0.5 % EMS (Waghmare and Mehra, 2000). The increased plant height has been reported in 10 KR treatment in green gram (Kulshreshtha and Singh, 1984) and increase in branching with increased number of fruits in *Brassica juncea* (Nayar and George, 1969).

The plant height was observed in 25 and 30 KR treatment relative to control treatment in the present assessment. The reduction in internodes length may be due to the reduction of cell length or the reduction of cell number (Weber and Gottschalk,1973) Similar findings has been reported in *Solanum melanogena* (L.) treated with chemical mutagen (Alka *et al.*, 2007; Krishna *et al.,*1984), in mungbean (Ansari *et al.,*1997) in Rhodes grass treated with gamma rays(Khan,1998).

The Number of primary and secondary branches were recorded more in T_{13} treatment as compared to control in M_2 generation and in conformity with previous study in grasspea (Waghmare and Mehra, 2000), chickpea (Wani and Anis, 2008). The mutation in 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) and present study revealed the conformity.

CONCLUSION

The chickpea is important legume crop and improve the soil fertility. The genetic variability in the cultigens narrowed to large extent therefore, and the mutation breeding could offer the basis for variation in the crop. The wild species of the chickpea is important on account of the resistance potential to various biotic and abiotic stresses. The useful traits in wild annual species of chickpea could be tapped for the betterment and improvement of the cultivated chickpea. The interspecific cross between the cultigens and wild could improve the quality of the cultigens. The mutagenesis brings the useful variation in the wild species and mutant may be appeared suitable for interspecific cross. The T_{13} treatment appeared the fairly good treatment among all treatments. ANOVA for the treatments were observed significant ($p<0.05$). The comparative result on overall variability in M_2 generation was observed significant in present study.

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Table 1: Effect of Mutagens on stem length and plant length in M_2 Generation.

Sr. No	Treatment	Mean stem length in cm 40DAS	Mean plant Length in cm 20DAS
1	T_1	3.03	18.63
2	T_2	3.96	21.03
3	T_3	3.06	20.8
4	T_4	3.23	23.06
5	T_5	3.2	19.93
6	T_6	2.96	18.93
7	T_7	2.93	19.2
8	T_8	2.93	20.63
9	T_9	2.96	19.23
10	T_{10}	2.9	14.56
11	T_{11}	2.9	17.2
12	T_{12}	3.03	18.2
13	T_{13}	3.13	16.8
14	T_{14}	3.26	15.43
15	T_{15}	2.86	9.93
	F-test	Significant	Significant
	SE(m±)	0.13	0.26
	CD at 5%	0.37	0.76

Table 2: Effect of Mutagens on number and length of primary branches in M_2 Generation.

Sr No.	Treatment	Number of Primary Branches Mean				Length of PrimaryBranches Mean (In cm)			
		Noof Primary Branches 20DAS	Noof Primary Branches 40DAS	Noof Primary Branches 60DAS	Noof Primary Branches 80DAS	Length of Primary Branches 20DAS	Length of Primary Branches 40DAS	Length of Primary Branches 60DAS	Length of Primary Branches 80DAS
1	T_1	2.86	3.66	4.8	4.93	12.76	18.96	30.2	30.2
2	T_2	1.93	4.46	4.6	4.93	8.4	24.1	27.23	27.86
3	T_3	1.73	4.2	4.06	4.93	8.6	23.4	25.03	26.73
4	T_4	--	3.13	4.26	5.4	--	20.6	25.3	26.43
5	T_5	--	2.93	4.06	5.66	--	24.1	24.43	26.2
6	T_6	1.53	3.13	4.13	5.06	7.2	24.3	25.73	27.06
7	T_7	--	3.2	3.93	4.73	--	24.5	26.43	26.73
8	T_8	--	3.4	4.93	5.46	--	25.26	29.3	29.96
9	T_9	--	3.0	4.06	4.86	--	23.13	26.53	27.53
10	T_{10}	2.2	3.4	4.6	4.73	10.13	22.4	33.9	33.9
11	T_{11}	2.0	4.93	5.2	5.4	9.36	24.6	31.23	31.3
12	T_{12}	2.33	4.2	5.6	5.6	12.2	23.3	32.43	32.46
13	T_{13}	--	3.86	6.73	6.73	--	22.9	34.03	34.03
14	T_{14}	--	4.0	5.4	5.46	--	23.1	32.43	32.43
15	T_{15}	--	3.26	4.26	4.6	--	16.03	28.4	28.93

F-test	Signif.	Signif.	Signif.	Signif.	Signif.	Signif.	Signif.	Signif.
SE(m±)	0.36	0.34	0.24	0.25	0.52	0.67	0.42	0.504
CD at 5%	1.05	0.99	0.69	0.74	1.52	1.95	1.22	1.45

Table 3: Effect of Mutagens on number and length of secondary branches in M_2 Generation.

Sr No.	Treatment	Number of Secondary Branches Mean			Length of Secondary Branches Mean (In cm)		
		No of Secondary Branches 40DAS	No of Secondary Branches 60DAS	No of Secondary Branches 80DAS	Length of Secondary Branches 40DAS	Length of Secondary Branches 60DAS	Length of Secondary Branches 80DAS
1	T_1	4.2	4.73	4.86	7.06	11.73	11.73
2	T_2	--	4.13	5.06	--	10.26	10.6
3	T_3	--	3.53	4.86	--	8.46	8.86
4	T_4	--	2.73	4.13	--	6.5	7.06
5	T_5	--	2.6	4.2	--	6.63	7.16
6	T_6	--	3.13	4.73	--	5.56	7.43
7	T_7	--	3.2	4.6	--	6.26	6.9
8	T_8	--	2.93	4.13	--	9.46	9.46
9	T_9	--	2.73	4.26	--	6.7	7.0
10	T_{10}	3.26	4.86	4.93	9.83	14.9	14.96
11	T_{11}	3.2	4.8	4.8	12.9	15.26	15.4
12	T_{12}	4.4	5.26	5.26	9.2	15.86	15.86
13	T_{13}	4.2	6.13	6.13	10.4	16.46	16.46
14	T_{14}	4.13	5.4	5.46	9.06	16.4	16.4
15	T_{15}	2.33	5.06	5.2	6.03	14.93	14.93
F-test		Significant	Significant	Significant	Significant	Significant	Significant
SE(m±)		0.24	0.26	0.27	0.22	0.59	0.54
CD at 5%		0.702	0.75	0.80	0.64	1.71	1.57

Fig 1.T_1 treatment

Fig 2.T_{13} treatment

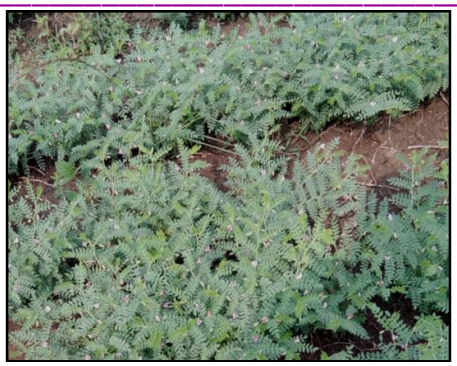

Fig 3. T_{14} treatment