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AN INDUCED FASCIATED MUTANT OF CHICKPEA (*CICER ARIETINUM* L.)

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ABSTRACT

A fasciated mutant characterized by broadened and flattened stem, irregular leaf arrangement and clustering of pods at the stem tip was induced in chickpea (*Cicer arietinum* L.) cv. 'JG-315' through mutagenesis with ethyl methane sulphonate (EMS). It was isolated in the M_2 derived from seeds treated with 0.4% EMS for 6 h. The mutant had delayed maturity, larger seed size and yielded less as compared to its parental cultivar. It was designated as 'Jawahar gram mutant-2' (JGM-2). The fasciation was found to be governed by a single recessive gene which segregated independently of the loci *slv* (simple leaf), *mlv* (multipinnate leaf), *blv* (bronze leaf) and *B* (blue flower). The fasciation has been transferred to different genetic background.

Key Words : Chickpea, *Cicer arietinum*, induced mutation, inheritance, fasciation

Spontaneous fasciated mutants have been identified in several leguminous crops including pea [1], pigeonpea [2], mungbean [3], soybean [4] and chickpea [5]. Induced fasciated mutants have also been reported in pea [6] and lentil [7, 8].

The fasciated mutants are valuable genetic resource and may benefit plant breeding programmes aimed at improving yield and lodging resistance. Fasciated mutants of pea [9] and lentil [8] were found higher yielding than their parental cultivars. Several promising recombinants were obtained in pea [9] and soybean [10, 11] by utilizing fasciated mutants in hybridization.

This article reports an induced fasciated mutant of chickpea (*Cicer arietinum* L.). Genetics of fasciation, its linkage relations with other morphological traits and morphological features of fasciated mutant have been described.

MATERIALS AND METHODS

Seeds of the chickpea (*Cicer arietinum* L. cv. JG-315) were treated with ethyl methane sulphonate (EMS) for induction of new traits. JG-315 (Jawahar gram - 315) is a wilt-resistant, high yielding cultivar of desi chickpea grown widely in Madhya

Pradesh. Seeds, presoaked in distilled-water for 2 hrs, were treated with EMS at 6 different concentrations (0.1, 0.2, 0.3, 0.4, 0.5 and 0.6%) and two different durations (6 and 8 hrs). The M_1 from each treatment was grown in a two-row plot of 3 m length and harvested in bulk. The M_2 from each treatment was grown in 6 to 12 row-plot (depending on availability of seeds) of 6 m length and thoroughly examined to identify mutants. Several mutants for plant growth habit, leaf type, foliage colour, floral morphology and seed attributes were isolated. The fasciated mutant was isolated in the treatment of 0.4% EMS for 6 hrs. This mutant was designated Jawahar gram mutant - 2 (JGM-2).

The fasciated mutant (JGM-2) was crossed with IC 5316 (multipinnate leaf), ICC 10301 (simple leaf), ICC 5783 (bronze leaf), and ICC 12450 (blue flower) to study the inheritance of fasciation and its linkage relationships with other morphological traits. The F_1 and F_2 were grown under normal field conditions and observations were recorded for each segregating qualitative trait on individual F_2 plants. Inheritance and linkage analyses were performed using the computer programme LINKAGE-1 [12]. Chi- square test was done to test the goodness of fit for the assumed segregation ratio.

RESULTS AND DISCUSSION

The fasciated mutant was isolated in the M_2 derived from the treatment of 0.4% EMS for 6 hrs. The mutant was characterized by broad strap-like stems (Figs. 1 and 2). The width of the fasciated stem varied considerably among plants. The broadest fasciated stem had a width of 4 cm. The leaf arrangement was irregular in the fasciated stem and the most common irregularity was the origin of 2 to 4 leaves from the same axis. The leaf rachis was branched in few leaves. The secondary branches generally arose either above or below the fasciated region. A comparison of the fasciated mutant (JGM-2) and the normal plants of the cv. JG 315 is given in Table 1.

The mutant was about one week late in maturity, 8 cm shorter in height and had reduced number of primary as well as secondary branches in comparison to its parental cultivar. The fasciation was found to have an adverse effect on yield. The fasciated mutant had reduced number of pods/plant, poor harvest index and reduced yield/plant. However, the seeds of the mutant were slightly larger.

The spontaneous fasciated mutant of chickpea reported earlier was also found to be inferior to its parental cultivar in yield. Similar to the induced fasciated mutant reported here, it had delayed flowering and larger seed size as compared to its parental cultivar [5]. The spontaneous fasciated mutants of pigeonpea [2, 13] and

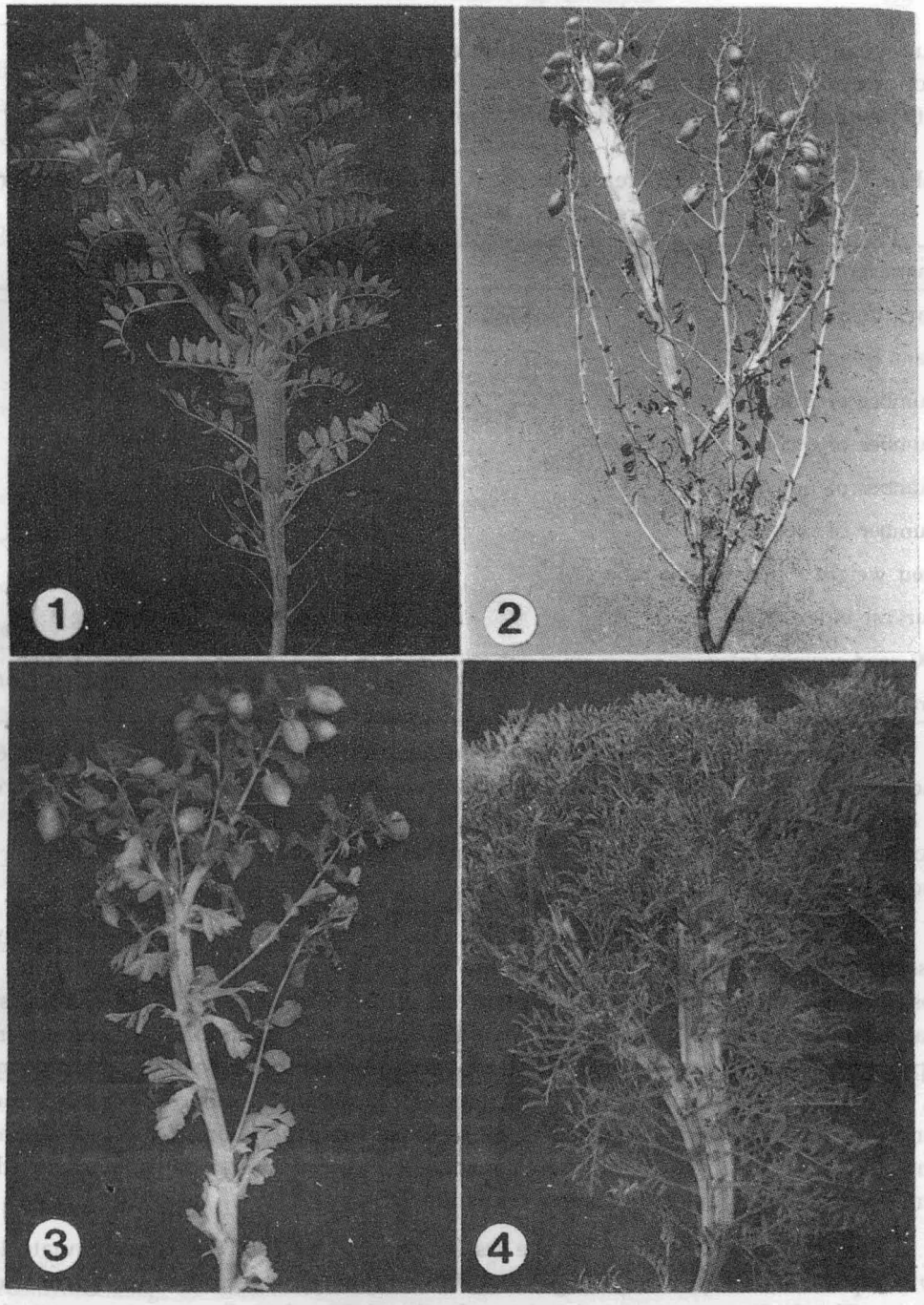

Fig. 1-4. An induced fasciated mutant of Chickpea

mungbean [3] were also agronomically inferior to their parental varieties, but the spontaneous fasciated mutant of soybean, though had delayed flowering, was at par with its parental line with regard to number of seeds per plant and seed size [4].

Table 1. Morphological features of JGM-2 (fasciated mutant) and the normal plants of its parental cv. JG-315

Character	JGM-2	JG-315
Days to maturity	126 ± 2.01	118 ± 1.41
Plant height (cm)	34.2 ± 0.62	42.6 ± 0.51
Number of primary branches	3.6 ± 0.05	4.5 ± 0.05
Number of secondary branches	9.6 ± 0.18	13.1 ± 0.19
Number of pods/plant	31.0 ± 1.70	53.0 ± 2.10
Number of seeds/pod	1.22 ± 0.01	1.20 ± 0.01
Seed weight - pod weight ratio (%)	0.81 ± 0.02	0.85 ± 0.01
Harvest index (%)	36.1 ± 1.06	48.6 ± 1.17
100 seed weight (g)	15.1 ± 0.18	14.3 ± 0.14
Grain yield/plant (g)	5.7 ± 0.34	9.2 ± 0.37

Induced fasciated mutants have been found to be very promising in pea [6, 9] and lentil [8]. The fasciated mutants of pea gave high seed production due to increase in number of flowers and pods per plant [9]. The fasciated mutants of lentil had more number of branches, larger seeds, higher biological yield, higher harvest index and higher seed yield per plant [8].

Inheritance of fasciation was studied in F_2 families of four crosses involving fasciated mutant (JGM-2) as one of the parent. A good fit for the 3:1 ratio was observed for normal and fasciated plant in all the four crosses (Table 2) suggesting that a single recessive gene control the stem fasciation. Fasciation has been generally reported to be of recessive nature and monogenically controlled, e.g. pea [1], pigeonpea [2, 13], soybean [4], lentil [8] and chickpea [5]. However, presence of one additional gene (*fas*) has also been proposed to be essential for expression of the pea fasciation gene (*Fa*) [14]. In another study on genetics of induced fasciated pea mutants, three genes were found to control stem fasciation [15].

The linkage relationship of the *fas* locus with the loci *mlv* (multipinnate leaf), *slv* (simple leaf), *blv* (bronze foliage) and *B* (blue flower) was studied using contigency X^2 test. The *fas* locus segregated independently of these loci. Segregants were isolated

combining fasciation trait with different leaf types, foliage colour and flower colour. Fasciated plants with sample leaf (Fig. 3) and with multipinnate leaf (Fig. 4) looked attractive. These plants, especially the fasciated plants with multipinnate leaf, indicate the possibility of the development of an ornamental chickpea.

Table 2. Goodness-of-fit (X^2) tests for 3:1 single-locus F_2 segregation of fasciation in chickpea

	F_2 phenotype		Goodness-of-fit	
	Normal	Fasciated	X^2	P
JGM-2 × ICC 5316	160	44	1.28	0.26
JGM-2 × ICC 5783	180	53	0.63	0.43
JGM-2 × ICC 10301	266	84	0.19	0.66
JGM-2 × ICC 12450	168	47	1.13	0.29
Pooled data			2.69	0.10
Heterogeneity			0.53	0.91

The fasciated mutants of chickpea are agronomically inferior to their parental cultivars and, thus, do not seem to have a direct use in chickpea improvement. It may be possible to obtain promising recombinants by using these mutants in hybridization. Nevertheless, fasciation is a easily scorable morphological trait and a welcome addition to the genetic markers available for gene mapping. The chickpea linkage map contain mainly isozyme and DNA markers and only a few morphological traits [16-19]. The gene for fasciation has already been mapped in pea [20] and soybean [21]. Work on mapping of chickpea fasciation gene using isozyme markers is presently in progress in our laboratory.

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