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Two unique induced mutants identified in fenugreek for growth habit and leaf characteristics

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ABSTRACT

Fenugreek *(Trigonella foenum-graecum* L.) is an annual crop belonging to the legume family. As such variability is present for many characters in this crop as it is grown from a long time in different agro-eco situations of Indian subcontinent. Two varieties of fenugreek namely RMt-1 and RMt-305 were treated with five different doses of gamma rays viz. 5, 10, 15, 20 and 25 kR during 2007 and one more promising genotype UM-344 was treated with 10, 20, 30, 40 and 50 kR. Two unique mutants namely AFgM-1 and AFgM-2 were isolated. Single stem Mutant (AFgM-1) mutant was identified in the M_2 generation of UM-344 treated with 40 kR gamma rays. The mutant AFgM-1 was different from the parent line with respect to plant height, internode length, branching habit, number of pods per plant and seed yield per plant. Rosette Leaf Mutant (AFgM-2) mutant was identified in the M_3 generation of RMt-305 treated with 25 kR gamma rays. The identified mutant AFgM-2 was different from the parent line with respect to plant height, growth habit, branching habit, number of pods per plant and seed yield per plant. This mutant is unique for its leaf growth habit, the younger leaves of the plant forms a rosette leaf structure i.e. cluster of about 20-24 leaves which can be seen from a distance.

Key words: Fenugreek, Mutation, *Trigonella foenum-graecum*.

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eFkh nyguh leg dh ,d okf"kd Qly gA eFkh dh nks itkfr;ka vkj-,e-Vh-&1 vkj vkj-,e-Vh-&305 dk o"k 2007 e xkek fofdj.kksa dh ikp Lrjksa ij mipkfjr fd;k x;kA lkFk gh itkfr ;-,e-&344 dk Hkh iFkd ikp Lrjksa ij xkek fofdj.kksa }kjk mipkfjr fd;k x;kA itkfr ;-,e-&344 ,oa vkj-,e-Vh-&305 dh 40 ,oa 25 **kR** }kjk mipkfjr chtksa dh ,e-&2 ,oa ,e-&3 lrfr ls nks fo'k"k idkj dk mRifjorh ¼**AFgM-1** ,oa **AFgM-2**½ ikIr fd;s x;sA nksuksa gh mRifjorh viuh tud ls e[; x.kksa ;Fkk ikni mpkbZ] ioa yEckbZ] 'kk[kk 0;ogkj] Qfy;ksa dh l[;k rFkk dy cht ifr ikni ls fofHkUurk fy;s gq, FkA mRifjorh **AFg-M-1** e ioa lf/k yEckbZ vf/kd ik;h x;h tcfd **AFgM-2** e if{k;ksa dk of} 0;ogkj fofHkUurk fy;s gq, FkkA tks fd fljs ij ,d xPNs d :i e n[kk x;kA

Fenugreek *(Trigonella foenum-graecum* L.) is an annual crop belonging to the family leguminaceae. It is regarded as the oldest known medicinal plant in recorded history. Seed and leaves of fenugreek have medicinal value to reduce blood sugar and lower blood cholesterol in humans and animals. Centre of origin of fenugreek is South-Europe, Mediterranean area and Western Asia. As such variability is present for many characters in this crop as it is grown from a long time in different agro-eco situations of Indian subcontinent. Mutation breeding studies is being done in fenugreek for the past three decades in India and many promising mutants have been identified for higher yield and other agro-morphological traits (Raje *et al.* 1, Kaushik & Dashora, 3). In the ongoing study mutation was found to be effective to generate hyper variable lines and it was a chance that some unique mutants were also identified which is new of its type ever reported.

Two varieties of fenugreek namely RMt-1 and RMt-305 were treated with five different doses of gamma rays viz. 5, 10, 15, 20 and 25 kR during 2007 and one more promising genotype UM-344 was treated with 10, 20, 30, 40 and 50 kR during 2008 thereafter individual plants were selected in advanced generations and maintained through pedigree method.

In M_2 generation significant amount of variability was

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found in all the three varieties RMt-1, RMt-305 and UM-344 which were subsequently carried forward to M_4 and M_5 generations (unpublished data). In the subsequent mutant generations few unique mutants were identified & isolated for distinct characteristics than their respective parents. These kinds of mutants are reported for the first time. Two unique mutants namely AFgM-1 (Ajmer Fenugreek Mutant – 1) and AFgM-2 (Ajmer Fenugreek Mutant – 2) were isolated, their detail morphological description with respect to parents are presented and discussed below. These two mutants are very resourceful to strengthen the gene pool of fenugreek. This kind of variability helps to understand the genetics of respective traits.

- **Single Stem Mutant (AFgM-1)** : This mutant was identified in the M_2 generation of UM-344 treated with 40 kR gamma rays. The genotype UM-344 is high yielding branched genotype having indeterminate growth habit, the mutant AFgM-1 was different from the parent line with respect to plant height, internode length, branching habit, number of pods per plant and seed yield per plant. This mutant had single main stem with generally no primary and secondary branches. Only one or two primary branches may occur only when there is topping of the main stem. (Table 1 and Fig.1a). The resulting mutants may be isogenic or variable for only few genes. The mutant AFgM-1 having single stem can help us to understand genetics of branching behavior which is a main component trait for the seed yield.

- **Rosette Leaf Mutant (AFgM-2):** This mutant was identified in the M_3 generation of RMt-305 treated with 25 kR gamma rays. The genotype RMt-305 is high yielding branched genotype having determinate growth habit and is a mutant of RMt-1 which is indeterminate. The identified mutant AFgM-2 was different from the parent line with respect to plant height, growth habit, branching habit, number of pods per plant and yield per plant. This mutant is unique for its leaf growth habit, the younger leaves of the plant forms a rosette leaf structure i.e. cluster of about 20-24 leaves which can be seen from a distance. This mutant flowers 15-20 days late than the parent (Fig.1b). The cluster of leaves at the top of AFgM-2 offers easy clean harvest simply by topping. Normal fenugreek leaves are consumed after removing from stock individually whereas from the rosette leaf structure the cluster of leaves can be removed from stock as a whole or can be directly cooked.

Mutation has offered a good amount of variability in fenugreek. In the recent era of molecular breeding the mutants can be utilized efficiently to understand the nucleotide differences and the genes responsible for the expression of target traits. The recent technique of TILLING (Targeting Induced Local Lesions in Genomes) are based on the same concept of developing hyper variable lines for target traits and simultaneously doing their molecular analysis for identifying the genomic region governing the traits (Colbert *et al.* 2). Molecular analysis of these mutants may lead to identification of markers tightly linked with the mutated region.

Table 1. Details of morphological variation observed in parent UM-344 and single stem mutant AFgM-1 (Mean of two years observation)

Traits	UM-344	Single stem mutant (AFgM-1)
Plant height (cm)	55.1	111.2
Inter-node length (First) cm	2.6	10.0
Inter-node length (Second) cm	5.2	12.0
No. of Primary Branches	4.0	0-2*
No. of Secondary Branches	11.8	0.0
Branch angle from main stem	>45^o	<45^o
No. of pods per plant	75.6	11.8
Pod length (cm)	10.2	10.1
No. of seeds per pod	15.1	11.2
100 seed Weight (g)	1.85	2.23
Yield per plant (g)	19.8	2.1

* Only emerges when there is topping

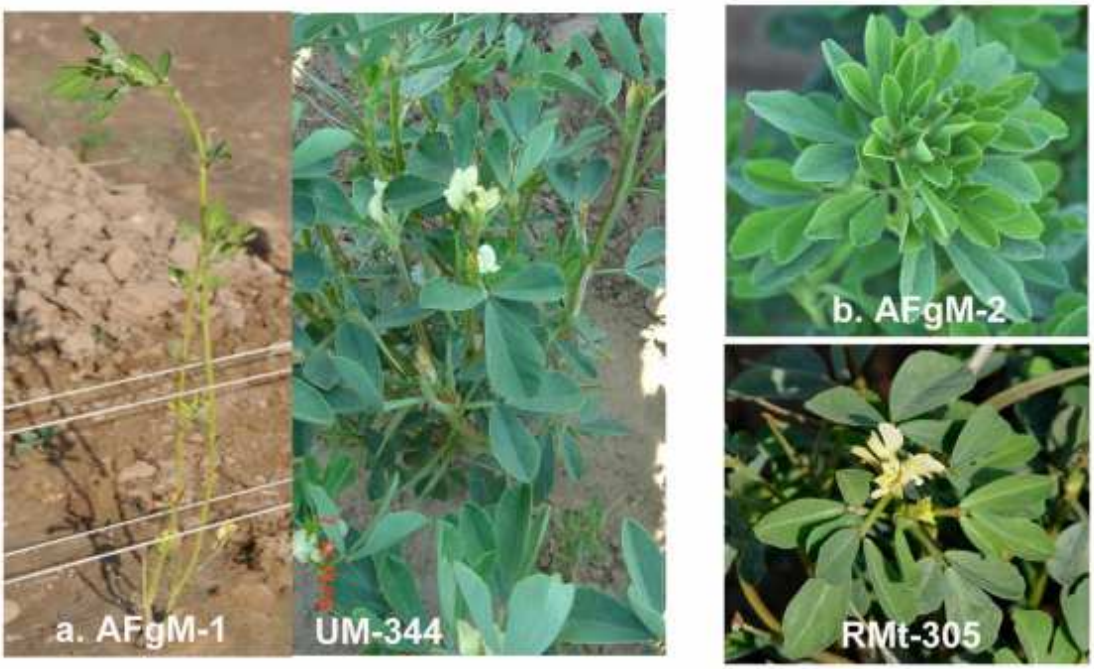

Fig 1. Unique characters of the mutant with respect to the parents.
(a) AFgM-1 vs UM-344 and (b) AFgM-2 vs RMt-305

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