

THE HOMOLOGUE OF THE AGROBACTERIAL GENE OF CUCUMOPINE SYNTHASE IS EXPRESSED IN NATURALLY TRANSGENIC PEANUTS

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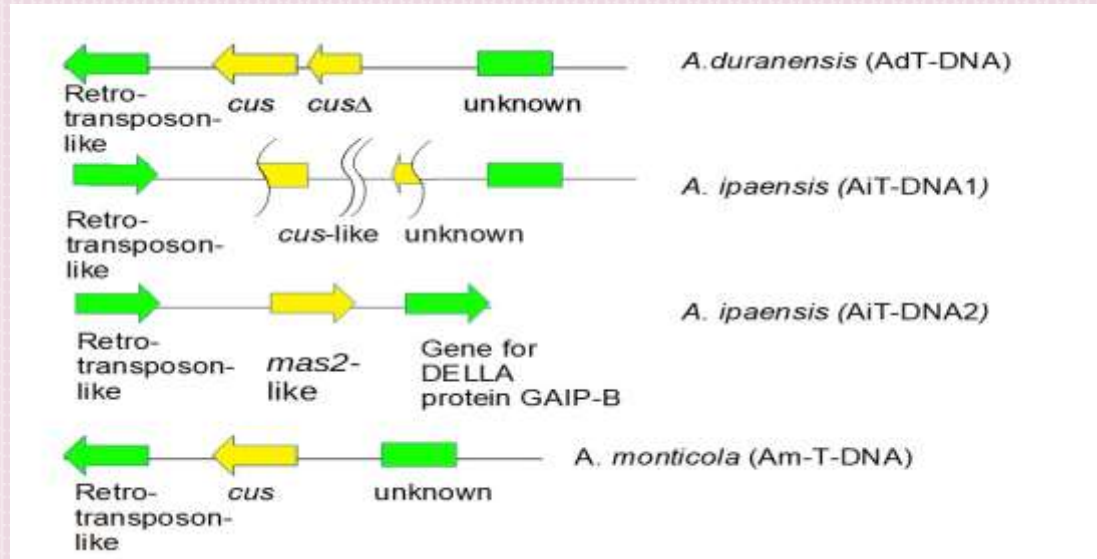
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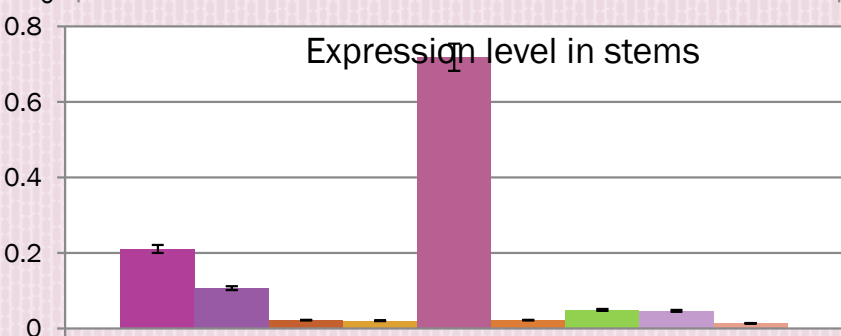
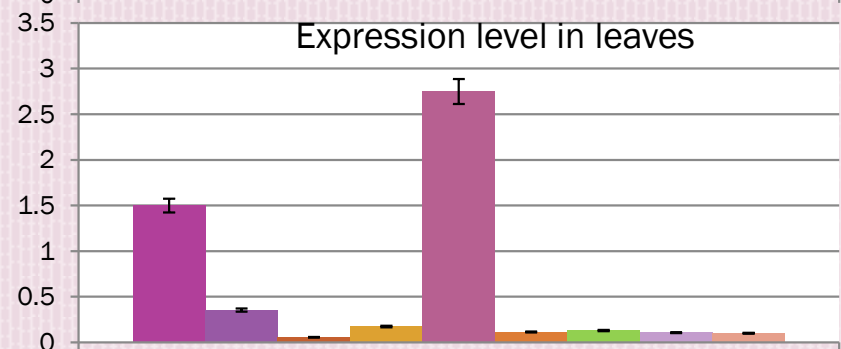
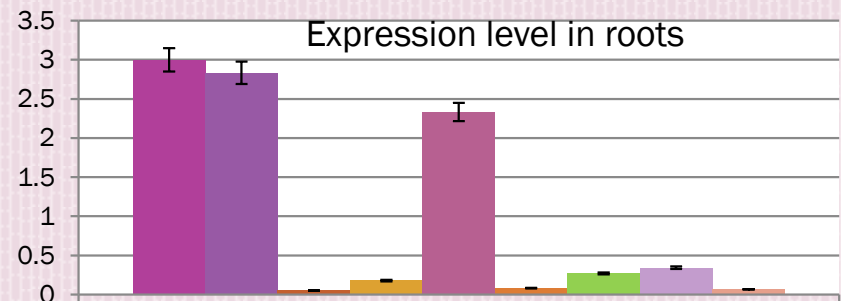
Arachis hypogaea L.

Recent studies show that horizontal gene transfer from agrobacteria to plants occurs in evolution with a fairly high frequency: about 7 percent of dicotyledonous plant species are naturally transgenic. They contain homologues of *Agrobacterium* T-DNA genes in their genomes. The most common of them are opine synthesis genes.

The genomes of several species of the genus *Arachis*, contain homologues of agrobacterial cucumopine synthase (*cus*) and synthase of deoxyfructosylglutamine (*mas2*) genes. There are full-length *cus* genes with intact ORFs in *A. duranensis*, *A. stenosperma*, *A. hypogaea* and *A. monticola*. However, whether the gene is being expressed has remained to be unknown.



Tis-tue-specific expression of the *cus* gene in peanut



- 168
- 416
- 555
- 626
- 751
- 939
- 1157
- 1252
- 1905

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- 416
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No	VIR catalog number	Name	Origin
1	168	-	China
2	416	Deur199	Argentina
3	555	-	India
4	626	Natal Runner T.M.V.3	India
5	751	Spanish Bunch	Portugal
6	939	Tatui	Brazil
7	1157	70-112	Cameroon
8	1252	Local	Africa
9	1905	-	Turkey

Within the framework of this research, the expression of the *cus* gene in various organs of 9 lines of cultivated peanuts from the VIR collection was investigated. Tis-tue-specific expression of the *cus* gene in peanut samples was revealed and lines contrasting in the level of its expression were found. The highest expression was observed in the roots, which suggests that the gene may be related to the interaction of nodule bacteria. A high level is noted in the roots of samples kk-168, 416 and 751. Also, in sample 168, an increased expression is noted in the roots and leaves; in sample 751, the level of expression in the leaves and stem is the highest in comparison with others.

Results of two-way analysis of variance

Factor	df	SS	MS	F	p	The share of the influence of the factor
Genotype	10	3728	373	4,01	0	0,09
Place of reproduction	1	24840	24840	267,33	0	0,64
Genotype*Place	10	1687	169	1,82	0	0,04

SS – sum of squares, df – degrees of freedom, MS – middle square, F – Fisher's empirical test, p – probability H_0

To check the effect of the place of reproduction on maturation, a two-way ANOVA was carried out using data for all 60 peanut samples. According to the results, maturation is more influenced by the place of reproduction and environmental conditions, rather than the genotype of the samples.

A pre-liminary assessment of economically valuable traits of peanuts (maturity, yield) when growing plants on nitrogen-rich soils does not show their relationship with the intensity of expression of the cus gene. It seems promising to assess these traits of peanut lines contrasting in expression of cus when cultivated on nitrogen-poor soils.