

## Prospects for the use of natural transgenic cultivated peanut (*Arachis hypogaea* L.) in breeding

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Common peanut (*Arachis hypogaea* L.), or peanut, is an annual herbaceous plant from the legume family (*Fabaceae*). Russia is one of the largest buyers of peanuts, and at the same time, in the south of the country, a number of zones meet the requirements for the cultivation of this crop. However, at present there are no commercial peanut crops in Russia, and selection work is almost not carried out. It is necessary to identify a new source material for breeding and breeding new high-yielding varieties. In the genomes of species of the genus *Arachis*, homologues of agrobacterial opine synthase genes, cucumopine synthase (*cus*) and deoxyfructosylglutamine synthase (*mas2'*), have been identified. The expression of these genes can affect the economically valuable traits of the plant, since the synthesis of various opines affects the composition of the microbiome in the rhizosphere. We have analyzed the expression of the *cus* gene in various organs of 9 peanut lines from the VIR collection, which have different geographical origin, belong to different cultivar types, and differ in morphological characters. As a result of the analysis, the organ-specific expression was shown; samples were identified that were contrasting in terms of the level of *cus* gene expression, including those with a high level of expression in the roots (kk-168, 416, 751). For the first time, data were obtained on the work of the *cus* gene at different stages of plant development on accessions k-168 and k-1157. An increase in the level of expression in the roots during flowering was revealed; during seed germination, the expression is lower. Further analysis and search for a correlation between the expression level of the *cus* gene and the manifestation of economically valuable traits in peanuts can provide new material for creating promising varieties.

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