https://doi.org/10.17816/ecogen567891

The transformation and genome editing of *Pisum sativum*: protocols and their modifications

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Pea (*Pisum sativum*) is an important agricultural crop and a model object in various fields of plant research. At the same time, the genetic modification of pea is still a difficult task, which, apparently, is associated with its low ability to regenerate. There are a lot of different pea transformation protocols, however, for most of them, the transformation efficiency, i.e. the number of transgenic plants per explant, is extremely low. In addition, none of the protocols known to us has demonstrated itself to be universal, i.e. suitable for all varieties and lines of peas. We searched for studies on the transformation and regeneration of peas and systematized the data obtained. The resulting database made it possible to identify the most effective protocols for the transformation and regeneration of *P. sativum*, as well as to analyze statistically the general features of the methods used, such as the source of the explant, the composition of the culture media, the duration of cultivation, and so on. We assume that our system for the analysis of publications devoted to *in vitro* cell cultures can also be used for similar data on other plant species.

This research was supported by the Sirius University of Science and Technology project: PBB-RND-2243.

Keywords: somatic embryogenesis; legumes; reporter genes.

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