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Development of a testing system for regeneration regulators in *Pisum sativum* L.

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Pisum sativum L. (pea) is one of the most important agricultural crops, because its seeds have high protein content, and, due to its ability have symbiotic relationships with nitrogen-fixing bacteria, these plants need less fertilizers. Nevertheless, we are faced with the need to improve old and create new methods for obtaining novel varieties of peas and other agricultural plants. The formation of regenerated pea plants is difficult to achieve in the *in vitro* culture. Accordingly, transformation of this species is a laborious process. In this regard, the search for morphogenic regulators of somatic embryogenesis (SE) in pea is an urgent problem. A number of publications reported on the genes regulating the SE process in a model plant from the legume family, *Medicago truncatula* [1]. In our study, we search for the *in vitro* cultivation system in peas, suitable to test the effect of putative SE regulators in this species. We tested several pea transformation techniques using different explant variants: embryonic axes from mature and immature seeds, as well as shoot apexes. Out of the tested options, the transformation of mature seeds turned out to be optimal. We also designed a set of DNA constructs *in silico*, which are suitable for the search of morphogenic regulators in peas.

REFERENCE

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