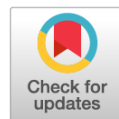


Genetically modified legume plants as a basis for studying the signal regulation of symbiosis with nodule bacteria



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The development of legume-rhizobium symbiosis is based on signal exchange between partners, which leads to the formation of nitrogen-fixing root nodules. Under the influence of rhizobial signal molecules, the Nod factors, the signal transduction cascade is activated, where the LysM-type receptor kinases and a complex of intracellular regulators, a significant part of which are still unknown, can play an important role.

Using transcriptomic and proteomic analysis, we searched for new regulators of the signal pathway in pea *Pisum sativum* L., which are activated under the influence of Nod factors. Phospholipases C and D, GTPases, calcium-dependent protein kinases, and mitogen-activated protein kinases (MAPKs) have been identified among such novel regulators. The influence of one of such regulators, the MAPK6, on the development of symbiosis was studied in more detail. Using genetic engineering approaches, we increased the transcriptional activity of *MAPK6* in transgenic roots, which led to an increase in the number of nodules and the biomass of pea plants. A similar effect was also found for the homologous *MAPK6* gene in another legume *Medicago truncatula*, which has a type of nodulation similar to that one in pea. New approaches have been developed to obtain stable pea transformants with enhanced level of *MAPK6* transcription using the constitutive p35S promoter. A comprehensive study of such plants inoculated with rhizobia was carried out. In addition, the approaches for genome editing of pea plants have been designed using the CRISPR/Cas system, when the *MAPK6* gene was used as a target. Thus, the possibility of using genetic engineering methods to obtain plants with increased symbiosis efficiency was investigated.

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Keywords: legume plants; symbiosis; nodule bacteria.

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