

Homologues of octopine/vitopine synthase genes in natural GMOs

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The process of horizontal gene transfer causes the appearance of natural genetically modified organisms. At the moment, it is known that over 7% of dicotyledonous plant species are naturally transgenic, i.e. nGMO [1]. These plants contain the genes of agrobacteria, which are integrated in the nuclear genome during infection. In some species of naturally transgenic plants, agrobacterial genes have been preserved for millions of years of evolution. Among these genes, genes encoding octopine/vitopine synthase (*ocs/vis*) can be distinguished [2].

The study of homologues of octopine/vitopine synthase genes in naturally transgenic plants: their structures and diversity, products of encoded enzymes will allow us to establish the functions and evolutionary role of homologues in nGMO. Currently, bioinformatic and genetic engineering methods are used to solve these problems.

ocs/vis-like were found in 7 species: *Albizia julibrissin* Durazz., *Cenostigma pyramidale* (Tul.) Gagnon & G.P.Lewis, *Paulownia fortunei* (Seem.) Hemsl., *Pterocarya stenoptera* C.DC., *Rehmannia glutinosa* Steud., *Santalum album* L., *Viscum album* L. In total twenty one *ocs/vis* sequences are known in 17 nGMO species. Twenty sequences are intact. This may indicate the functional significance of these genes for nGMO.

Phylogenetic analysis of currently known *ocs/vis*-like genes of *Agrobacterium*, *Rhizobium* and natural GMOs suggests that diversity of studied genes is wider, than it was estimated based on agrobacterial sequences. On the phylogenetic tree constructed by the neighbor-joining method, 6 clusters for *ocs/vis* can be distinguished. Three clusters contain nGMOs and "agrobacteria", showing the relationship of the T-DNA sequences of nGMO with those of currently known strains of *Agrobacterium/Rhizobium*. Three clusters contain only nGMOs. One of them consists of species that belong to the Cannabaceae family. Other clusters are heterogeneous. No significant ecological similarities were found among the studied species.

The obtained results can be used to study the diversity of ancient and modern strains of agrobacteria, their host specificity and the possible role of their genes in plant evolution.

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Keywords: octopine/vitopine synthase; nGMO; horizontal gene transfer.

REFERENCES

1. Matveeva TV. Why do plants need agrobacterial genes? *Ecological genetics*. 2021;19(4):365–375. (In Russ.) DOI: 10.17816/ecogen89905
2. Matveeva TV, Otten L. Widespread occurrence of natural genetic transformation of plants by *Agrobacterium*. *Plant Mol Biol*. 2019;101(4–5):415–437. DOI: 10.1007/s11103-019-00913-y

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