

New cellular T-DNAs in naturally transgenic plants

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Naturally transgenic plants represent the result of *Agrobacterium*-mediated gene transfer. T-DNA of soil bacteria *Agrobacterium* integrated into plant's genome is called cellular T-DNA (cT-DNA) [1]. Today, more than 50 species of naturally transgenic plants, or natural GMO (nGMO) are known [2, 3]. The function of cT-DNA in plants remains unknown. It is assumed that the fixation of transgenes could give plants different selective advantages depending on which genes had been integrated into the plant [4]. In order to clarify this issue, it is necessary to study more naturally transgenic plants. Until recently, the list of nGM plants contained less than 2 dozen species, but a search through genomic and transcriptomic sequencing data made it possible to more than double this list [2]. In this work, we used the same approach, looking for cT-DNA genes in whole genome sequencing data that have appeared in the NCBI WGS since 2021. We found 14 new species of naturally transgenic plants, among which the most extended cT-DNAs were found in *Triadica sebifera*, *Lonicera japonica*, and *Lonicera maackii*. The cT-DNAs in these species are organized as imperfect inverted repeats. In the genomes of the species *Paulownia fortunei*, *Apocynum venetum*, *Elaeagnus angustifolia*, *Erythroxylum havanense*, *E. densum*, *E. daphnites*, *E. cataractarum*, *Ceriops decandra*, *Camellia oleifera*, *Silene uniflora*, short cT-DNAs containing only opine synthesis genes were found. We also estimated the approximate age of the cT-DNAs. The first described examples date back to the Late Paleogene, and the process continues to the present. Thus, we can conclude that natural GMOs are a widespread phenomenon, many aspects of which remain unclear, requiring additional research on the topic.

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