

PLANTGEN'23

10-15 July

Kazan, Tatarstan, Russia



Abstracts

VII International
scientific conference

PLANT GENETICS,
GENOMICS,
BIOINFORMATICS &
BIOTECHNOLOGY



<https://plantgen2023.ofr.su>



Natural GMOs as models for studying the role of *Agrobacterium* genes in plant evolution

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Plants containing homologs of “*Agrobacterium*” T-DNA in their genomes are called natural GMOs (nGMOs). Such T-DNA was named cellular (cT-DNA). NGS data shows, that about 6% of dicots are nGMOs. The extended cT-DNAs in their genomes are usually organized as imperfect inverted repeats. Based on the analysis of the divergence of these repeats, it was proposed that nGMOs began to appear about 15 mya and have been appearing till present time. They have been used by humans throughout their history as food, drinks and drugs. Natural GMOs differ in the composition of intact and expressed genes within cT-DNAs. Accordingly, these genes perform different functions. T-DNA in toadflax enhances their regenerative capacity and activates secondary metabolism, the *rolB/C*-like gene of sweet potato leads to the early flowering in transgenic *Arabidopsis*, and the genes of tobacco, dodder, peanut, and hop opine synthase lead to the synthesis of opiines, which can be used for microbes feed, changing the biological environment of plants. These plant species are used to study different functions of cT-DNA and their evolutionary role.

Supported by RSF 21-14-00050

The main publications of authors on the subject of the abstract:

*Matveeva, T. V., Otten, L. Widespread occurrence of natural genetic transformation of plants by *Agrobacterium*// Plant molecular biology, 2019. 101(4-5): 415–437.*

Matveeva T, Otten L. Opine biosynthesis in naturally transgenic plants: Genes and products// Phytochemistry. 2021 Sep;189:112813.

Matveeva, T. New naturally transgenic plants: 2020 update. Biological Communications, 2021. 66(1), 36–46.

Take-home message:

Natural GMOs appeared without human intervention millions of years ago and continue to appear till nowadays. Different species maintain intact and expressed different sets of “*Agrobacterium*” genes, which play different evolutionary roles

