

## Natural GMOs in the genus *Nicotiana* L.

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Soil bacteria "*Agrobacterium*" are able to transfer fragments of their plasmids, so-called T-DNA, into plants. T-DNA integrated into plant's genome is called cellular T-DNA (cT-DNA) [1]. Plants transformed in nature are considered natural genetically modified organisms (nGMOs). For the first time, nGMOs were described within the genus *Nicotiana*. To date, more than 50 nGM species are known [2, 3], among which nGMO in the genus *Nicotiana* are the most well studied. Within this genus 3 subgenera are distinguished, those are *Tabacum*, *Petunioides*, and *Rustica*. CT-DNAs in natural genetically modified representatives of the subgenus *Tabacum* are studied in detail [4, 5]. We know how many cT-DNA those species carry as well as the composition of the cT-DNA, which allows us to propose scenarios for the acquisition of cT-DNA by these species during their evolution. Species *N. noctiflora* and *N. glauca* belong to the subgenus *Petunioides* and they are not so well studied. We sequenced and assembled the genomes of *N. noctiflora* and *N. glauca*, to analyze their cT-DNAs. In the *N. glauca* genome we confirmed the presence of one cT-DNA, gT, discovered in 1983, and showed no other inserts. In the genome of *N. noctiflora* 2 cT-DNAs of different composition were found, NnT-DNA1 and NnT-DNA2. The data suggest a single agrotransformation act in the evolution of the species *N. glauca*, while the species *N. noctiflora* was transformed several times. Further study of cT-DNA in *Nicotiana* representatives belonging to different evolutionary branches of the genus will help to clarify the evolutionary history of the genus *Nicotiana*. In addition, the identification of changes that have occurred in the cT-DNA since its entry into the plant genome will help to elucidate the processes that occur with transgenes in plant genomes over long time intervals.

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