

## Structure and functional analysis of cT-DNAs in the genus *Nicotiana*

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The genus *Nicotiana* contains at least six different species (*Nicotiana tabacum*, *tomentosiformis*, *tomentosa*, *otophora*, *kawakamii* and *glauca*) with cellular T-DNAs. These DNAs are believed to derive from natural infection of *Nicotiana* ancestors by *Agrobacterium rhizogenes* strains, followed by spontaneous regeneration of hairy roots. The paternal tobacco ancestor *Nicotiana tomentosiformis* contains 4 different cT-DNAs (TA to TD), apparently acquired by four successive transformations (1). An important question is whether these cT-DNAs are expressed and could modify plant growth in some way. The TB region contains a *mas2'* gene which encodes the synthesis of the Amadori-type opine desoxyfructosyl-glutamine (DFG) in hairy roots. We have shown that the TB-*mas2'* gene is highly expressed in root tips of some tobacco cultivars and leads to detectable amounts of DFG (2). A unique cT-DNA was found in *Nicotiana otophora*, and called TE. I will report on the mapping of the TE region and the study of one of its potential ORFs, coding for a *6b*-like gene. *6b* genes have so far only been found in *A. tumefaciens* and *A. vitis* and belong to the *plast* gene family. The T-*6b* and AB-*6b* genes from *A. vitis* cause large changes in tobacco development probably due to uptake and retention of sucrose (3). We have expressed the TE-*6b* gene from *N. otophora* in tobacco under 35S promoter control and obtained an unusual phenotype that is not typical for *6b* genes. I will describe this phenotype in more detail and discuss how it might be related to the classical *6b* phenotype and to what extent it may play a role in the growth and development of *N. otophora*.

(1) Chen K, Dorlhac de Borne F, Szegedi E, Otten L (2014) Deep sequencing of the ancestral tobacco species *Nicotiana tomentosiformis* reveals multiple T-DNA inserts and a complex evolutionary history of natural transformation in the genus *Nicotiana*. *Plant J.* 80:669-682.

(2) Chen K, Dorlhac de Borne F, Julio E, Obszynski J, Pale P, Otten L (2016) Root-specific expression of opine genes and opine accumulation in some cultivars of the naturally occurring GMO *Nicotiana tabacum*. *Plant J.* doi: 10.1111/tpj.13196. [Epub ahead of print].

(3) Chen K, Otten L (2016) Morphological analysis of the *6b* oncogene-induced enation syndrome. *Planta* 243:131-148.