

Natural DNA transfer by *Agrobacterium* and plant evolution

Léon Otten, Emeritus Professor at the University of Strasbourg

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I. wing lecture hall (Kriilo Ivana Supeka), IRB

Starting from 1985, plant genetic engineering has become established as an essential technique, both in basic science and for the development of new agricultural varieties. Plant genetic engineers often use the soil bacterium *Agrobacterium tumefaciens* as a convenient tool for gene transfer. Indeed, *Agrobacterium* has a unique and efficient capacity to transfer a precise DNA fragment (T-DNA) into the nuclei of plant cells. This is based on a complex molecular mechanism, originally used in bacterial conjugation. As a result of a long evolutionary selection process, the T-DNA genes are expressed in plant cells, and lead to the synthesis of new compounds, called “opines”, used by the bacterium for its growth. Additional T-DNA genes amplify the opine-producing cells by inducing ectopic growth, visible as galls or fast-growing “hairy roots”. Plant cells with stably integrated T-DNAs are “genetically transformed”. *Agrobacteria* and their T-DNAs are highly diverse and have been around for hundreds of millions of years. In 2019, we showed that up to 10% of flowering plant species carry T-DNAs in their genomes, they are called natural genetically modified organisms, or nGMOs. They probably result from spontaneous regeneration of “hairy roots” into fertile plants in the course of evolution. Surprisingly, several nGMOs carry multiple T-DNAs, showing they were re-transformed several times. Some of the T-DNA genes in nGMOs have been shown to be active and produce opines. In my talk, I will present the latest data from this emerging field, and discuss the possible role of *Agrobacterium*-induced transformation in plant evolution.



Professor Emeritus Léon Otten from the University of Strasbourg (born 1950) studied biology and obtained his Ph.D. (1979) from the University of Leiden in the Netherlands. He did his PhD in the group of Prof. Schilperoort on Lysopine dehydrogenase and nopaline dehydrogenase from Crown Gall tumour tissues. In 1975-1976 he was Euratom fellow at the University of Orsay, France. Between 1979-1985 he was a Post-doc and Max-Planck fellow at the Max-Planck Institute for Plant Breeding in Cologne in the group Prof. Jeff Schell and then became a

professor of Molecular Plant Pathology at the University of Strasbourg, and member of the “Institut de Biologie Moléculaire des Plantes du CNRS” in Strasbourg in 1985. During his prolific career, he published over 100 papers and is a recognized expert in the field of *Agrobacterium* biology, analysis of T-DNA genes and studies of naturally transgenic plants. Recently, he and his collaborators discovered the unexpectedly widespread presence of *agrobacterium* T-DNA in flowering plants, which attracted worldwide attention (Altmetric score 549 – in the top 5% of all research outputs scored by Altmetric). He is Emeritus Professor at the University of Strasbourg since 2018.

Recent publications:

Chen, K., Liu, H., Blevins, T., Hao, J., Otten, L. (2023) Extensive natural *Agrobacterium*-induced transformation in the genus *Camellia*. *Planta* 258:81.

Chen K, Zhurbenko P, Danilov L, Matveeva T, Otten L (2022) Conservation of an *Agrobacterium* cT-DNA insert in *Camellia* section *Thea* reveals the ancient origin of tea plants from a genetically modified ancestor. *Front Plant Sci* 13:997762.

Otten L (2021) T-DNA regions from 350 *Agrobacterium* genomes: maps and phylogeny. *Plant Mol Biol* 106:239-258.

Matveeva TV, Otten L (2019) Widespread occurrence of natural transformation of plants by *Agrobacterium*. *Plant Mol Biol* 101:415-437.

Otten L (2018) The *Agrobacterium* phenotypic plasticity (*plast*) genes. *Curr Top Microbiol Immunol* 418:375-419.

Chen K, Otten L (2017) Natural *Agrobacterium* transformants: recent results and some theoretical considerations. *Front Plant Sci* 8. e1600.

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* 87:258-269.

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.