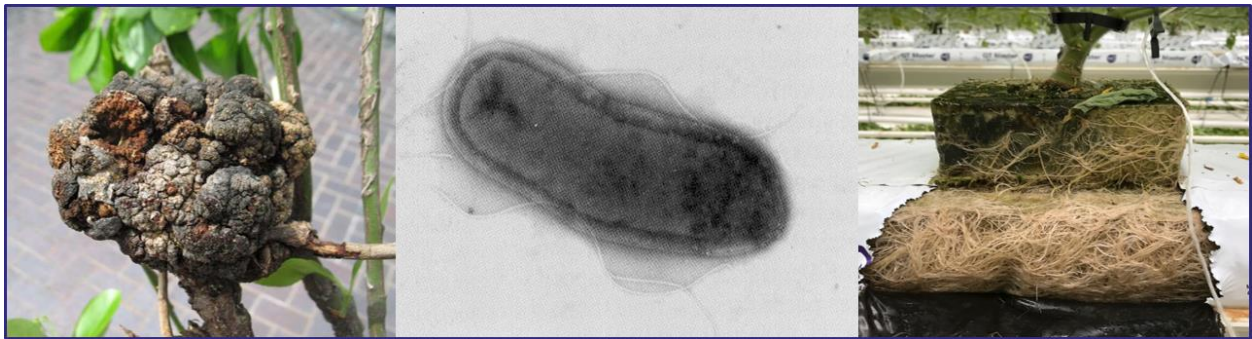


AGROBACTERIUM 2021

Welcome to the 41st American Crown Gall meeting and the
3rd European Agrobacterium conference



11-12 October Leuven, Belgium



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Naturally transgenic plants: recent results and generalizations

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«Agrobacterium» is the most common tool for creating of commercial lines of transgenic plants. Such genetically engineered organisms (GMOs) are constantly attacked as alien to nature organisms. An important argument supporting GMOs was the discovery of plants transformed by Agrobacterium in natural conditions millions of years ago [1]. DNA sequences in their genomes, homologous to T-DNA, were named cellular T-DNA (cT-DNA). Until recent, nGMOs have been described within three genera *Nicotiana*, *Linaria* and *Ipomoea* [2-4].

The development of methods for sequencing genomes and algorithms for their assembly led to an avalanche-like increase in the number of available sequenced plant genomes. The search for sequences similar to agrobacterial ones in the genomes of land plants revealed several dozens of new natural GMOs. And this list continues to grow. New examples of natural GMOs are described mainly among dicotyledonous plants and account for about 7% of their number [5-6]. Based on the new data, it can be concluded that genes for the synthesis of opines dominate among the agrobacterial genes transferred to plants. Moreover, there are many intact potentially functional sequences among them [7]. Extended cT-DNA sequences containing not only opine synthase genes but also oncogenes are characterized in most cases by the structure of inverted repeats. Comparative analysis of cT-DNA of closely related plant species makes it possible to use it in phylogenetic studies, which will be illustrated by the example of species from the genera *Vaccinium*, *Nicotiana* and *Camellia*

Data on the presence in plant genomes of cT-DNA sequences indicates that mankind throughout its history has encountered GMOs, using them for food, drinks, drugs etc.

Acknowledgments:

The presented research was supported by a grant from the Russian Science Foundation 21-14-00050.

Poster 1.6