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In the meantime a publication reported about positioning *M. truncatula* FUT2 (α-1.3-fucosyltransferase) genes by FISH method on five chromosomes (LG1,4,5,7,8), one of them inserted in the NOR region. Based on this information we checked if FUT2 gene was present also in *M. sativa* NOR region or not. Southern blot experiments suggested that FUT2 gene has lower copy number in the *M. sativa* genome and no position inside the rDNA region was detected. This further suggests a low synteny between these regions in the two *Medicago* species.

Insertional mutagenesis technology is important tool for isolation of new genes by phenotypes (forward genetics) or study their function (reverse genetics). We have found a number of plants with leaf phenotype similar to *stl* among *M. truncatula* insertional mutants carrying tobacco *Tnt1* retrotransposons. Sequence of *Tnt1* flanking regions of these mutant lines were determined by AFLP-PCR method. These sequences have been analyzed by their potential coding function as well as by their map position. Possible candidates were identified based on location (Mt LG5, LG6 or unknown) and are subject for further studies.

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Typing of bacterial symbionts of entomopathogenic nematodes, and their potenital use as biocontrol agents

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The extensively used biocontrol organisms, entomopathogenic nematodes belong to the *Heterorhabditis* and *Steinernema* genus are symbiotically associated with *Photorhabdus* and *Xenorhabdus* bacteria. The bacterial partners have an outstanding role in the life-cycle of their nematode hosts: they produce wide range of toxins, hydrolitic exoenzymes and antibacterial compounds that are responsible for the death and bioconversion of the infected insect larvae and prevent other soil organisms from degradating the insect cadavers. The bacterial partners highly determine the effectiveness of the symbiotic complex against different insects, therefore bacteria have an interests from the viewpoint of biocontrol practice. The aim of this study was to survey the diversity of the Hungarian *Photorhabdus* isolates, and to obtain comprehensive view about their potential use as industrial entomotoxin and antimicrobial compound producers.

Photorhabdus strains from entomopathogenic nematodes isolated from Hungarian soils (Tóth 2006) were characterized by morphological, physiological and genetic properties to survey the diversity of bacterial symbionts of *Heterorhabditis* species of commercial importance. Entomopathogenic bacteria (EPB) were isolated from 245 entomopathogenic nematode strains originated from different part of Hungary. There were 156 *Photorhabdus* and 77 *Xenorhabdus* from the successfully cultured 233 EPB isolates. 65 *Photorhabdus* isolates representing the whole collection from the point of view of geographical and nematode host distribution were analysed. First stage bacteria cells selected on NBTA indicator plates were used to determine the morphological traits and to perform physiological tests using Biolog GN microplates and API20E strips. Cytotoxic and antibacterial properties of cell-free culture broth were measured against *Drosophila melanogaster* S2 and *Spodoptera frugiperda* Sf9 cell lines or *Stpahylococcus aureus* and *Bacillus subtilis* bacteria, respectively. Morphologically and physiologically homogenous groups of *Photorhabdus* isolates were characterized by partial sequencing of 16S rRNA and *gyr*B subunit gene.

High physiological and morphological diversity were proved among the *Photorhabdus* isolates, and all of physiological and morphological bacteria types could be isolated both from *Heterorhabditis megidis* and *H. downesi*. A number of bacteria isolates were shown only moderate 16S rRNA gene sequence similarities with type strains of all described *Photorhabdus* species/subspecies. Using *gyrB* sequences to the phylogenetic analysis, these isolates were proved to be part of the species *Photorhabdus temperata*, with clear separation from both palearctic and American strains (phylogenetic distances are 93.1% and 92.1%, respectively). The physiological and carbon source utilization characters supported the phylogenetic position of these strains, therefore a new subspecies, *Photorhabdus temperata* subsp. *cinerea* (Tóth and Lakatos 2008).

The 39% and 13% of all studied isolates were uneffective against *S. aureus* and *B. subtilis*, respectively, while 26% and 7% were much more effective, than 100 ppm streptomycine, which was the control. About 10% of the studied isolates do not produce effective ingredients against *S. aureus* and *B. subtilis* bacteria, while 10% of them were highly effective against both bacteria.

59% and 8% of isolates had no cytotoxic effect on S2 and Sf9 cells, while 3% and 21% were highly toxic to dipteran and lepidopteran cells. There was not any *Photorhabdus* isolates, of which fermentation liquid was toxic to both cell types.

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