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## Bacterial endophytes in crops – molecular identification and biodiversity

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Bacterial endophytes reside in a large number of plant species as part of their microbiome. Endophyte community structure exhibits a high diversity of species within a plant. This diversity is determined by abiotic and biotic factors such as soil conditions, biogeography, plant species, microbe–microbe interactions and plant–microbe interactions. The purpose of this study was to assess the degree of genomic diversity, relationship and molecular identification of bacteria isolated from the endosphere of maize, broad bean, wheat, rye, horsetail and burdock (root and stem). The tests were performed on 45 strains. The genetic identification of bacterial population was performed based on comparative sequence analysis of the 16S rDNA. On the basis of 16S ribosomal RNA sequences, all strains of bacteria were assigned to 10 genera: *Rhizobium* (19 isolates), *Delftia* (11 isolates), *Agrobacterium* (5 isolates), *Stenotrophomonas* (3 isolates), *Brevundimonas* (2 isolates), *Novosphingobium* (1 isolate), *Variovorax* (1 isolate), *Collimonas* (1 isolate), *Achromobacter* (1 isolate) and *Comamonas* (1 isolate). The assessment of the diversity of potential plant growth promoting bacteria, including 11 species *Delftia* sp, was conducted based on the BOX-PCR, ERIC-PCR and PCR-DGGE techniques. The genetic profile shows similarity among tested bacteria strains. The microorganism group was related to the type of the host plant.

### Recent Publications:

1. Costa L. E. D. O., Queiroz M. V. D., Borges A. C., Moraes C. A. D. and Araújo E. F. D. (2012) Isolation and characterization of endophytic bacteria isolated from the leaves of the common bean (*Phaseolus vulgaris*). Brazilian Journal of Microbiology 43: 1562-1575.
2. De Bruijn F. J. (1992) Use of repetitive (repetitive extragenic palindromic and enterobacterial repetitive intergeneric consensus) sequences and the polymerase chain reaction to fingerprint the genomes of *Rhizobium meliloti* isolates and other soil bacteria. Applied and Environmental Microbiology 58: 2180-2187.
3. Katara J., Deshmukh R., Singh N. K. and Kaur S. (2012) Molecular typing of native *Bacillus thuringiensis* isolates from diverse habitats in India using REP-PCR and ERIC-PCR analysis. The Journal of General and Applied Microbiology 58: 83-94.
4. Sun L., Qiu F., Zhang X., Dai X., Dong X. and Song W. (2008) Endophytic bacterial diversity in rice (*Oryza sativa* L.) roots estimated by 16S rDNA sequence analysis. Microbial Ecology 55: 415-424.

### Biography

Małgorzata Woźniak obtained a master degree in biology with specialization microbiology in 2015. She studied at Maria Curie-Skłodowska University (UMCS) in Lublin, Poland. She work in Department of Agricultural Microbiology, Institute of Soil Science and Plant Cultivation in Poland. She is principal Investigator (head of the project) in two projects: the research project in the statutory activity of IUNG-PIB, Title of project: "Molecular and biochemical identification of the endophytic bacteria and it application in plant growth promoting" and Preludium project, the National Science Center, Title of project: "The influence of fast-growing *Paulownia* Clon In Vitro 112 (*P.elonagata* x *P.fortunei*) on microbiological and physico-chemical properties of the soil in Poland".

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