Genome sequence of the natural antagonist Pseudomonas fluorescens 2-79 against fungal plant diseases

In agriculture we have to deal with a huge variety of diseases caused by phytopathogenic bacteria, fungi or insects for instance. Many of these plant pathogens live in the soil and attack the respective cultivar at the roots and can lead to considerable yield loss.

In the root surrounding, the rhizosphere, researchers discovered several soil organisms that intensively interact with each other and with the plant. The concentration and composition of these communities can be rather unique for different plant species and environmental habitat conditions. Some microorganisms even colonize the root surface and produce metabolites which possess antibiotic properties against other soil-living organisms. This way these antagonistic microbes even can be used as natural warriors against undesired disease organisms that infect farmer's crops. Especially in absence of appropriate pesticides this bioconrol strategy can be quite promising.

It was shown that fluorescent pseudomonads, a soil-living bacterial group, play a major role in suppressing the fungal plant pathogen Gaeumannomyces graminis var. tritici causing the widely-spread take-all disease of wheat. In 1979 Weller and Cook isolated bacteria from roots of wheat plants grown in take-all suppressive soils in Washington state, USA. Pseudomonas fluorescens 2-79, the strain analyzed in this study, was characterized as a strong biological control agent suppressing G. graminis. Wheat plants infected with G. graminis and additionally treated with P. fluorescens 2-79 resulted in taller plants, more heads, and fewer symptoms of root disease compared to the control plants without bacterial treatment. The bacteria could increase the yield up to 147%. P. fluorescens 2-79 produces mycotoxic phenazines, which are assumed to represent a key element in the suppression of pathogenic fungi.

Genomic DNA of P. fluorescens 2-79 was isolated and sequenced by a next-generation sequencing technique from the US-company Illumina. In the draft genome sequence we found 1 ribosomal RNA cluster, 47 transfer RNA genes, 4,286 genes that encode for a predicted protein function, and 1,388 genes coding for hypothetical proteins. In a further analysis of genes involved in secondary metabolism we found the complete phenazine gene cluster as well as an essential gene for the synthesis of hydrogen cyanide (hcnA) a bioactive compound that is secreted by some Pseudomonas species. An antifungal metabolite that is also often discussed in the biocontrol context using fluorescent pseudomonads is 2,4-diacetylphloroglucinol. The gene phlD necessary for the synthesis DAPG is absent in P. fluorescens 2-79.

The sequence of the antagonistic strain Pseudomonas fluorescens 2-79 can contribute to a wider base for further investigation of its biocontrol mechanisms. Finally this knowledge should be utilized to control the growth of fungal plant pathogens in agriculture.

The whole genome sequence has been deposited at DDBJ/EMBL/GenBank (www.ncbi.nlm.nih.gov/genbank) under the accession number JXCQ00000000. The version described in this paper is the first version, JXCQ01000000.

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Publication

Draft Genome Sequence of the Phenazine-Producing Pseudomonas fluorescens Strain 2-79.
Nesemann K, Braus-Stromeyer SA, Thuermer A, Daniel R, Mavrodi DV, Thomashow LS, Weller DM, Braus GH.
Genome Announc. 2015 Mar 26