

Sequence of the plant beneficial biocontrol agent *Pseudomonas fluorescens* DSM 8569

Pseudomonas represents an abundant bacterial group that can live in the soil. In this habitat many organisms like fungi, bacteria, plants or insects live together, often intensively interacting in close communities. The composition of these communities is quite characteristic for different plant species and environmental conditions. For several fluorescent pseudomonads a beneficial plant promoting effect was shown. Even a direct antagonistic biocontrol effect against plant pathogens and this way an additional indirect plant promotion effect was investigated. In 1994 *Pseudomonas fluorescens* DSM 8569, the strain analyzed in this study, was isolated from soil surrounding roots, the so called rhizosphere, of oilseed rape in Rostock, Germany. Oilseed rape is one host plant of the phytopathogenic fungus *Verticillium*, that lives in the soil and infects its host via the root system. In 2006 a strong biocontrol potential towards *Verticillium* was described for *P. fluorescens* DSM 8569. It is assumed that the biocontrol potential of antagonistic rhizobacteria is due to the secretion of various metabolites with toxic properties. For fluorescent pseudomonads a variety of secreted secondary metabolites with antimycotic impact are known, such as 2,4-diacetylphloroglucinol (DAPG), pyoluteorin, hydrogen cyanide (HCN), or pyrrolnitrin. A two-component system, called *gacA-gacS*, was discovered in the strain *Pseudomonas protegens* CHA0, which regulates the synthesis and secretion of these compounds. The mycotoxic phenazines are produced by *P. fluorescens* 2-79 and described as the key element in its biocontrol strategy. Currently, it is unknown which suppressive mechanisms are responsible for the antagonistic potential of *P. fluorescens* DSM 8569. Genomic sequencing will be helpful in understanding the plant-promoting and antagonistic potentials of fluorescent pseudomonads.

The genomic DNA of the biocontrol strain *P. fluorescens* DSM 8569 was isolated and sequenced by a next-generation sequencing technique from the US-company Illumina. In the draft genome sequence we found 2 ribosomal RNA cluster, 43 transfer RNA genes, 4,560 genes that encode for a predicted protein function, and 1,354 genes coding for hypothetical proteins. In a further analysis of genes involved in secondary metabolism in DSM 8569 we found two genes responsible for HCN synthesis. Genes necessary for pyoluteorin synthesis and the entire phenazine operon described for *P. fluorescens* 2-79 are absent in *P. fluorescens* DSM 8569. At least one gene (*phlG*) required for the regulation of DAPG synthesis is missing in DSM 8569.

With the sequence of the biocontrol strain *Pseudomonas fluorescens* DSM 8569 we want to support further research in biocontrol mechanisms. This way it hopefully will be possible to improve the usage of beneficial *Pseudomonas* rhizobacteria to control crop diseases in agriculture.

The whole genome sequence has been deposited at DDBJ/EMBL/GenBank (www.ncbi.nlm.nih.gov/genbank) under the accession number JXOE00000000. The version described in this paper is the first version, JXOE01000000.

Kai Neseemann, Gerhard H. Braus
*Institut für Mikrobiologie und Genetik Georg-August-Universität
Göttingen, Germany*

Publication

[Draft Genome Sequence of the Beneficial Rhizobacterium *Pseudomonas fluorescens* DSM 8569, a Natural Isolate of Oilseed Rape \(*Brassica napus*\).](#)

Neseemann K, Braus-Stromeyer SA, Thuermer A, Daniel R, Braus GH
Genome Announc. 2015 Mar 26