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**Draft Genome Sequence of MCPA-Degrading *Sphingomonas* sp. Strain ERG5, Isolated from a Groundwater Aquifer in Denmark**

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*Sphingomonas* sp. strain ERG5 was isolated from a bacterial community, originating from a groundwater aquifer polluted with low pesticide concentrations. This bacterium degrades 2-methyl-4-chlorophenoxyacetic acid (MCPA) in a wide spectrum of concentrations and has been shown to function in bioaugmented sand filters. Genes associated with MCPA degradation are situated on a putative conjugative plasmid.

Herbicides such as 2-methyl-4-chlorophenoxyacetic acid (MCPA) are widely used for crop protection across the world, with the implication that they frequently occur in groundwater reservoirs, for example, in the European Union, where they are threatening an important and sensitive source of freshwater (1).

The MCPA-degrading bacterium *Sphingomonas* sp. strain ERG5 was previously isolated from an enriched bacterial community that originated from an aquifer located below a conventionally treated agricultural field at Fladerne Creek in Denmark (2). This strain can readily mineralize MCPA at both low and high concentrations (10 μg·L⁻¹ to 10 mg·L⁻¹), making it a strong candidate for bioremediation purposes (3). *Sphingomonas* sp. ERG5 was previously sequenced, in order to investigate the genes encoding the degradation pathway. It was discovered that the entire putative pathway is encoded within an approximately 33-kbp transposon, which in turn is placed on a 138-kbp putative plasmid that also harbors the genes associated with conjugative transfer via the type IV secretion system, as well as multiple plasmid stability genes (4). The *Sphingomonadaceae* family is often associated with degradation of xenobiotics, and several strains have been isolated from polluted environments and have been shown to have their degradative genes situated on large plasmids (5). Members of this family appear to often harbor conjugative plasmids that are rarely transferred to other bacterial families (6).

*Sphingomonas* sp. ERG5 was streaked on a R2A plate (Sigma-Aldrich, St. Louis, MO, USA) and incubated at 20°C for 4 days. A single colony from this plate was picked for DNA extraction using an Ultra-Clean Microbial DNA isolation kit (MoBio Laboratories, Inc., Carlsbad, CA, USA). Genomic DNA was prepared for paired-end sequencing on the Illumina MiSeq platform using the Nextera XT DNA sample preparation kit (Illumina, San Diego, CA, USA). Libraries were sequenced using the MiSeq version 2 reagent kit (Illumina, San Diego, CA, USA). Genomic DNA was prepared for paired-end sequencing on the Illumina MiSeq platform using the Nextera XT DNA sample preparation kit (Illumina, San Diego, CA, USA). Genomic DNA was prepared for paired-end sequencing on the Illumina MiSeq platform using the Nextera XT DNA sample preparation kit (Illumina, San Diego, CA, USA). Genomic DNA was prepared for paired-end sequencing on the Illumina MiSeq platform using the Nextera XT DNA sample preparation kit (Illumina, San Diego, CA, USA).

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