

Draft Genome Sequence of the Marine *Streptomyces* sp. Strain PP-C42, Isolated from the Baltic Sea[∇]

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***Streptomyces*, a branch of aerobic Gram-positive bacteria, represents the largest genus of actinobacteria. The streptomycetes are characterized by a complex secondary metabolism and produce over two-thirds of the clinically used natural antibiotics today. Here we report the draft genome sequence of a *Streptomyces* strain, PP-C42, isolated from the marine environment. A subset of unique genes and gene clusters for diverse secondary metabolites as well as antimicrobial peptides could be identified from the genome, showing great promise as a source for novel bioactive compounds.**

Streptomyces, a branch of aerobic Gram-positive bacteria, represents the largest genus of actinobacteria, with more than 900 described species. Streptomycetes are characterized by the formation of mycelia and spores during their life cycle and by a complex secondary metabolism. They produce more than two-thirds of the clinically used natural antibiotics (4, 11) and represent an important source of novel bioactive compounds. Furthermore, many enzymes produced by streptomycetes are important for food manufacturing (3) and for diverse industrial applications (7). *Streptomyces* strains have been isolated and characterized from a large variety of habitats (10, 13). Although more than five *Streptomyces* genomes have been completely sequenced in recent years, numerous genome sequencing projects with different *Streptomyces* species are still ongoing. Streptomycetes have linear chromosomes (approximately 8 to 12 Mb) with a high G+C content (11). More than 20 diverse secondary metabolic gene clusters in their genome have been described to date (11, 12).

Streptomyces sp. strain PP-C42 was isolated from the surface layer of a sediment core taken at a water depth of 241 m from the Gotland Deep in the Baltic Sea. The sampling was taken through a small gravity corer during an expedition with the research vessel *Alkor* AL156 in the year 2000.

Raw data of the genome were generated from two independent sequencing lanes using Illumina GA II and assembled with the Velvet program (18). The released genome sequence of the *Streptomyces* strain IFO 13350 (12) served as a reference. GeneMarkS (2), tRNAscan-SE (14), and RNAmmer (8) were utilized to predict protein-coding genes, tRNAs, and rRNAs, respectively. The GSP software (<http://gsizepred.sourceforge.net>) was used to estimate the genome size of the strain (5, 9).

The draft genome sequence of strain PP-C42 comprises 7,167,114 bases representing approximately 74.5% of the 9.6-Mb estimated size of the PP-C42 genome. The genome of strain PP-C42 has a high G+C content of 72.5%. The draft genome sequence contains 4,410 open reading frames (ORFs), 62 tRNAs, and 24 rRNAs. Of 4,410 ORFs, 2,774 genes have orthologs in *Streptomyces* strain IFO 13350 (12) (BLASTP < 1e−5), while 1,076 ORFs were not found in any of the five released genome sequences of other *Streptomyces* strains (1, 11) and 1,068 ORFs did not give any hits in the current public databases. This may be a reflection of a high degree of the strain specificity of the PP-C42 genome. So far, 19 diverse secondary metabolic genes have been identified; these genes are located on the PP-C42 genome in various gene clusters, which exhibit high genomic synteny to those of various *Streptomyces* species. Also, a set of hits was retrieved (BLASTP < 1e−5) from various antimicrobial peptide databases (6, 15, 16, 17) but with striking sequence variations at both DNA and amino acid levels when compared to their orthologs from other *Streptomyces* species. Thus, the unique genome information provided by the draft sequence of PP-C42 has great importance for basic as well as applied microbial genomic researches.

Nucleotide sequence accession numbers. This whole genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession AEWS00000000. The version described in this paper is the first version under accession number AEWS01000000.

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