

Draft Genome Sequence of the Biocontrol Bacterium *Chromobacterium* sp. Strain C-61

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***Chromobacterium* sp. strain C-61 is a plant-associated bacterium with proven capacities to suppress plant diseases. Here, we report the draft genome sequence and automatic annotation of strain C-61. A comparison of this sequence to the sequenced genome of *Chromobacterium violaceum* ATCC 12472 indicates the novelty of C-61 and a subset of gene functions that may be related to its biocontrol activities.**

Chromobacterium sp. strain C-61 was isolated from eggplant rhizosphere in Korea based on its ability to solubilize chitin and antagonize *Rhizoctonia solani* *in vitro* (7). The strain was subsequently tested as a microbial biopesticide *in planta*, and it displayed significant capacities to suppress a variety of fungal diseases of pepper, particularly when used in combination with other biocontrol agents (2). It has also been shown to be useful as part of a bacterial inoculant mixture targeting the suppression of fungal diseases of ginseng (3). Initial work on the mode of action of strain C-61 indicated that its antagonistic activity against *R. solani* depended on its ability to produce an active chitinase, designated Chi54 (5). Because chitinases are of interest industrially, mutational analyses of the *chi54* gene were undertaken and led to the identification of active residues in the enzyme and the creation of a more active gene product (6). But more recent work indicates that *in planta*, the production of a novel cyclic lipopeptide, chromobactomycin, is more important for biological control activity against plant pathogens (H. J. Kim, H. S. Choi, S. Y. Yang, I. S. Kim, M. R. Park, T. Yamaguchi, J. K. Sohng, J. H. Kim, H. H. Baek, S. K. Park, J.-C. Kim, B. B. McSpadden Gardener, and Y. C. Kim, submitted for publication).

The genomic DNA of *Chromobacterium* sp. strain C-61 was isolated, and a library was prepared from a sheared DNA fraction of ~300 bp using Illumina paired-end sample preparation kits according to the manufacturer's instructions. This library was sequenced with an Illumina genome analyzer II (Illumina, San Diego, CA) for 76 cycles, generating over 6 million good-quality paired-end reads, amounting to over 400 million nucleotides. The short-read sequences were assembled using Velvet version 0.7.55 software (8, 9) with an empirically determined optimal hash length of 37 nucleotides (nt) and a minimum contig length of 150 nt. The assemblies were uploaded to the automated annotation platform Rapid Annota-

tion using Subsystems Technology (RAST) server maintained by the National Microbial Pathogen Data Resource (1) and visualized with the SEED viewer (4).

This shotgun genome sequence of *Chromobacterium* sp. strain C-61 has a total of 5,115,736 nt. The annotation indicates that 730 of the 1,118 contigs harbor a total of 4,685 protein-encoding genes (PEGs). Sequence coverage was 94-fold or greater for 99% of the annotated genes. Additionally, 99% of the annotated PEGs were greater than 450 nt in length. The assembly did not adequately reconstruct the rRNA genes, but 49 tRNA sequences were identified. Only 3,547 (75.7%) of the annotated PEGs were mapped to the genome of *Chromobacterium violaceum* ATCC 12472, its closest relative in the public SEED database, with an average DNA sequence identity of 69.4%. Of the 1,138 PEGs predicted to be unique to strain C-61, 466 (40.9%) had predicted functions, including synthesis of nonribosomal lipopeptides and metabolite transport.

Nucleotide sequence accession numbers. The assembled shotgun genome sequence and annotations of *Chromobacterium* sp. strain C-61 were deposited in the European Nucleotide Archive (<http://www.ebi.ac.uk/genomes/wgs.html>) under the accession numbers CAEE01000001 to CAEE01001118.

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