

Draft Genome Sequence of *Streptomyces* Strain S4, a Symbiont of the Leaf-Cutting Ant *Acromyrmex octospinosus*[∇]

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***Streptomyces* spp. are common symbionts of the leaf-cutting ant species *Acromyrmex octospinosus*, which feeds on basidiomycete fungus leaf matter and harvests the lipid- and carbohydrate-rich gongylidia as a food source. *A. octospinosus* and other ant genera use antifungal compounds produced by *Streptomyces* spp. and other actinomycetes in order to help defend their fungal gardens from parasitic fungi. Herein, we report the draft genome sequence of *Streptomyces* strain S4, an antifungal-producing symbiont of *A. octospinosus*.**

The well-studied leaf-cutting ant species *Acromyrmex octospinosus* forms a mutualism with a single basidiomycete fungus, *Leucoagaricus gongylophorus*, in which the ants exchange food as well as protection and transport services with the fungus (4). The fungal garden can be parasitized by a variety of microorganisms (6, 10, 11). The ants groom and weed their garden to remove parasites and produce antifungal secretions from their metapleural glands (8). The ants also host *Amycolatopsis*, *Pseudonocardia*, and *Streptomyces* exosymbionts (5, 7, 9, 14). These symbionts produce antifungal compounds that are thought to be applied as weed killers by the ants (3, 5, 7, 9, 13, 14). Both the chemical identities of these antifungal compounds and the means by which symbionts are selected have been the subject of several recent studies (3, 9, 14). One of these studies demonstrated that genome sequencing of ant symbionts can aid the identification of antifungal compounds that may be important in this mutualism and could also help us understand how the selection of leaf-cutting ant symbionts occurs (2, 3).

A combination of shotgun, 3-kbp and 8-kbp paired-end libraries were constructed to sequence the *Streptomyces* strain S4 genome on the GS FLX sequencer (Roche) using the GS FLX Titanium series chemistry kit, generating >335 Mbp of sequence. Reads were assembled using the gsAssembly version 2.3 software (Roche), generating 12 scaffolds containing 211 large contigs (>500 bp) spanning 7.47 Mbp of sequence, which is within the size range reported for other streptomycetes. The genome was shown to consist of one linear chromosome; one linear plasmid, pS4L1; and one circular plasmid, pS4C1. These were annotated using the Rapid Annotation Subsystem Technology (RAST) server, and the predicted open reading frames were manually inspected and the annotation was adjusted using Artemis, release 12 (1, 12).

The *Streptomyces* S4 genome, as with other streptomycetes,

contains multiple biosynthetic gene clusters coding for known and predicted bioactive secondary metabolites. Notably, *Streptomyces* S4 contains a biosynthetic gene cluster that directs the biosynthesis of the antifungal candidicin, which was proposed to be an antifungal used by *A. octospinosus* to protect the fungal garden and was previously demonstrated to be produced by *Streptomyces* strain S4 (3, 7). The genome of *Streptomyces* strain S4 is also predicted to make mannopeptimycin-like and gramicidin-like antibacterial compounds as well as biosynthetic gene clusters predicted to encode anticancer compounds similar to fredericamycin and kendomycin as well as four cryptic biosynthetic gene clusters whose products are unknown. The presence of multiple biosynthetic gene clusters makes *Streptomyces* strain S4 an attractive symbiont and could possibly explain the isolation of a taxonomically very similar strain that produces candidicin from *A. octospinosus* in Panama (7). The biosynthesis of predicted antibacterials also has implications for the bacterial community present on the ant cuticle, suggesting that leaf-cutting ant symbionts may be involved in determining which bacterial species compose the ant microbiome (2).

Nucleotide sequence accession number. The genome sequence has been deposited in DDBJ/EMBL/GenBank under the accession number CADY00000000. The version described in this paper is the first version, CADY01000000.

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