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GENOME SEQUENCES

# Draft Genome Sequences of *Saccharopolyspora* sp. Strains and *Streptomyces* sp. Strains, Isolated from Social Wasps (Vespidae; Polistinae: Epiponini)

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**ABSTRACT** Strains of the genera *Saccharopolyspora* and *Streptomyces* were isolated from *Protopolybia* sp. and *Metapolybia* sp. social wasps in Costa Rica. Draft genome sequences were obtained for six isolates, ranging from 6.4 Mb to 9.1 Mb long and having GC contents of 71 to 73%.

Underexplored sources of natural products have recaptured the interest of scientists, and these include new bacterial strains from social insects as promising sources of novel molecules (1). Interest in these microbes is due to their ability to adapt and compete with a broad spectrum of insect pathogens, which has allowed their evolutionary success over the time (2) and might provide them with an untapped diversity of metabolites. Under this premise, *Saccharopolyspora* sp. and *Streptomyces* sp. symbiotic strains associated with social wasps from the genera *Metapolybia* and *Protopolybia* were isolated.

Actinobacteria strains were isolated from the cuticle and salivary glands of social wasps collected at three different locations in Costa Rica (Table 1). For bacterial isolation from the cuticle, one worker wasp was rubbed directly onto a petri dish using sterile forceps. For actinobacterial isolation from the salivary glands, thoracic glands were homogenized in 30 $\mu$l PBS + 100 mM sodium acetate (pH 5), and 20 $\mu$l was plated. Three different media supplemented with nystatin (0.1%) and nalidixic acid (10 $\mu$g/ml) were used for isolation: 1% Luria-Bertani (LB; Miller) medium and International Streptomyces Project 1 and 2 (ISP1 and ISP2) media. The plates were incubated at room temperature (~22°C) for 1 month; colonies exhibiting macroscopic morphologies of actinobacteria were transferred and purified onto new LB, ISP1, or ISP2 plates (Table 1). Genomic DNA from six pure isolates was obtained by phenol-chloroform extraction as described by Chun and Goodfellow (3), using 1 mg of bacterial colonies, aerial mycelia, and spores of each strain after 7 days' culture at room temperature on their respective media. Genomic libraries were prepared using the Nextera XT DNA library preparation kit (Illumina, San Diego, CA) and sequenced using a paired-end strategy of 2 × 150 nucleotides on the Illumina NextSeq 500 platform. The raw sequencing reads were both quality controlled and trimmed using fqCleanER (https://gitlab.pasteur.fr/GIPhy/fqCleanER) with all the "-s" options activated and clipping of the Illumina Nextera index. *De novo* assemblies were obtained from trimmed reads using SPAdes v3.14.1 (4) with the following options: -k 21,33,55,77 --only-assembler --careful. The quality of the assembled genomes was verified using CheckM v1.1.3 (5). Default parameters were used for data processing except where otherwise noted.

Six draft genome sequences were obtained, from 6.4 Mb to 9.1 Mb long. The relevant genome characteristics are presented in Table 1. A taxonomic comparison made using JSpeciesWS (6) based on average nucleotide identity (ANI) showed four *Saccharopolyspora* sp. strains sharing >99% genome identity among them and two different *Streptomyces* sp. strains. However, none of the comparisons showed results above the species threshold

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**TABLE 1** Characteristics of six *Actinobacteria* isolates associated with social wasps and sequencing general results

| Metric | Data for strain:[a] | | | | | |
|---|---|---|---|---|---|---|
| | ***Saccharopolyspora* sp. 6M** | ***Saccharopolyspora* sp. 6T** | ***Saccharopolyspora* sp. 6V** | ***Saccharopolyspora* sp. 7B** | ***Streptomyces* sp. 7G** | ***Streptomyces* sp. 8L** |
| Source (individual ID) | Cuticle of *Metapolybia* sp. (insect 1) | Cuticle of *Metapolybia* sp. (insect 1) | Cuticle of *Metapolybia* sp. (insect 2) | Cuticle of *Metapolybia* sp. (insect 3) | Salivary gland of *Protopolybia* sp. (insect 4) | Cuticle of *Protopolybia* sp. (insect 5) |
| Sampling date (yr-mo-day) | 2019-6-20 | 2019-6-20 | 2019-9-19 | 2019-9-19 | 2019-8-16 | 2020-2-12 |
| Sampling location | Santa Cruz, Guanacaste (10° 16′22.8″N, 85° 31′43.5″W) | Santa Cruz, Guanacaste (10° 16′22.8″N, 85° 31′43.5″W) | Santa Cruz, Guanacaste (10° 16′22.8″N, 85° 31′43.5″W) | Santa Cruz, Guanacaste (10° 16′22.8″N, 85° 31′43.5″W) | Research Station La Selva, Heredia (10° 25′19″N, 84° 00′54″W) | Golfito, Puntarenas (8° 39′15.8″N, 83° 10′45.1″W) |
| Isolation and culture medium | LB | LB | ISP1 | ISP2 | ISP1 | ISP2 |
| Total no. of reads | 4,447,755 | 4,414,784 | 5,429,465 | 4,959,684 | 5,077,834 | 6,368,654 |
| Genome size (bp) | 6,438,697 | 6,587,366 | 6,571,055 | 6,480,769 | 7,848,592 | 9,078,753 |
| No. of genes annotated with PGAP (7) | 5,764 | 5,898 | 5,942 | 5,725 | 7,357 | 8,045 |
| No. of RNAs annotated with PGAP (7) | 54 | 56 | 56 | 55 | 73 | 78 |
| % GC | 73 | 72 | 72 | 73 | 71 | 71 |
| No. of contigs | 360 | 355 | 242 | 291 | 1,081 | 991 |
| $N_{50}$ (bp) | 29,651 | 38,839 | 50,652 | 40,461 | 12,009 | 15,698 |
| Completeness (%) | 99.65 | 99.47 | 99.47 | 99.82 | 99.33 | 98.19 |
| Contamination (%) | 1.48 | 1.45 | 1.12 | 1.45 | 1.99 | 2.17 |
| Sequencing depth (×) | 100 | 98 | 112 | 107 | 99 | 103 |
| BioSample accession no. | SAMN21501660 | SAMN21501661 | SAMN21501662 | SAMN21501663 | SAMN21501664 | SAMN21501665 |
| GenBank WGS[b] accession no. | JAIUJZ000000000 | JAIUKA000000000 | JAIUKB000000000 | JAIUKC000000000 | JAIUKD000000000 | JAIUKE000000000 |
| GenBank assembly accession no. | GCA_020176775.1 | GCA_020177455.1 | GCA_020176785.1 | GCA_020177435.1 | GCA_020177475.1 | GCA_020176795.1 |
| SRA accession no. for raw reads | SRX13158144 | SRX13158145 | SRX13158146 | SRX13158147 | SRX13158148 | SRX13158149 |

[a]Strain identification was based on ANI comparison with available species of the closest genus.
[b]WGS, whole-genome sequencing.

(>95%) with available genomes of the genera, suggesting that these isolates might be new species.

**Data availability.** The data from this study are available under BioProject accession number PRJNA764377. The BioSample material, assembled genomes, and raw reads have been deposited at DDBJ/ENA/GenBank under the accession numbers listed in Table 1.

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