



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

Mariela Gutiérrez-Araya, Kattia Núñez-Montero, Javier Pizarro-Cerdá, Laura Chavarría-Pizarro

► To cite this version:

Mariela Gutiérrez-Araya, Kattia Núñez-Montero, Javier Pizarro-Cerdá, Laura Chavarría-Pizarro. Draft Genome Sequences of *Saccharopolyspora* sp. Strains and *Streptomyces* sp. Strains, Isolated from Social Wasps (Vespidae; Polistinae: Epiponini). *Microbiology Resource Announcements*, 2022, 11 (1), pp.e0093521. 10.1128/MRA.00935-21 . pasteur-03666839

HAL Id: pasteur-03666839

<https://pasteur.hal.science/pasteur-03666839>

Submitted on 12 May 2022

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.



Distributed under a Creative Commons Attribution 4.0 International License



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

Mariela Gutiérrez-Araya,^a  Kattia Núñez-Montero,^{a,b} Javier Pizarro-Cerdá,^c  Laura Chavarría-Pizarro^a

^aCentro de Investigación en Biotecnología, Instituto Tecnológico de Costa Rica, Cartago, Costa Rica

^bLaboratorio de Biología Molecular Aplicada, Centro de Excelencia en Medicina Traslacional, Universidad de La Frontera, Temuco, Chile

^cInstitut Pasteur, Université de Paris, Yersinia Research Unit, Paris, France

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 µl PBS + 100 mM sodium acetate (pH 5), and 20 µl was plated. Three different media supplemented with nystatin (0.1%) and nalidixic acid (10 µg/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

Editor Irene L. G. Newton, Indiana University, Bloomington

Copyright © 2022 Gutiérrez-Araya et al. This is an open-access article distributed under the terms of the [Creative Commons Attribution 4.0 International license](#).

Address correspondence to Laura Chavarría-Pizarro, laura.chavarria@itcr.ac.cr.

The authors declare no conflict of interest.

Received 19 September 2021

Accepted 1 December 2021

Published 6 January 2022

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

| Metric | Data for strain: ^a | <i>Saccharopolyspora</i> sp. 6M | <i>Saccharopolyspora</i> sp. 6T | <i>Saccharopolyspora</i> sp. 6V | <i>Saccharopolyspora</i> sp. 7B | <i>Saccharopolyspora</i> sp. 7G | <i>Streptomyces</i> sp. 8L |
|--|--|--|--|--|--|--|---|
| Source (individual ID) | Cuticle of <i>Metapolybia</i> sp. (insect 1) | Cuticle of <i>Metapolybia</i> sp. (insect 1) | Cuticle of <i>Metapolybia</i> sp. (insect 1) | Cuticle of <i>Metapolybia</i> sp. (insect 2) | Cuticle of <i>Metapolybia</i> sp. (insect 3) | Salivary gland of <i>Protopolybia</i> sp. (insect 4) | Cuticle of <i>Protopolybia</i> sp. (insect 5) |
| Sampling date (yr-mo-day) | 2019-6-20 | 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) | 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 | ISP2 |
| Total no. of reads | 4,447,755 | 4,414,784 | 5,429,465 | 4,959,684 | 5,077,834 | 6,368,654 | 6,368,654 |
| Genome size (bp) | 6,438,697 | 6,587,366 | 6,571,055 | 6,480,769 | 7,848,592 | 9,078,753 | 9,078,753 |
| No. of genes annotated with PGAP (7) | 5,764 | 5,898 | 5,942 | 5,725 | 7,357 | 8,045 | 8,045 |
| No. of RNAs annotated with PGAP (7) | 54 | 56 | 56 | 55 | 73 | 78 | 78 |
| % GC | 73 | 72 | 72 | 73 | 71 | 71 | 71 |
| No. of contigs | 360 | 355 | 242 | 291 | 1,081 | 991 | 991 |
| N_{50} (bp) | 29,651 | 38,839 | 50,652 | 40,461 | 12,009 | 15,698 | 15,698 |
| Completeness (%) | 99.65 | 99.47 | 99.47 | 99.82 | 99.33 | 98.19 | 98.19 |
| Contamination (%) | 1.48 | 1.45 | 1.12 | 1.45 | 1.99 | 2.17 | 2.17 |
| Sequencing depth (\times) | 100 | 98 | 112 | 107 | 99 | 103 | 103 |
| BioSample accession no. | SAMN21501660 | SAMN21501661 | SAMN21501662 | SAMN21501663 | SAMN21501664 | SAMN21501665 | SAMN21501665 |
| GenBank WGS ^b accession no. | JAIUJZ000000000 | JAIUKA000000000 | JAIUKB000000000 | JAIUKC000000000 | JAIUKD000000000 | JAIUKE000000000 | JAIUKE000000000 |
| GenBank assembly accession no. | GCA_020176775.1 | GCA_020177455.1 | GCA_020176785.1 | GCA_020177435.1 | GCA_020177445.1 | GCA_02017745.1 | GCA_02017745.1 |
| SRA accession no. for raw reads | SRX13158144 | SRX13158145 | SRX13158146 | SRX13158147 | SRX13158149 | SRX13158149 | SRX13158149 |

^aStrain identification was based on ANI comparison with available species of the closest genus.

^bWGS, 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.

ACKNOWLEDGMENTS

The research was funded by Instituto Tecnológico de Costa Rica (VIE-1510090 and 1510143 projects) and by Institut Pasteur (Yersinia Research Unit).

We thank CONAGEBIO for the collection permits (R-CM-ITCR-001-2019-OT and R-CM-ITCR-002-2019-OT) and Cyril Savin and Rémi Beau for technical help.

REFERENCES

- Sholkamy EN, Muthukrishnan P, Abdel-Raouf N, Nandhini X, Ibraheem IBM, Mostafa AA. 2020. Antimicrobial and antineoplastic metabolites from *Streptomyces cuspisporus* strain SA4 against selected pathogenic bacteria, fungi and nematode. *Saudi J Biol Sci* 27:3208–3220. <https://doi.org/10.1016/j.sjbs.2020.08.043>.
- Halim M, Aman-Zuki A, Syed Ahmad SZ, Mohammad Din AM, Abdul Rahim A, Mohd Masri MM, Badrul BM, Yaakop S. 2018. Exploring the abundance and DNA barcode information of eight parasitoid wasps species (Hymenoptera), the natural enemies of the important pest of oil palm, bagworm, *Metisa plana* (Lepidoptera: Psychidae) toward the biocontrol approach and its [sic] application in Malaysia. *J Asia Pac Entomol* 21:1359–1365. <https://doi.org/10.1016/j.aspen.2018.10.012>.
- Chun J, Goodfellow M. 1995. A phylogenetic analysis of the genus *Nocardioides* with 16S rRNA gene sequences. *Int J Syst Bacteriol* 45:240–245. <https://doi.org/10.1099/00207713-45-2-240>.
- Bankevich A, Nurk S, Antipov D, Gurevich AA, Dvorkin M, Kulikov AS, Lesin VM, Nikolenko SI, Pham S, Prijibelski AD, Pyshkin AV, Sirotkin AV, Vyahhi N, Tesler G, Alekseyev MA, Pevzner PA. 2012. SPAdes: a new genome assembly algorithm and its applications to single-cell sequencing. *J Comput Biol* 19:455–477. <https://doi.org/10.1089/cmb.2012.0021>.
- Parks DH, Imelfort M, Skennerton CT, Hugenholtz P, Tyson GW. 2015. CheckM: assessing the quality of microbial genomes recovered from isolates, single cells, and metagenomes. *Genome Res* 25:1043–1055. <https://doi.org/10.1101/gr.186072.114>.
- Richter M, Rosselló-Móra R, Oliver Glöckner F, Peplies J. 2016. JSpeciesWS: a Web server for prokaryotic species circumscription based on pairwise genome comparison. *Bioinformatics* 32:929–931. <https://doi.org/10.1093/bioinformatics/btv681>.
- Tatusova T, Dicuccio M, Badretdin A, Chetvernin V, Nawrocki EP, Zaslavsky L, Lomsadze A, Pruitt KD, Borodovsky M, Ostell J. 2016. NCBI Prokaryotic Genome Annotation Pipeline. *Nucleic Acids Res* 44:6614–6624. <https://doi.org/10.1093/nar/gkw569>.