



# Complete Genome Sequence of *Spiroplasma phoeniceum* Strain P40<sup>T</sup>, a Plant Pathogen Isolated from Diseased Plants of Madagascar Periwinkle [*Catharanthus roseus* (L.) G. Don]

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**ABSTRACT** The phytopathogen *Spiroplasma phoeniceum* was isolated from diseased plants of Madagascar periwinkle [*Catharanthus roseus* (L.) G. Don]. Here, we report the nucleotide sequence of the 1,791,576-bp circular chromosome and three plasmids of strain P40<sup>T</sup>. This information serves as a resource for comparative analyses of spiroplasmal adaptations to diverse ecological niches.

**S**piroplasmas are helical and motile members of the class *Mollicutes* (1). Following discovery of spiroplasma in diseased plants (2–6) and subsequent erection of the genus *Spiroplasma* (7), nearly 40 *Spiroplasma* spp. have been described. Three phytopathogenic *Spiroplasma* spp. are known, *S. citri*, *S. kunkelii*, and *S. phoeniceum* (7–9). Complete genome sequences have been reported for *S. kunkelii* CR2-3X (10) and *S. citri* R8-A2<sup>T</sup> (11).

Here, we report the complete genome sequence of *S. phoeniceum* strain P40<sup>T</sup> (ATCC 43115<sup>T</sup>). Strain P40<sup>T</sup> was isolated in culture from plants of Madagascar periwinkle [*Catharanthus roseus* (L.) G. Don] in Syria (8). Genomic DNA was extracted from *S. phoeniceum* P40<sup>T</sup>, grown as previously described at 30°C in M1D broth (1), using a PowerMicrobial Maxi DNA isolation kit (Mo Bio Laboratories, Inc., Carlsbad, CA). A primer-annealed 20-kb SMRTbell library was prepared, and nucleotide sequencing was carried out using a Pacific Biosciences (PacBio) single-molecule real-time (SMRT) sequencing system, in which 14,859 reads were obtained, totaling 210,862,768 nucleotides (nt). The  $N_{50}$  read length was 21,682 nt, the mean read length was 14,190 nt, and the average reference consensus concordance was 99.99%. Using R\_HGAP\_Assembly.3 with preassembler filter parameters, the minimum subread length was 500 nt, the minimum polymerase read quality was 0.80, and the minimum polymerase read length was 100 nt. The genome was assembled using SMRT Portal 2.3.0.140893. Within SMRT Portal, *de novo* assembly was performed with the R\_HGAP\_Assembly.3 pipeline (default parameters). The overlap was removed and the reads were remapped to the consensus using the RS\_Resequencing.1 pipeline, also contained within the SMRT portal, to join the 5' and 3' ends of the nascent assembly of the chromosome.

The assembled 1,791,576-bp circular chromosome has an overall base composition of 25.25 mol% G+C; average coverage per base position was 110.5×. The plasmids were 24,478, 38,732, and 53,490 bp in size and had base compositions of 28.40, 28.77, and 26.74 mol% G+C, respectively. The chromosome and plasmids were put through GeneMark.hmm (12) annotation. The programs tRNAscan-SE 1.21 and RNAmmer (13) predicted 43 tRNA genes and 1 set of rRNA genes. The chromosome has 1,573 protein-coding regions; BLASTN searches against a library of plectroviruses downloaded from the NCBI database and BLASTP searches against the NCBI protein database

**Citation** Davis RE, Shao J, Zhao Y, Wei W, Bottner-Parker K, Silver A, Stump Z, Gasparich GE, Donofrio N. 2019. Complete genome sequence of *Spiroplasma phoeniceum* strain P40<sup>T</sup>, a plant pathogen isolated from diseased plants of Madagascar periwinkle [*Catharanthus roseus* (L.) G. Don]. *Microbiol Resour Announc* 8:e01612-18. <https://doi.org/10.1128/MRA.01612-18>.

**Editor** John J. Dennehy, Queens College  
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**Received** 27 November 2018

**Accepted** 19 February 2019

**Published** 21 March 2019

revealed chromosomal insertions of plectrovirus sequences and a tailed prophage, respectively.

Spiroplasmas are now known as part of the internal and external microbiomes of plants, and as symbionts of insects, ticks, and crustaceans (14–18). Suspected spiroplasmas have been reported in jellyfish, a deep-sea chiton, and a hadopelagic zone sea cucumber (19–22). Certain spiroplasmas can present a risk of human infection (23–25). Together with the complete genome sequences of related *S. kunkelii* and *S. citri* strains (26, 27), the complete genome sequence of *S. phoeniceum* P40<sup>T</sup> presents a valuable resource for elucidating the evolutionary biology of plant-infecting spiroplasmas.

**Data availability.** This complete genome project has been deposited in GenBank under BioProject accession number [PRJNA435429](https://ncbi.nlm.nih.gov/bioproject/PRJNA435429), SRA accession number [SRX5075236](https://ncbi.nlm.nih.gov/sra/SRX5075236), and BioSample accession number [SAMN08579949](https://ncbi.nlm.nih.gov/biosample/SAMN08579949) for *Spiroplasma phoeniceum* P40<sup>T</sup> (taxonomy ID 1276259), and accession numbers [CP031088](https://ncbi.nlm.nih.gov/nuccore/CP031088) (chromosome), [CP031089](https://ncbi.nlm.nih.gov/nuccore/CP031089) (plasmid pSPH535), [CP031090](https://ncbi.nlm.nih.gov/nuccore/CP031090) (plasmid pSPH387), and [CP031091](https://ncbi.nlm.nih.gov/nuccore/CP031091) (plasmid pSPH245). The sequence versions described in this paper are CP031088.1, CP031089.1, CP031090.1, and CP031091.1.

## ACKNOWLEDGMENT

This work was supported through U.S. Government funds.

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