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Complete Genome Sequence of *Spiroplasma turonicum* Strain Tab4c^T, a Parasite of a Horse Fly, *Haematopota* sp. (Diptera: Tabanidae)

Robert E. Davis,[a] Jonathan Shao,[a] Yan Zhao,[a] Gail E. Gasparich,[b] Brady J. Gaynor,[b] Nicole Donofrio[c]

Molecular Plant Pathology Laboratory, USDA, Agricultural Research Service, Beltsville, Maryland, USA[a]; Department of Biological Sciences, Towson University, Towson, Maryland, USA[b]; Department of Plant and Soil Sciences, University of Delaware, Newark, Delaware, USA[c]

***Spiroplasma turonicum* was isolated from a *Haematopota* sp. fly in France. We report the nucleotide sequence of the circular chromosome of strain Tab4c^T. The genome information will facilitate evolutionary studies of spiroplasmas, including symbionts of insects and ticks and pathogens of plants, insects, crustaceans, and humans.**

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Address correspondence to Robert E. Davis, robert.davis@ars.usda.gov.

Although the helical, motile, and cell wall-less bacteria termed spiroplasmas were first discovered in plants, spiroplasmas have been isolated from diverse insects, ticks, and crustaceans (1–10). These discoveries and the identification of a human-infecting spiroplasma as a strain of the horse fly (*Haematopota* sp.) symbiont, *Spiroplasma turonicum* (11), support the prediction that spiroplasmas exhibit a constant link with arthropods (2).

Here, we report the complete nucleotide sequence of the circular chromosome of *S. turonicum* strain Tab4c^T (American Type Culture Collection, ATCC 700271), which was isolated in axenic culture from a *Haematopota* sp. fly in France (6). Genomic DNA was extracted from a culture of *S. turonicum* Tab4c^T grown in liquid M1D broth medium, as previously described (12). Nucleotide sequencing was carried out using the next-generation sequencing (NGS) platform of the Pacific Biosciences (PacBio) single-molecule real-time sequencing (SMRT) system, in which 86,887 reads were obtained, totaling 1,193,390,409 nucleotides. The N_{50} read length was 17,755 nucleotides, the mean read length was 13,734 nucleotides, and the average reference consensus concordance was 100.00%. The assembled circular chromosome of 1,261,374 bp has an overall base composition of 24.20 mol% G+C; the average coverage per base position was 616.05×. The assembled chromosome was put through GeneMark.hmm (13) annotation and was curated by manual inspection using Artemis (14) as an annotation platform. The programs tRNAscan-SE 1.21 and RNAmmer (15) were used to predict regions containing tRNAs and rRNAs, respectively. The chromosome has 1,085 protein coding regions (CDSs), 1 set of rRNA genes, 29 tRNA genes, and a 2,940-bp clustered regularly interspaced short palindromic repeat (CRISPR) locus.

Phylogenetically, *S. turonicum* clusters with other wall-less bacteria in the class *Mollicutes* and is a member of the Apis clade, which includes *Spiroplasma apis*, a pathogen of honey bees (12, 16). The availability of the *S. turonicum* complete genome sequence will facilitate studies to elucidate the evolutionary biology of spiroplasmas.

Nucleotide sequence accession numbers. This genome project has been deposited in GenBank under the BioProject ID PRJNA291635, BioSample accession no. SAMN03948565, and GenBank accession no. CP012328.

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