1 Complete genome sequences of two new strains of the shipworm
2 endosymbiont, *Teredinibacter turnerae*

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16 Running Title: Complete genomes of two new strains of *T. turnerae*

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18 Abstract

19 We present the complete genome sequences of two strains of *Teredinibacter turnerae*,

20 SR01903 and SR02026, shipworm endosymbionts isolated from the gills of *Lyrodus pedicellatus*

21 and *Teredo bartschi*, respectively, and derived from Oxford Nanopore sequencing. These

22 sequences will aid in the comparative genomics of shipworm endosymbionts and

23 understanding of host-symbiont selection.

Announcement

25 *Teredinibacter* species are cultivable intracellular symbionts of xylotrophic, bivalve wood-borers

26 (Teredinidae) (1–4) and have been shown to secrete lignocellulolytic enzymes that aid in host

27 digestion (5, 6). Wood containing live specimens of *Lyrodus pedicellatus* and *Teredo bartschi*

28 was collected from the Indian River Lagoon, Merit Island, FL. (N 28.40605 W 80.66034) on

29 January 24, 2020, and subsequently maintained in laboratory culture. Strain SR01903 was

30 isolated from the gill of a single specimen of *L. pedicellatus* immediately after collection from

31 the wild. Strain SR02026 was isolated from the gill of a fourth-generation lab-reared specimen

32 of *T. bartschi.* Bacterial isolations were performed as in O'Connor *et al.*, 2014. Briefly, gills were

33 removed by dissection and homogenized in 1.0 mL of SBM medium (7) in an autoclave-

34 sterilized glass dounce homogenizer. Homogenates were streaked onto culture plates

35 containing 1.0% Bacto agar prepared in shipworm basal medium (SBM) at pH 8.0 supplemented

36 with 0.2% w/v powdered cellulose (Sigmacell Type 101; Sigma-Aldrich) and 0.025% NH_4Cl.

37 Plates were then incubated at 30 °C. When individual colonies appeared, a single colony was

38 picked, re-streaked, and regrown. This process was repeated until clonal isolates were

39 achieved. Genomic DNA was extracted from the resulting clonal isolates, as in O'Connor *et al.*,

40 2014 using the Qiagen DNeasy Blood and Tissue Kit following the manufacturer's recommended

41 protocol for cultured cells with the exception that DNA was eluted with two 75 µL volumes of

42 AE buffer preheated to 56 °C. DNA quality and length were assessed on Tapestation (Agilent

43 Technologies, US). Nanopore (Oxford Nanopore Technologies, UK) sequencing was performed

44 without DNA fragmentation or size selection. The sequencing library was prepared using the

45 Q20+ chemistry Ligation Sequencing Kit (SQK-LSK112) and sequenced on a MinION (Mk1B)

46 instrument using a R10.4 (FLO-MIN112) flow cell. Bases were called using Guppy v6.4.6 with the

47   high-accuracy (HAC) algorithm, and default read quality filtering. Adapters were trimmed from

48   reads using Porechop v0.2.4 (https://github.com/rrwick/Porechop) and filtered to remove

49   reads less than 1 Kb using Filtlong v0.2.1 (https://github.com/rrwick/Filtlong). De novo

50   assembly was performed with Flye v2.9.2 (https://github.com/fenderglass/Flye) (8) followed by

51   contig correction and consensus generation with Racon v1.5.0 (https://github.com/lbcb-

52   sci/racon) and Medaka v1.8.0 (https://github.com/nanoporetech/medaka). Assemblies were

53   then circularized and rotated to start at *dnaA,* predicted by prodigal v2.6.3 (9) with Circlator

54   v1.5.5 (https://github.com/sanger-pathogens/circlator) (10). Chromosomal assemblies were

55   produced for both strains and annotated using the NCBI Prokaryotic Genome Annotation

56   Pipeline (PGAP) (Table 1). All software was run using default settings unless otherwise noted.

57   The primary sequences were 98.67% identical based on the calculated average nucleotide

58   identity (ANI) (11) and highly syntenic (Fig. 1) (12).

59   *Table 1 Genome sequencing, assembly, and annotation of Teredinibacter strains*

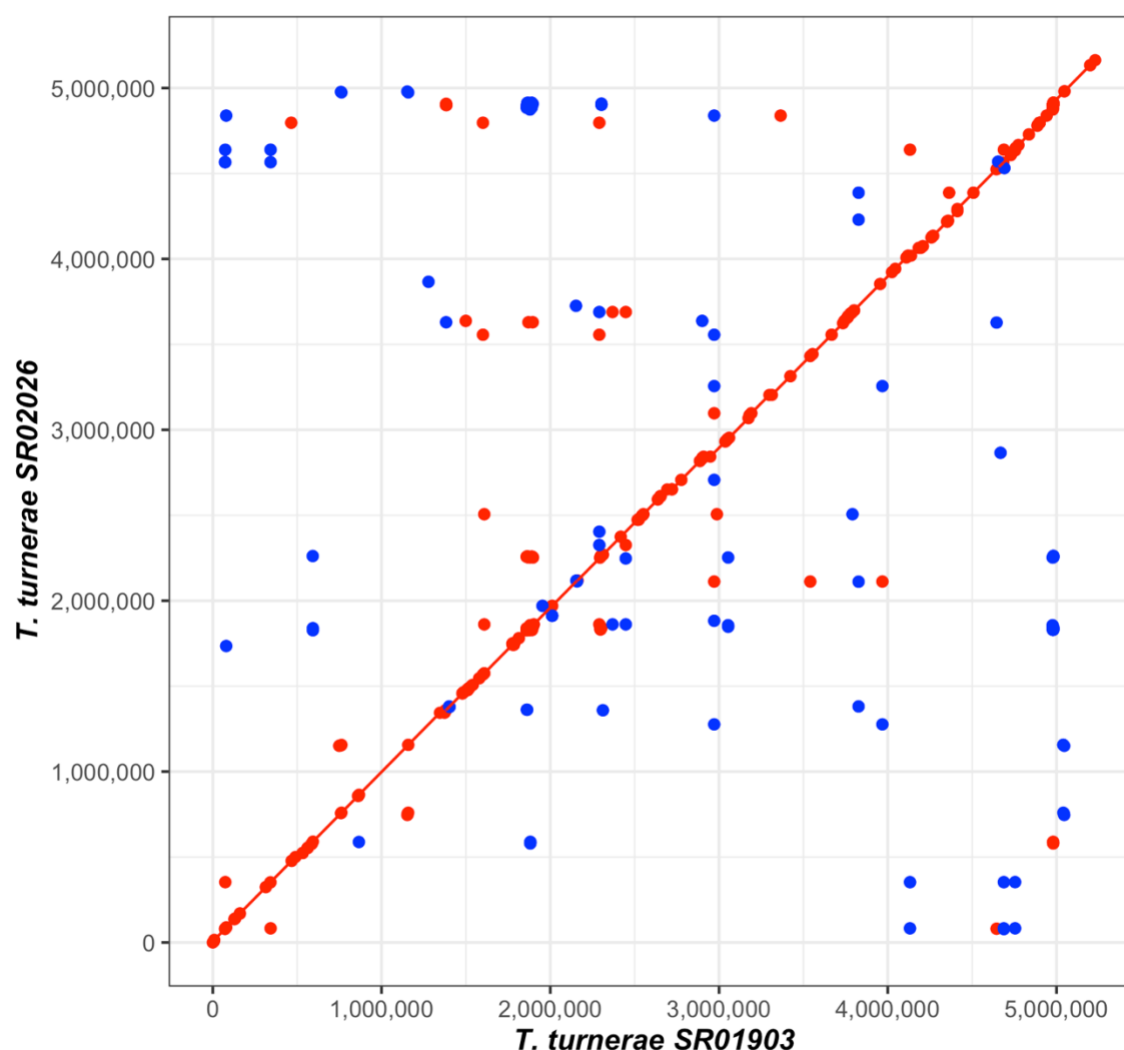| Strain	SR01903	SR02026
Host	*L. pedacellatus*	*T. bartschi*
Reads	77,041	253,198
Bases (M)	289.9	306.2
Read N50	11,088	2,331
Assembly (bp)	5,229,132	5,163,139
Coverage	52x	44x
GC content (%)	50.9	50.9
Genes	4,207	4,142
CDS	4,152	4,086
rRNA (complete)	3	3

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63 *Figure 1 Synteny plot comparing the genome sequences of SR01903 and SR02026. A MUMmer3 plot was generated with*
64 *NUCmer v3.1 (12) using NUCmer to assess synteny and completion. Minimum exact matches of 20bp are represented as a dot*
65 *with lines representing match lengths >20bp. Forward matches are displayed in red, while reverse matches are shown in blue.*

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67 ## Data availability

68 The complete genome sequences for SR01903 and SR02026 have been deposited in GenBank

69 under the accession numbers CP149818 and CP149819, respectively. The Oxford Nanopore

70 sequencing reads are available from the NCBI Sequence Read Archive (SRA) under the accession

71 numbers SRR28421271 and SRR28421270, respectively.

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