



DATA NOTE

The chromosome-level genome sequences of the freshwater sponge, *Spongilla lacustris* (Linnaeus, 1759) and the chlorophyte cobiont *Choricystis* sp., and the associated microbial metagenome sequences

[version 1; peer review: 2 approved]

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Keywords

Spongilla lacustris, freshwater sponge, genome sequence, chromosomal, Spongillida; microbial metagenome assembly



This article is included in the [Tree of Life](#) gateway.

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Author roles: **Leys SP:** Investigation, Resources, Writing – Original Draft Preparation; **Hentschel U:** Investigation, Resources, Writing – Review & Editing; **Oatley G:** Investigation; **Sinclair E:** Investigation; **Aunin E:** Formal Analysis; **Gettle N:** Formal Analysis; **Santos C:** Formal Analysis; **Paulini M:** Formal Analysis; **Erpenbeck D:** Formal Analysis; **Niu H:** Project Administration; **McKenna V:** Project Administration;

Competing interests: No competing interests were disclosed.

Species taxonomy: host

Eukaryota; Opisthokonta; Metazoa; Porifera; Demospongiae; Heteroscleromorpha; Spongillida; Spongillidae; *Spongilla*; *Spongilla lacustris* (Linnaeus, 1759) (NCBI:txid6055).

Species taxonomy: eukaryote cobiont

Eukaryota; Viridiplantae; Chlorophyta; core chlorophytes; Trebouxiophyceae; Trebouxiophyceae *incertae sedis*; *Choricystis* clade; *Choricystis*; unclassified *Choricystis* (NCBI:txid3025909).

Background

Spongilla lacustris (Linnaeus 1758) is a freshwater sponge with a Holarctic distribution (Manconi & Pronzato, 2008). It is one of the most commonly encountered sponges in shallow 0–4 m depths in lakes and rivers of Europe and North America, where

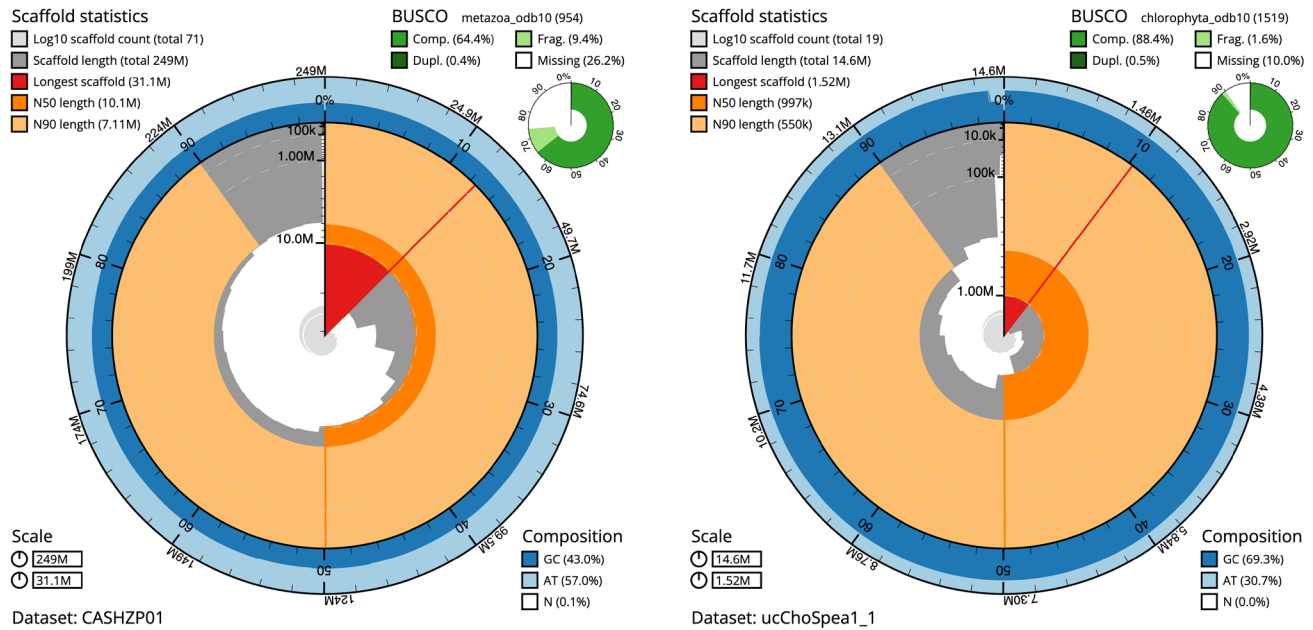
Im siecke, 1993; Saller, 1988; Saller & Weissenfels, 1985), as well as symbioses (Brøndsted & Brøndsted, 1953; Francis *et al.*, 2016; Gernert *et al.*, 2005; Graffius *et al.*, 2023; Harrison *et al.*, 1981; Pröschold & Darienko, 2020). Such a breadth of knowledge on one species makes this an excellent model system for a diversity of future work.

Genome sequence report for the host and chlorophyte cobiont

The genome was sequenced from a specimen of *Spongilla lacustris* grown in the laboratory at the University of Alberta, Edmonton, Canada (latitude 53.53, longitude -113.53). For the host organism, an estimated 34x coverage in Pacific Biosciences single-molecule HiFi long reads was generated. For the *Choricystis* sp. cobiont, 16x coverage was obtained, based on the estimated genome size. In both cases, the primary assembly contigs were scaffolded with chromosome conformation Hi-C data. Manual assembly curation corrected 239 missing joins or mis-joins and removed 160 haplotypic duplications, reducing the assembly length by 3.50% and the scaffold number by 77.02%, and increasing the scaffold N

Table 1. Genome data for *Spongilla lacustris*, odSpoLacu1.1.

Project accession data		
Assembly identifier	odSpoLacu1.1	
Species	<i>Spongilla lacustris</i>	
Specimen	odSpoLacu1	
NCBI taxonomy ID	6055	
BioProject	PRJEB58940	
BioSample ID	SAMEA8580182	
Isolate information	odSpoLacu1	
Raw data accessions		
PacificBiosciences SEQUEL II	ERR10802379, ERR10798424, ERR10802378	
Hi-C Illumina	ERR10786015, ERR10786016, ERR107	



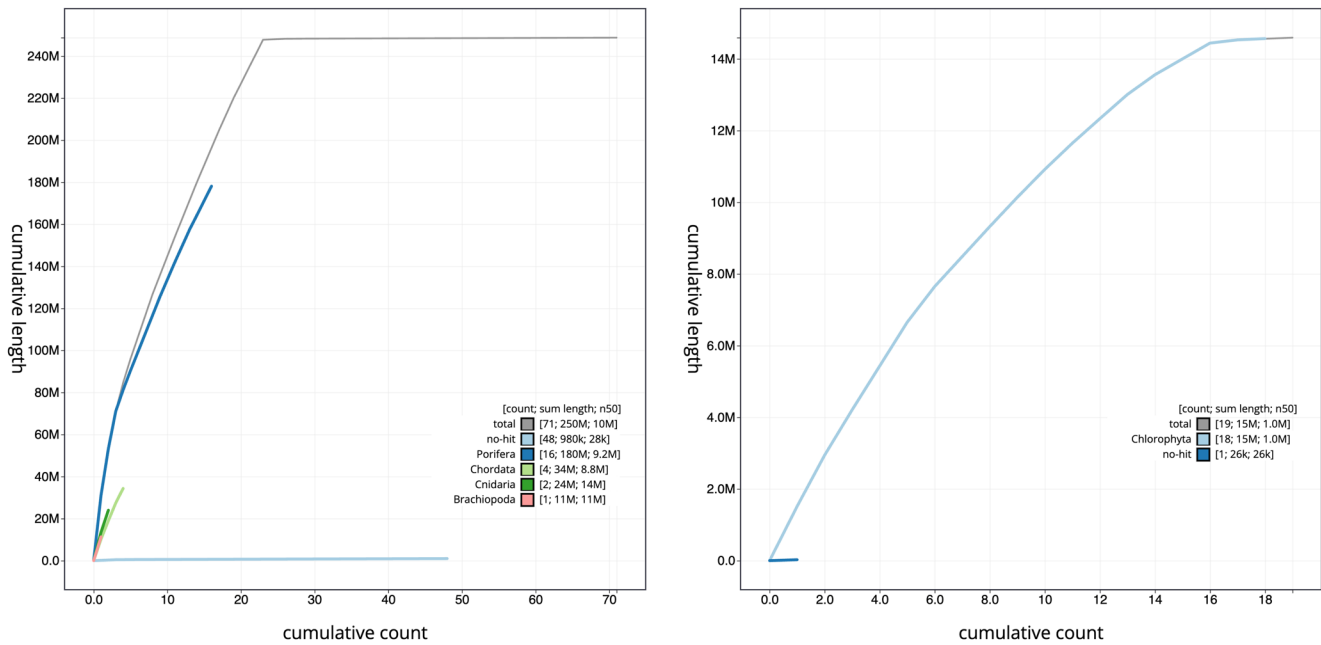


Table 2. Chromosomal pseudomolecules in the genome assembly of *Spongilla lacustris*, odSpoLacu1.

INSDC accession	Chromosome	Length (Mb)	GC%
OX442415.1	1	31.14	43.0
OX442416.1	2	22.15	42.5
OX442417.1	3	17.78	43.0
OX442418.1	4	13.56	42.5
OX442419.1	5	11.34	42.5
OX442420.1	6	10.42	42.5
OX442421.1	7	10.12	44.0
OX442422.1	8	10.27	42.5
OX442423.1	9	9.18	42.5
OX442424.1	10		

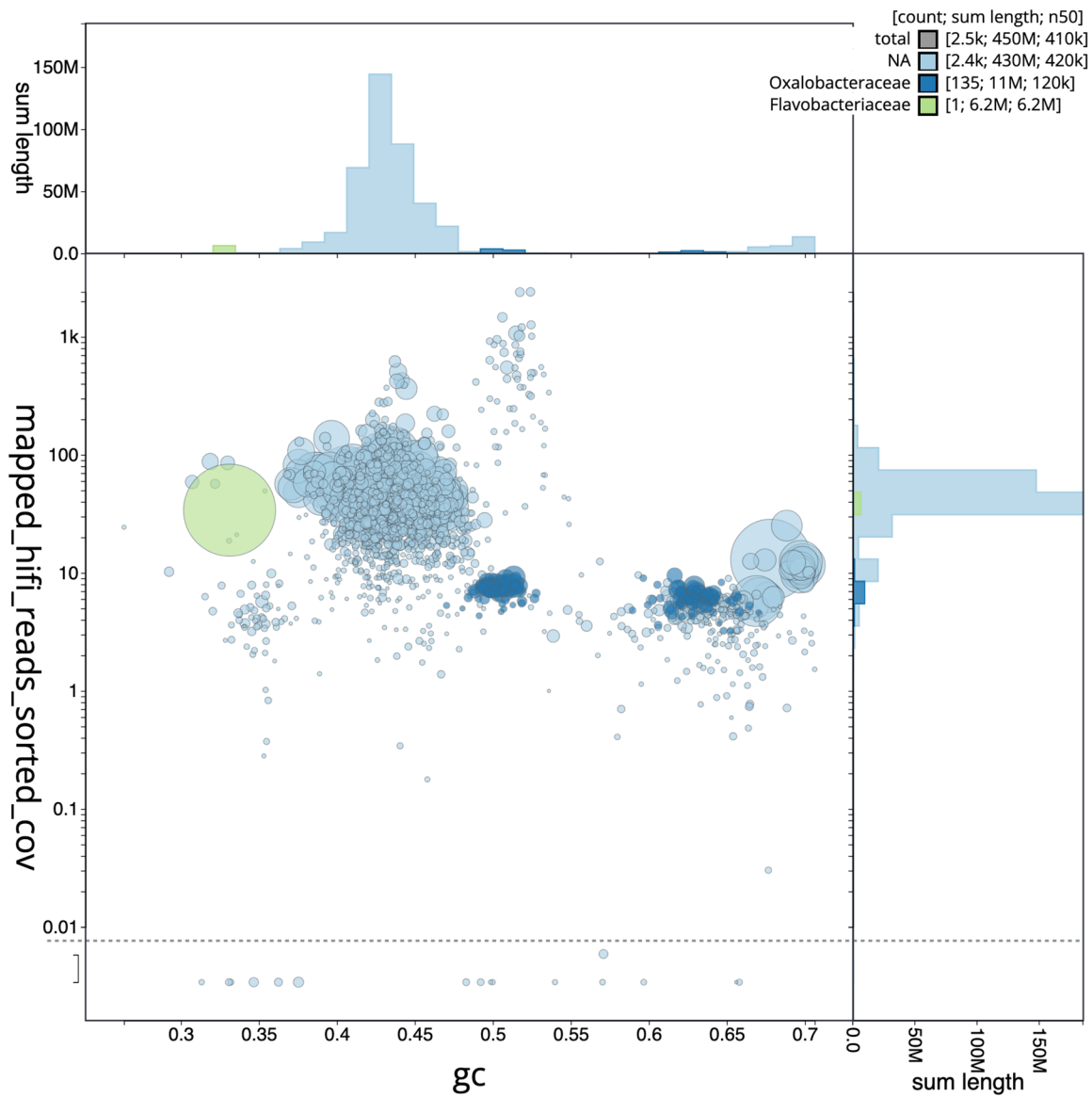


Figure 6. Blob plot of base coverage in mapped against GC proportion for sequences in the *Spongilla lacustris* metagenome. Binned contigs are coloured by family. Circles are sized in proportion to

Taxonomic verification

Molecular markers obtained from the assembly were used to reconstruct the phylogenetic position of the sample. For this, a comprehensive dataset of all published freshwater sponge ITS1-5.8S-ITS2 sequences was generated ($n = 358$) using MAFFT (Katoh & Standley, 2013), including all 29 specimens currently published as *Spongilla lacustris* from its wide range of its Holarctic distribution. Currently, ITS is regarded as most suitable marker in Spongillida molecular taxonomy (Erpenbeck et al., 2019). Phylogenetic Analysis with RAXML (Stamatakis, 2014) recovered the specimen nested among all other samples currently recognised as *S. lacustris* with 97% bootstrap support.

Evaluation of the final assembly

A Hi-C map for the final host and eukaryote cobiont assemblies were produced using bwa-mem2 (Vasimuddin et al., 2019) in the Cooler file format (Abdennur & Mirny, 2020). The MerquryFK tool (Rhie et al., 2020), run within a Singularity container (Kurtzer et al., 2017), was used to evaluate k -mer completeness and assembly quality for the primary and alternate

haplotypes, using the k -

Software tool	Version	Source
PROKKA	1.14.5	https://github.com/vdeja/prokka
purge_dups	1.2.3	https://github.com/dfguan/purge_dups
RAXML	8	https://github.com/amkozlov/raxml-ng
TreeVal	1.0.0	https://github.com/sanger-tol/treeval
YaHS	1.1a.2	https://github.com/c-zhou/yahs

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- Ethical review of provenance and sourcing of the material
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Open Peer Review

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expertise to confirm that it is of an acceptable scientific standard.

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The article provides a well-structured and informative background on the sponge species

Competing Interests: No competing interests were disclosed.

Reviewer Expertise: Sponge symbiosis, marine microbiology

I confirm that I have read this submission and believe that I have an appropriate level of expertise to confirm that it is of an acceptable scientific standard.
