Data Article

Genome sequence data of the antagonistic soil-borne yeast *Cyberlindnera sargentensis* (SHA 17.2)

Maria Paula Rueda-Mejia, Lukas Nägeli, Stefanie Lutz, Raúl A. Ortiz-Merino, Daniel Frei, Jürg E. Frey, Kenneth H. Wolfe, Christian H. Ahrens, Florian M. Freimoser

ABSTRACT

*Cyberlindnera sargentensis* strain SHA 17.2, isolated from a Swiss soil sample, exhibited strong antagonistic activity against several plant pathogenic fungi *in vitro* and was highly competitive against other yeasts in soil. As a basis for identifying the mechanisms underlying its strong antagonistic activity, we have sequenced the genome of *C. sargentensis* (SHA 17.2) by long- and short read sequencing, *de novo* assembled them into seven contigs/chromosomes and a mitogenome (total genome size 11.4 Mbp), and annotated 5455 genes. This high-quality genome is the reference for transcriptome and proteome analyses aiming at elucidating the mode of action of *C. sargentensis* against fungal plant pathogens. It will thus serve as a resource for identifying potential biocontrol genes and performing comparative genomics analyses of yeast genomes.
Specifications Table

| Subject                          | Agricultural Microbiology |
|---------------------------------|---------------------------|
| Specific subject area           | Genome analysis of a yeast that strongly antagonises fungal plant pathogens. |
| Type of data                    | High-quality draft genome sequence data, genome annotation, table and figure |
| How data were acquired          | Genomic DNA sequencing by Oxford Nanopore Technologies (ONT), Illumina MiSeq, and PacBio platforms, de novo assembly |
| Data format                     | Raw data: annotated draft genome assembly |
| Parameters for data collection  | Genomic DNA was extracted from a pure culture of *C. sargentensis* (SHA 17.2) using a phenol/chloroform protocol. |
| Description of data collection  | **Sequencing**: Oxford Nanopore Technologies (ONT), Illumina MiSeq, PacBio **Assembly**: filtering using length cut-offs, de novo assembly of PacBio reads, scaffolding with long ONT reads, reference-based assembly of the mitogenome. **Annotation**: Yeast Genome Annotation Pipeline (YGAP) and KEGG Orthologs assignment with KofaKOALA. |
| Data source location            | Cyberlindnera sargentensis SHA 17.2 was isolated from a fallow farmland soil sample collected near Wädenswil (47.223140 °N, 8.676699 °E, 470 m.a.s.l.), Switzerland. The strain is available at the Culture Collection of Switzerland under CCOS1011. |
| Data accessibility              | The assembled genome is deposited at NCBI’s Genbank under the BioProject PRJNA763105 and the accession numbers CP083464-CP083471 (https://www.ncbi.nlm.nih.gov/bioproject/?term=PRJNA763105). Additional data (PacBio and ONT long read data; Illumina miSeq short read data; genome annotation) is available at https://dataverse.harvard.edu/dataverse/Csar_genome. |
| Related research article        | Hilber-Bodmer, M., Schmid, M., Ahrens, C.H., Freimoser, F.M., 2017. Competition assays and physiological experiments of soil and phyllosphere yeasts identify *Candida subhashii* as a novel antagonist of filamentous fungi. BMC Microbiol. 17, 4. 10.1186/s12866-016-0908-z |

Value of the Data

- The genome of *C. sargentensis* (SHA 17.2; 7 contigs/chromosomes plus mitogenome) is the basis for identifying the biocontrol mode of action of this strongly antagonistic yeast.
- The annotated genome sequence released here can be used by biologists, microbiologists or mycologists who study fundamental aspects of microbial interactions or who are interested in developing new and improved biocontrol applications. Bioinformaticians and genome biologists may include the genome in comparative analyses and evolutionary studies.
- The high-quality genome of *C. sargentensis* (SHA 17.2) presented here is a reference for functional genomics studies and represents the basis for potential biocontrol genes and similarly active biocontrol strains through genome mining.

1. Data Description

*Cyberlindnera sargentensis* (SHA 17.2; CCoS1011) was isolated from an agricultural soil sample collected near Wädenswil (47.223140 °N, 8.676699 °E, 470 m.a.s.l.) in Switzerland. The strain was identified based on the ITS sequence as the species hypothesis SH1545207.08FU, which is currently labelled as *Cyberlindnera sargentensis* (Wick. & Kurtzman) Minter [1–3]. The isolate was
Table 1
Overview of the final, nearly complete C. sargentensis (SHA 17.2) de novo genome assembly.

| Contigs | Chromosomes | Scaffolds |
|---------|-------------|-----------|
|         | I           | II        | III       | IV        | V         | VI        | VII       | Mitogenome |
| Length [bp]: | 2,886,691 | 2,560,583 | 1,739,817 | 1,341,035 | 1,204,786 | 1,140,646 | 438,574   | 66,400     |
| PacBio > 5 kb: |            |           |           |           |           |           |           |            |
| Coverage Mapped | 53x | 54x | 58x | 63x | 64x | 69x | 64x | 1418x |
| ONT > 20 kb: |            |           |           |           |           |           |           |            |
| Coverage Mapped | 4x | 5x | 5x | 7x | 6x | 8x | 8x | 298x |
| Illumina 2 x 300 bp: |            |           |           |           |           |           |           |            |
| Coverage Mapped | 65x | 67x | 74x | 79x | 82x | 97x | 105x | 64x |
| No. of telomere patterns 5': | 20 | 18 | 24 | 22 | 21 | 0 | 18 |          |
| No. of telomere patterns 3': | 48 | 40 | 34 | 26 | 65 | 32 | 0 | Not annotated |
| No. of genes | 1403 | 1254 | 841 | 650 | 560 | 542 | 205 |          |
| No. of tRNAs | 49 | 44 | 14 | 16 | 22 | 21 | 1 |          |

Comments:
- I, II, IV, and V: Complete
- III: Complete apart from 10 kb of scaffolded Ns at 670 kb
- Mitogenome: Complete, circular
- VI: First 10 kb consist of collapsed rRNA operons. Two copies are present. The coverage is, however, ~20x higher. Thus, there should be ~40 copies, which can only be resolved using very long reads.
- VII: Scaffolds VI and VII might be on the same chromosome since the telomeres are missing at one end, and thus, are not complete. They also have a very similar coverage.

one of the most strongly antagonistic yeasts against a range of saprophytic and plant pathogenic filamentous fungi (e.g., Botrytis, Fusarium, and Monilinia strains) and was also highly competitive against other yeasts in soil [2,4]. Cybelindnhera sargentensis (SHA 17.2) has thus been selected as a promising yeast for potential biocontrol applications and for further characterising the mechanisms responsible for the strong biocontrol phenotype.

The initial de novo assembly of the C. sargentensis (SHA 17.2) genome consisted of 13 contigs, which, after ONT scaffolding, extensive polishing and manual curation, were reduced to a total of seven chromosomes and one mitogenome (Table 1). In order to correctly assemble the mitogenome, a reference-based approach was followed (see Methods), which resulted in the assembly of the 66 kb circular mitogenome. No additional plasmids could be identified. The total genome size was 11’378’532 bp. Variant calling detected only 55 and 12 variants in the Illumina and PacBio data, respectively, which suggested that C. sargentensis SHA 17.2 is a haploid strain. This was confirmed by the presence of only the MATa1 and MATa2 genes (CYS0D04350 and CYS0D04340, respectively) and the flanking genes SLA2 (CYS0D04360) and VPS75 (CYS0D04330), which often adjoin yeast MAT loci [5,6]. C. sargentensis is thus a heterothallic species and the strain SHA 17.2 a haploid of the mating type a. Overall, the small
number of contigs and high coverage of the genome assembly (see Table 1) suggest the C. sargentensis SHA 17.2 genome to be of high quality and completeness.

The C. sargentensis nuclear genome contained 5455 protein coding genes and 167 tRNA genes. The mitochondrial genome was not annotated. Of all protein coding genes, 5019 sequences were annotated with at least one KEGG orthology identifier (KO identifier, K number). Overall, 3,157 K numbers with a score above the predefined thresholds for individual KOs were assigned to 3044 predicted C. sargentensis genes. Many KEGG pathway modules, functional units of gene sets in metabolic pathways, were complete or missed only few blocks as indicated by the KEGG Mapper Reconstruct tool [7] (Fig. 1). Based on the KofamKOALA KEGG Orthology analysis of the annotated genome, only one secondary metabolite biosynthesis gene (CYSA_0A07570; K06998, similar to a trans-2,3-dihydro-3-hydroxyanthranilate isomerase [EC:5.3.3.17]) was identified. However, the fungal antiSMASH v.6.0 online tool [8] identified two potential secondary metabolite clusters. The first represented a NRPS-like cluster predicted to consist of 15 genes that was localised on scaffold 1 (CYSA_0A11890-CYSA_0A12070). Furthermore, a predicted terpene cluster with seven genes was identified on scaffold 5 (CYSA_0E04890-CYSA_0E04950). Since antiSMASH uses different principles to predict genes, the annotations of the predicted secondary metabolite cluster genes were not identical to those from YGAP. Specific transcriptome and proteome analyses that are enabled by the C. sargentensis SHA 17.2 reference genome will help identifying a set of potential biocontrol genes by the strategy recently used for Aureobasidium pullulans [9].

2. Experimental Design, Materials and Methods

Genomic DNA was extracted using a phenol/chloroform extraction protocol. Oxford Nanopore Technologies (ONT) sequencing was carried out in-house. The ONT library was prepared using a 1D2 Sequencing Kit (SQK-LSK308) and sequenced on a FLO-MIN107 (R9.5) flow cell (all from Oxford Nanopore Technologies, Oxford, UK). One 2 × 300 bp Illumina paired end library was prepared in-house using the Nextera XT DNA kit and sequenced on a MiSeq platform (all from Illumina, Inc., San Diego, CA, USA). PacBio sequencing was carried out at the Functional Genomics Centre Zurich (FGCZ) on a Sequel machine (1 SMRT cell shared between three strains)
(PacBio, Menlo Park, CA, USA). Size selection was performed using the BluePippin system (Labgene Scientific, Châtel-St-Denis, Switzerland).

PacBio and ONT subreads were filtered with Filtlong (v0.2.0) using a length cut-off of 5 kb and 20 kb, respectively. The Illumina reads were filtered and trimmed using trimmomatic (v0.39; parameters: phred 33, “LEADING:3 TRAILING:3 SLIDINGWINDOW:4:15 MINLEN:36”, only keep paired reads) [10]. The filtered PacBio reads were assembled using Flye (v2.4; default parameters, except: estimated genome size of 11 Mb) [11], an assembly algorithm capable of resolving long, nearly identical repeat sequences [12]. Three short contigs were submitted to BLAT [13] and subsequently removed since they appeared spurious. The remaining 10 contigs were polished with the PacBio reads using 3 Arrow runs. The polished contigs were further scaffolded using the longer ONT reads (> 20 kb) and LRScaf (v1.1.6). To correctly assemble the mitogenome, the mitogenome sequences of three Cyberlindnera strains (NC_022167.1, NC_022163.1, KC993181.1) were downloaded from NCBI and PacBio reads were individually mapped to the three references using minimap2 (set parameters: -a, -x map-pb). Mapping reads were filtered from the bam file using samtools (-F 4) and extracted into a fastq file using bam2fastq (v1.1.0). The reads were filtered by length (> 10 kb) and randomly subsampled (500 sequences) using awk to achieve a suitable coverage. The reads were assembled using Flye in plasmid mode (v2.4; default parameters, except: estimated genome size of 50 kb, –plasmid) [11]. The circularity and completeness of the mitogenome were confirmed by mapping the PacBio reads to the start-aligned contig using miniasm (set parameters: -a, -x map-pb) and visual inspection in the Integrative Genomics Viewer (IGV) [14]. All contigs were polished using the PacBio reads and 8 Arrow runs. The contigs were further polished using the Illumina reads and 3 Freebayes (v1.2.0) [15] runs to correct potential small errors (e.g., homopolymer errors). The PacBio (> 5 kb), ONT (> 20 kb) and Illumina reads were mapped to the polished contigs using miniasm for PacBio (-x map-pb) and ONT (-x map-ont) and bwa for Illumina to verify the completeness and contiguity of the assembly by visual inspection in the IGV. PlasmidSpades [16] was run on the Illumina data in order to detect smaller plasmids. The mean telomere lengths (pattern “TGTGGTGCTGGA”) could not be calculated using the Illumina reads and computel (v1.2) [17]. The number of telomere patterns at both ends of each contig was thus counted manually (see Table 1). The ploidy level of the genome was estimated with the Illumina data by using PloidyNGS (v3.1.2) [18] and nQuire [19]. Variants were called using the Illumina data and Freebayes (v1.2.0; parameter: -c 5 (minimum count of observations supporting an alternate allele)) [15]; as well as the PacBio data and longshot (v0.3.3) [20]. The variants were filtered using vcffilter and a quality cut-off of 20 (parameter: -f “QUAL > 20”).

The C. sargentensis (SHA 17.2) genome was annotated using the Yeast Genome Annotation Pipeline (YGAP) [21]. Predictions were assessed for errors (i.e., internal stop codons, no ATG start codon) and manually corrected (indicated by the suffix “ed” in gene names). KEGG Orthologs (KOs; K numbers) were assigned to the predicted proteins by KofamKOALA [22]. The KEGG Mapper Reconstruct tool was used to assign the KOs to pathway modules [7].

Declaration of Competing Interest

The authors declare that they have no known competing financial interests or personal relationships, which have or could be perceived to have influenced the work reported in this article.

CRediT Author Statement

Maria Paula Rueda-Mejía: Investigation, Resources; Lukas Nägeli: Investigation, Resources; Stefanie Lutz: Software, Formal analysis; Raúl A. Ortiz-Merino: Software, Data curation, Formal analysis; Daniel Frei: Investigation, Resources; Jürg E. Frey: Resources, Supervision; Kenneth H. Wolfe: Software, Data curation, Supervision; Christian H. Ahrens: Conceptualization, Software, Supervision; Florian M. Freimoser: Conceptualization, Writing – review & editing, Supervision.
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