



Complete Genome Sequence of *Micrococcus luteus* Strain CW.Ay, Isolated from Indoor Air in a Hong Kong School

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ABSTRACT *Micrococcus luteus* strain CW.Ay was isolated from indoor air in Hong Kong. The complete genome (2,543,764 bp; GC content, 72.93%) was established by hybrid assembly and comprised a linear plasmid and a single chromosome featuring many genes to account for its broad distribution in very diverse habitats.

Micrococcus luteus (formerly *Micrococcus lysodeikticus*) is a Gram-positive, nonmotile, obligate aerobe found in a remarkable range of habitats, including soil (1, 2), seawater (3, 4), freshwater (5, 6), and surfaces such as clothing and human skin (7, 8). It is also airborne in dust and bioaerosols and has been recovered from samples of indoor air (9, 10) and urban air (11). *Micrococcus* spp. even comprise a major proportion of bacteria recovered from the lower stratosphere (12). Given its mobility and the variety of conditions *M. luteus* may encounter, the features encoded by its small genome (~2.5 Mbp) enable impressive versatility and resilience.

CW.Ay was isolated from indoor air in a school classroom in Cyberport, Hong Kong, using the IUL Spin Air Basic sampler passing 100 L/min onto the surface of Luria agar for 5 min. After incubation for 48 h at 27°C, selected yellow colonies were passaged 10 times on Luria agar. A single colony was incubated in Luria broth for 24 h before DNA extraction using a PureLink Genomic DNA Mini Kit (Invitrogen). Paired-end short-read sequencing libraries were prepared using the Nextera XT DNA library preparation kit and sequenced via the Illumina MiSeq platform using v3 chemistry (2 × 300 bp). Adapter sequences were removed using Trimmomatic v0.32 (13) and reads were quality filtered and trimmed, producing 703,669 read pairs, with an average length of 278 bp (~196 Mbp). Long-read libraries, which were prepared from the same extracted DNA using the rapid barcoding kit SQK-RBK004, were sequenced using an Oxford Nanopore Technologies SpotON flow cell (vR9), MinION sequencer, and MinKNOW v3.1.8 software, with base calling by Guppy v2.1.3. The final long-read data set, trimmed by Porechop v0.2.4 (14, 15), totaled 182,541 reads (2.21 Gbp), with a mean length of 12,121 bp (N_{50} , 20,668 bp). Default parameters were used for all software unless otherwise specified.

Assembly of short reads by Newbler v2.7 (Roche Diagnostics) suggested a draft genome of ~2.5 Mbp, based on 411 contigs (mean length, 6,202 bp). However, Unicycler v0.4.3 (16) combined the Illumina and MinION data sets to render a circular chromosome of 2,449,847 bp and a linear plasmid of 93,917 bp (mean coverage, 194×), which were submitted to NCBI PGAP v5.0 (17) and PATRIC (18) for annotation.

Mash/MinHash using PATRIC (19) found the CW.Ay chromosome and plasmid to be close to *Micrococcus luteus* strain SA211 (GenBank accession number [CP033200](#)) and *Micrococcus* sp. strain A7 plasmid pLMA7 (GenBank accession number [KJ599675.1](#)), respectively, with average nucleotide identities of 97.11% and 97.09%, respectively (20).

Table 1 lists a selection of CW.Ay genes directed toward heavy metal resistance. In antimicrobial susceptibility tests (discs from Liofilchem), CW.Ay exhibited resistance to ampicillin (10 μg), chloramphenicol (30 μg), colistin (10 μg), erythromycin (15 μg), and sulfanilamide (30 μg), with relevant genes being chromosomally encoded (21).

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TABLE 1 Heavy metal resistance genes in *Micrococcus luteus* CW.Ay

Gene(s) ^a	Protein(s)	Locus ^b	Reference(s)
<i>arsC</i>	Arsenate reductase (EC 1.20.4.4), thioredoxin coupled	10380	22
<i>arsC1-acr3-arsR-arsC-arsC</i>	Arsenic resistance operon, including arsenate-mycotoxin transferase (EC 2.8.4.2) and arsenate efflux Acr3	05330–05350	22
<i>trxB-trxA</i>	Thioredoxin reductase (EC 1.8.1.9)-thioredoxin (similar to <i>arsT-arsX</i> in an arsenic-resistant <i>Microbacterium</i>)	11190–11195	22, 23
<i>arsO</i>	Flavin-dependent monooxygenase ArsO	08970	24
<i>czcD</i>	Cobalt/zinc/cadmium resistance protein	00780, 02990, 10120, 03020	25
<i>csr-copZ, copZ</i>	Copper(I) chaperone CopZ	10385–10390, 06440	26
<i>copCD</i>	Periplasmic copper-binding proteins	09335–09350	27, 28
<i>merA, merR, merB</i>	Hg ²⁺ reductase, organomercury lyase	10085–10100, 03005–03010	29
<i>cadD</i>	Cadmium resistance transporter	02990, 05315, 10110	30
<i>cadA</i>	Lead-, cadmium-, zinc-, and mercury-transporting ATPase (EC 7.2.2.21)	10150, 10175, 10395, 06435	31

^a Gene assignments by NCBI PGAP v5.0 and UniProt.

^b NCBI locus prefix K7G68_.

Data availability. The complete genome sequence and raw sequence data for *Micrococcus luteus* CW.Ay are available through NCBI under BioProject accession number [PRJNA758605](https://www.ncbi.nlm.nih.gov/bioproject/PRJNA758605), with GenBank accession numbers [CP082331](https://www.ncbi.nlm.nih.gov/genbank/CP082331) (chromosome) and [CP082332](https://www.ncbi.nlm.nih.gov/genbank/CP082332) (plasmid) and SRA accession numbers [SRX11980019](https://www.ncbi.nlm.nih.gov/sra/SRX11980019) (MinION reads) and [SRX11980018](https://www.ncbi.nlm.nih.gov/sra/SRX11980018) (Illumina MiSeq reads).

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