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Draft genome sequences of four *Morganella morganii* strains isolated from Colombian colorectal cancer patient stool specimens

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ABSTRACT We report the draft genome sequences of four *Morganella morganii* strains isolated from the stools of four patients diagnosed with colorectal cancer (CRC) in Medellín, Colombia. These genomes represent an important addition to the limited number of genomes of *M. morganii* strains originating from CRC patients currently available.

KEYWORDS *Morganella morganii*, colorectal cancer

Morganella morganii is a Gram-negative, facultative anaerobic commensal bacterium of the human intestinal tract recognized as an important opportunistic pathogen (1) in a wide range of nosocomial and community-acquired infections (2–4). In addition, it has been shown that *M. morganii* is enriched in the gut microbiota of inflammatory bowel disease and colorectal cancer (CRC) patients and it has even been shown to produce a previously undescribed family of genotoxins, termed the indolimines, and causing increased intestinal permeability and exacerbated colon tumorigenesis in gnotobiotic mice (5). However, to the best of our knowledge, only one *M. morganii* strain isolated from CRC patient stool specimens has been sequenced so far (6); hence, additional genomes are needed to facilitate comparative genomic analyses and to elucidate the potential role of *M. morganii* in the development of CRC.

Strains were isolated in 2022 from the stools of four adult males diagnosed with CRC and hospitalized after colonoscopy in Medellín, Colombia. Real-time PCR based on the 16S rRNA gene was used to detect *M. morganii* from stool specimens (7). Positive specimens were plated onto MacConkey agar (Becton Dickinson, USA) and, following overnight incubation at 37°C, a maximum of ten lactose-negative (colorless) colonies per plate were randomly chosen and identified by biochemical methods (API 20E, BioMérieux, France). Definitive identification of the presumptive *M. morganii* colonies was based on 16S rRNA gene PCR and sequencing (8). According to NCBI BLASTN results, the best match accession numbers were MN807694 (strains IPS008 and IPS040), KM269029 (IPS012), and MN006020 (IPS030).

Morganella morganii strains from our laboratory stocks were overnight cultivated in tryptic soy agar (Becton Dickinson) at 37°C. Genomic DNA was extracted and purified using the NZY Tissue gDNA Isolation Kit (NZYTech, Portugal), according to the manufacturer's instructions. A DNA library was generated using the Illumina DNA Prep Kit (Illumina, USA), according to the manufacturer's instructions, and whole-genome sequencing (WGS) was performed with the Illumina NextSeq 500 platform (Illumina) using 300 cycles and generating 150 bp paired-end reads. The reads were trimmed and filtered according to quality criteria using FastP v0.23.2 and FastQC v0.11.9, respectively (9). The quality-filtered reads were assembled using Unicycler v0.4.8 (10) with *Morganella*

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TABLE 1 Whole-genome characteristics of the sequenced *Morganella morganii* strains[a]

	Morganella morganii strain			
	IPS008	**IPS012**	**IPS030**	**IPS040**
No. of reads	5,492,226	5,927,468	5,012,278	5,871,056
Depth of coverage	155×	170×	131×	160×
GC content (%)	51.00	51.14	51.14	50.93
Total length (bp)	3,830,508	3,848,985	3,910,626	3,912,298
Genome fraction (%)	81.06	86.07	85.66	81.31
Number of contigs	18	23	24	22
Contig N50	473,353	402,904	378,793	682,475
Contig L50	2	4	3	2
No. of predicted genes	3,669	3,705	3,744	3,795
No. of RNA genes	77	82	79	78
No. of pseudogenes	44	34	38	47
BioSample number	SAMN37692576	SAMN37692577	SAMN37692578	SAMN37692579

[a]All statistics are based on contigs of size ≥ 500 bp.

morganii strain AR_0057 as the reference genome (accession number NZ_CP027177.1). Contigs shorter than 200 bp were removed to ensure sequencing quality and to meet the requirements for uploading to the NCBI Genome Database. All software was used with default settings unless otherwise specified. Complete genome sequences were obtained for all four *M. morganii* strains and genomes were annotated using the NCBI Prokaryotic Genome Annotation Pipeline v6.6. Detailed information about WGS parameters, assembly, and genome characteristics for individual strains is shown in Table 1.

Approval of the study protocol was obtained from the Ethics Committee of the Medical Research Institute [Faculty of Medicine, University of Antioquia (Ref. 00613.05.2021)], and the Technical Research Committee of the Hospital Alma Máter de Antioquia (Ref. IN32-2021).

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DATA AVAILABILITY

This whole-genome shotgun project has been deposited at DDBJ/ENA/GenBank as BioProject PRJNA1024498 under the accession numbers JAWLLN000000000 (strain IPS008), JAWLLO000000000 (strain IPS012), JAWLLP000000000 (strain IPS030), and JAWLLQ000000000 (strain IPS040). The versions described in this paper are JAWLLN010000000, JAWLLO010000000, JAWLLP010000000, and JAWLLQ010000000, respectively. Corresponding SRA data were deposited under accession numbers SRR26288169, SRR26288168, SRR26288167, and SRR26288166.

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