Draft genome sequence of a prodigiosin-hyperproducing
*Serratia marcescens* strain isolated from Cairo, Egypt

Nora M. Elkenawy,1,* Noha H. Youssef,2 Ramy K. Aziz,3,4,5 Magdy A. Amin,3,† and Aymen S. Yassin3,4,*

1Drug Radiation Research Department, National Center for Radiation Research &Technology, 11787 Cairo, Egypt,
2Department of Microbiology and Molecular Genetics, Oklahoma State University, Stillwater, OK 74078-5061, USA,
3Department of Microbiology and Immunology, Faculty of Pharmacy, Cairo University, 11562 Cairo, Egypt,
4The Center for Genome and Microbiome Research, Cairo University, 11562 Cairo, Egypt, and
5Microbiology and Immunology Research Program, Children’s Cancer Hospital Egypt 57357, 11617 Cairo, Egypt

*Corresponding authors: Email: Nelkenawy@gmail.com (N.M.E.); aymen.yassin@pharma.cu.edu.eg (A.S.Y.)
†Professor Magdy A. Amin was deceased on November 30, 2019; all authors agree that he contributed to that manuscript with full authorship rights.

**Abstract**

*Serratia marcescens* is a Gram-negative bacterium with both environmental and host-associated strains. Pigmentation is reportedly inversely correlated with infection frequency, and prodigiosin is one of *Serratia* pigments that has medical and industrial applications. Here, we report the draft genome sequence of prodigiosin-hyperproducing *Serratia marcescens* strain N2, isolated from Cairo, Egypt. The sequence is assembled into 142 contigs, with a combined size of 5,570,793 bp. The assembled genome carries typical *S. marcescens* genes, with potential prodigiosin-biosynthesizing genes detected.

**Keywords:** *Serratia marcescens*; prodigiosin; bioinformatics; genome annotation; genome assembly

**Introduction**

*Serratia marcescens* is a Gram-negative rod-shaped bacterium, belonging to family *Enterobacteriaceae*. It has been isolated from various environmental and nosocomial sources. In the last decades, *S. marcescens* has been recognized as a significant opportunistic human pathogen, as it was found responsible for a variety of symptoms in hospitalized patients, including septicemia, meningitis, and infections of the urinary tract (Abreo and Altier 2019). Although some *S. marcescens* strains are associated with hospital infections, pigmented *S. marcescens* strains were shown to cause infections in a much lower frequency than nonpigmented strains. This observation implies that the infection risk is minimal during the mass production of pigment (Roy et al. 2014).

Prodigiosin is a red pigment produced as a secondary metabolite by *S. marcescens*, characterized by a distinctive tripyrrole structure, responsible for its reported multiple pharmacological effects as anti-cancer, anti-microbial, anti-oxidant, and immuno-suppressant, as well as its unique application as a natural dye for olefins and textiles (Lin et al. 2019). Factors such as temperature, pH, dissolved oxygen levels, light and medium composition influence the production of prodigiosin (Aruldass et al. 2014). Here, we report the genome sequencing of *S. marcescens* strain N2, which was isolated from a local hospital in Cairo, Egypt. This strain is capable of producing 870 unit/cell of prodigiosin after 6 days of incubation (Elkenawy et al. 2017).

**Materials and methods**

**DNA extraction**

Genomic DNA was extracted by the PrepMan® ultra sample preparation reagent (Applied Biosystems, USA). Phylogenetic identity was confirmed by 16S rRNA gene sequencing, performed by the MicroSeq® 500 identification protocol (Applied Biosystems, USA), as previously described (Fontana et al. 2005).

**Sequencing**

The genome of *S. marcescens* strain N2 was sequenced on an Illumina MiSeq platform at Novogene (Beijing, China), following the standard Illumina protocols. A 300 × 2 paired-end chemistry was used, with an average library insert size of 700 bp. The Nextera XT DNA library prep kit (Illumina, San Diego, CA, USA) was used for the preparation of sequencing libraries from extracted DNA, as per the manufacturer’s instructions.

**Preprocessing and assembly**

Reads were quality-filtered by Trimmomatic, version 0.36 (Bolger et al. 2014), with adaptor clipping option, a sliding window size of 4 and a sliding window minimum quality of 15. High-quality reads were assembled by three different tools: (1) IDBA assembler (v1.1.3) with minimum contig length of 2000 bp (Feng et al. 2012); (2) SPAdes assembler (v3.12.0), which is part of the Pathosystems Resource Integration Center (PATRIC) services (Antonopoulos et al. 2012); (3) IDBA-UD assembler. The assembled genome sequence is assembled into 142 contigs, with a combined size of 5,570,793 bp. The assembled genome carries typical *S. marcescens* genes, with potential prodigiosin-biosynthesizing genes detected.

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et al. 2019; Davis et al. 2020), with minimum contig length of 500 bp, and (3) Unicycler assembler (v0.4.8), within PATRIC services as well, with minimum contig length of 500 bp (Table 1).

**Genome annotation**

The assembled genome was annotated by PATRIC (version 3.6.9) annotation service (Antonopoulos et al. 2019; Davis et al. 2020), which uses the RASTtk algorithm (Aziz et al. 2008; Brettin et al. 2015).

**Results and discussion**

The sequencing yielded 13.3 Gb of paired-end reads, with an average read length of 150 bp.

All three genome assemblers produced high-quality contigs, ranging in number from 142 to 716, and an N50 from 41,216 to 238,944 (Table 1). Based on the comparison between the three assemblers, Unicycler assembly was further considered for downstream annotation and analysis steps. The 142 contigs had a combined size 5,570,793 bp with an N50 of 238,944 bp, an L50 of 8, and a G + C content of 59.05%.

Genome annotation resulted in 5615 coding sequences (CDS), 86 tRNAs, and 6 tRNA-encoding genes. The CDS included 1200 hypothetical proteins and 4415 proteins with functional assignments, of which 2064 proteins were assigned EC number, 1068 were assigned gene ontology (GO) terms, and 1471 proteins were assigned to known pathways. PATRIC assigned the proteins to 5024 genus-specific families (PLfams) and 5170 cross-genus families (FGfams). The assembled genome was also analyzed by NCBI prokaryotic genome annotation pipeline service (Tatusova et al. 2016), which is usually more conservative in gene calling and functional assignments. NCBI analysis predicted 5393 CDS, a combined size 5,570,793 bp with an N50 of 5024 bp, an L50 of 8, and a G + C content of 59.05%.

Finally, the use of PATRIC similar genome finder (Antonopoulos et al. 2019), which uses the Mash/MinHash algorithm (Ondov et al. 2016) predicted the closest genome neighbor to strain N2 to be S. marcescens strain ATCC 274 (NCBI accession number: AP021873). Further analyses of the genome sequence, coupled with high-throughput techniques such as random transposon mutagenesis (in vitro) and genome-wide metabolic reconstruction (in silico), will enable the identification of genes putatively involved in prodigiosin promotion and provide more insight into the biosynthesis and regulation of structurally diverse secondary metabolites.

**Data availability**

Raw reads are available under SRA accession SRX10696011. The whole-genome shotgun project has been deposited at DDBJ/ENA/GenBank under Bioproject ID PRJNAS25074, Biosample ID SAMN11041520, and WGS accession SPSG00000000. The version described in this paper is version SPSG02000000. The annotated genome the PATRIC database is deposited under genome number 615.1488.

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**Conflicts of interest**

The authors declare that there is no conflict of interest.

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