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Short Communication

Draft genome sequence and nomenclature adjustment of *Rhodococcus qingshengii* CS98, a cesium-accumulating strain isolated in Japan

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ABSTRACT

Strains within the *Rhodococcus* genus have the ability to endure a range of recalcitrant compounds and metabolise a variety of pollutants. As a result there is increasing interest in these robust prokaryotes for their applications in bioremediation of contaminated environments and bioconversion of industrial wastes. In this announcement we present the draft genome sequence of *R. qingshengii* CS98, a soil isolate from Japan with the demonstrated ability to accumulate both stable and radioactive caesium.

1. Introduction

The genus *Rhodococcus* are gram-positive, non-motile, aerobic members of the family Nocardiaceae [1]. *Rhodococci* have a high G+C content (up to 73 %), large genomes and linear plasmids have been identified in species such as *R. opacus*, *R. faceans* and *R. erythropolis* [1,2]. These bacteria are found distributed throughout soil, freshwater and marine habitats, and have been shown to produce a range of enzymes involved in biodegradation and bioconversion reactions [3]. Their ability to metabolise wastes such as those associated with oil production and pollution (petroleum hydrocarbons), mining sites and vehicle exhausts (polycyclic aromatic hydrocarbons) and those found in fire retardants and solvents (polychlorinated biphenyls) continues to increase their profile as viable candidates for bioremediation of a vast array of pollutants [3].

R. quingshengii strains are able to tolerate a large variety of temperatures and environments, from the anoxic floor of the Arctic Ocean to sandy vegetable fields in Jiangsu, China (J.-L. [4]; Jing-Liang [5]). *R. quingshengii* species have been demonstrated to degrade the widely-used mutagenic and teratogenic fungicide carbendazim (Jing-Liang [5]), toxic triphenylmethane dyes [6] and hydrocarbons - both under heavy-metal rich [7] and high-pressure conditions. Thus, this bacteria is well positioned as a strong candidate for bioremediation purposes.

R. qingshengii CS98 is a caesium-accumulating soil isolate from Japan, formerly referred to as *Rhodococcus erythropolis* CS98 [8]. In liquid culture, the organism has demonstrated the ability to remove over 90 % of caesium from surrounding media, and it has been demonstrated to accumulate both stable and radioactive (Cs-137) caesium [9]. *R. qingshengii* CS98 immobilised in an agarose gel matrix has proven effective at removal of radiocaesium from aqueous environments, suggesting the organism as a potential candidate for bioremediation of radioactive waste affected regions such as Fukushima, Japan [10].

2. Materials and methods

The bacterial strain was a kind gift from Dr. Noriko Tomioka (National Institute for Environmental Studies, Japan). The strain was cultured in broth and DNA was harvested using a Wizard® Genomic DNA Purification Kit. The *R. qingshengii* CS98 genome was sequenced using next-generation Illumina paired-end sequencing technology MrDNA, Shallowater, Texas. Genome assembly and annotation was completed using the Rapid Annotation using Subsystem Technology (RAST) annotation pipeline, and genome analysis undertaken in the SEED viewer (version 2.0) [11,12]. The complete genome sequence of *R. qingshengii* CS98 has been deposited at NCBI under the accession number LYXB00000000.

3. Results

The 6,712,239 bp genome exhibits a GC content of 62 %, and was assembled from 25 gene-encoding contigs ranging from 569 bp to

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2,021,467 bp. A total of 6,528 coding sequences were identified, and of these 2,275 (35 %) features were covered by sub-systems (2,172 non-hypothetical proteins, 103 hypothetical). Sixty-nine RNAs were identified, and the strain's closest neighbours identified were *R. erythropolis* PR4 (score = 528) and *R. erythropolis* SK121 (score = 518).

Sub-system feature counts revealed a range of genes involved in DNA repair, ion transport and metabolism. Notably, 139 features involved in stress-response were identified and 74 involved with repair of DNA. Eighty-nine membrane transport features were identified, 22 of these noted as cation transporters and an additional 14 features were involved in potassium metabolism. A large number of features responsible for metabolism of aromatic compounds (104) and sulphur metabolism (96) were also present.

A total of 438 tandem repeats were identified via Tandem Repeat Finder across 17 contigs [13]. Of these, 125 were on contig 19. Plasmid partitioning proteins *ParA* and *ParB* were present on contigs 19, 16 and 31, suggesting the presence of multiple plasmids. The Phage Search Tool (PHAST) identified 1 intact and 1 incomplete prophage region within the sequence [14], and 3 questionable CRISPRs (clustered regularly interspaced short palindromic repeats) were found on contigs 19, 11 and 5 [15],

Footnotes

This bacteria was originally identified as *R. erythropolis* CS98 in 1992. Average Nucleotide Identity (ANI) scores of the submitted organism revealed a higher identity with *R. quingshengii* (identified 2007; ANI 98.136 %) *and R. enclensis* (identified 2015; ANI 98.768 %) than *R. erythropolis (95.*554 %*)* at the time of analysis (2016). Thus the identification of this bacterium has been amended to *R. quingshengii* CS98.

Declaration of Competing Interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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Appendix A. Supplementary data

Supplementary material related to this article can be found, in the online version, at doi:10.1016/j.btre.2019.e00415.

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