Short Communication

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

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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. faeans 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. qingshengii 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. qingshengii 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 LYXB0000000.

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
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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