Members of the genus *Rhodococcus* possess a wide range of metabolic capabilities applicable for biodegradation of diverse environmental pollutants (1, 2) and for various biotransformations (3, 4). The strain *Rhodococcus erythropolis* CCM2595 (NCIB8147; JCM3132; ATCC 11048) was isolated from soil. Originally, it was classified as a strain of the species *Jensenia canicruria* (5). Later, it was reclassified into the species *Rhodococcus erythropolis* (6). *R. erythropolis* CCM2595 has been shown to utilize phenol, catechol, resorcinol, hydroxybenzoate, hydroquinone, p-chlorophenol, p-nitrophenol, pyrimidines, and sterols (7, 12). The functions of the predicted protein-coding genes were assigned by the PGAAP pipeline (http://www.ncbi.nlm.nih.gov/genome/annotation_prok/). The annotation results were combined and verified within Artemis (24). In total, 5,830 predicted coding regions (CDSs), 12 rRNAs, 53 tRNAs, 1 tmRNA, and 5 ncRNAs were predicted and annotated.

Based on our results, we anticipate that *R. erythropolis* strain CCM2595 will display rich and complex metabolic capabilities, far beyond the utilization of benzene derivatives or catechol metabolism originally associated with this strain (7, 12).

**Nucleotide sequence accession numbers.** The genome sequences were deposited at DDBJ/EMBL/GenBank under the accession numbers CP003761 (chromosome) and CP003762 (plasmid pRECF1).

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