

Genome sequence of *Paraburkholderia kururiensis*, an environmental bacterial that reveals a great potential for bioremediation.

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Environmental pollution has become one of the major issues of the 21st century. A possible cost-effective minimization of this problem is bioremediation, which either microorganism, plants (phytoremediation) or both can be applied to control a myriad of chemical contaminants in the environment. The type strain *Paraburkholderia kururiensis* KP23^T (JCM10599, formerly *Burkholderia kururiensis* KP23^T) is a non-pathogenic environmental strain, isolated from an aquifer in Japan, showing promising bioremediation abilities. In this work, we have sequenced the whole genome of type strain *Paraburkholderia kururiensis* KP23^T. Extraction of the genomic DNA was performed with the Blood and Cell Culture DNA Maxi Kit from Qiagen. The sequencing method was Illumina 2x300 MiSeq in paired-end mode. The genome was assembled *de novo* using SPAdes v3.9.0, and the QUAST tool was used for the quality evaluation of this assembly. The novel genome sequence was subsequently compared to a previously published draft genome of strain M130, isolated from soil in Brazil. To perform a comparative analysis, both genomes were automatically annotated using PROKKA software. The genome sizes of KP23^T and M130 are 7.5 and 7.1Mb with GC content of 64.8% and 65.0%, respectively. The annotation identified 6596 and 6,266 coding sequences, respectively, in which an average of 90% proteins were assigned to COG categories. The two genomes contained 5,419 orthologous genes, which represent an average 84% of the total proteins encoding within these *P. kururiensis* strains. This large percentage indicates a surprisingly small variability among the strains, considering the geographical origins (KP23^T strain was isolated from Japan and M130 from Brazil). Also, the 16S ribosomal gene similarity between them is 100%. However, the comparative analysis revealed 981 unique genes to KP23^T strain, of which 67% were annotated as hypothetical proteins. The other genes are related to signal transduction, intracellular trafficking and secretion and secondary metabolites and degradation of aromatic compounds, including toluene, biphenyl, benzoate degradation and genes for other hydrocarbon-degrading enzymes, such as alkanesulfonate monooxygenase. These findings may provide significant support at unraveling the genes coding for enzymes that apply to several bioremediation strategies, alongside the large biotechnological potential of this bacterial species, more specifically the type strain KP23^T.

Keywords: Comparative Genomics; *Burkholderia*; *Paraburkholderia kururiensis*; Bioremediation

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