Bisphenol A (BPA), a synthetic chemical widely and abundantly used in the production of polycarbonates and epoxy resins in many consumer products, has aroused particular concerns due to its endocrine-disrupting effects and widespread human exposure (1). Partially removed BPA in treated wastewater also led to its ubiquitous distribution in the environment (2). Although microbial degradation has been shown to be important for BPA removal in the environment (3), little is known about the genetic mechanisms of BPA degradation in microorganisms.

To gain insight into the mechanisms involved in microbe-mediated BPA degradation, we determined the draft genome sequence of a novel BPA-degrading bacterium, *Sphingobium* sp. strain YL23, which was isolated from the sewage sludge of a full-scale domestic wastewater treatment plant in Fujian Province, China. The phylogenetic analysis based on 16S rRNA gene sequences indicated that YL23 was most closely related to two type strains, with 97.8% and 97% sequence identities, respectively. Further in-depth genomic analysis is needed to provide more information for elucidation of the genetic mechanism of BPA degradation, including genome organization and the evolution of the degradation pathway.

**Nucleotide sequence accession numbers.** This whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession number ASTG00000000. The version described in this paper is the first version, ASTG01000000. The version described in this paper is the first version, ASTG01000000.

**ACKNOWLEDGMENTS**

This work was supported by the Science and Technology Innovation and Collaboration Team Project of the Chinese Academy of Sciences, Technology Foundation for Selected Overseas Chinese Scholar of MOHRSS, China; the Hundred Talents Program of the Chinese Academy of Sciences, Science and Technology Planning Project of Xiamen, China (3502Z20102017, 3502Z20120012), and the CAS/SAFEA International Partnership Program for Creative Research Teams (KZCX2-YW-T08).

**REFERENCES**


