**Genome Sequence of *Sphingobium indicum* B90A, a Hexachlorocyclohexane-Degrading Bacterium**


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*Sphingobium indicum* B90A, an efficient degrader of hexachlorocyclohexane (HCH) isomers, was isolated in 1990 from sugarcane rhizosphere soil in Cuttack, India. Here we report the draft genome sequence of this bacterium, which has now become a model system for understanding the genetics, biochemistry, and physiology of HCH degradation.

**Sphingobium indicum** B90A was isolated from sugarcane rhizosphere soil in 1990 and became the first strain to degrade one of the most recalcitrant man-made compounds, β-hexachlorocyclohexane (β-HCH) (12). Since then, B90A has been the focus of many studies leading to novel discoveries, such as the association of *lin* genes with IS6100 (3, 7), enantioselective transformation of chiral ε-HCH by the *lin*A1 and *lin*A2 genes (15), the presence of efficient HCH dehydrochlorinase (4) and haloalkane dehalogenase systems (13), evolution of isomer-specific (α-, β-, γ-, δ-, and ε-HCH) degradation pathways (2, 6, 11), and potential application of B90A in HCH bioremediation (11).

The draft genome of *S. indicum* B90A was generated by using the Illumina Genome Analyzer platform. For this purpose, three paired-end libraries (2, 5, and 7 kb) were constructed, and ~2 Gb (35.2 × 10^10) paired-end reads; average length, 75 bp) of sequence data was generated. The sequencing data (88.3% of the total raw reads) were assembled into 149 contigs by using ABySS 1.2.7 assembler (14), set at a k-mer size of 41. The final assembly (N50 contigs, 54.5 kb) was validated based on the paired-end information. The draft genome was annotated using RAST version 4.0 (1) and the NCBI Prokaryotic Genomes Automatic Annotation Pipeline (PGAAP; http://www.ncbi.nlm.nih.gov/genomes/static/Pipeline.html).

The draft genome of B90A (4.08 Mb with a G + C content of 65%) with a coding density of ~88% contains a total of 3,919 protein coding sequences and 1,140 hypothetical proteins. A total of 54 tRNA genes encompassing all 20 amino acids and two rRNA operons (16S-23S-23S-5S and 16S-23S-5S) were identified by using tRNAscan-SE (8) and RNAmmer (5), respectively.

As reported earlier (6), all of the *lin* genes responsible for the degradation of HCH isomers were not integrated into a compact and consistently regulated operon but were scattered throughout the genome. IS6100 (7 copies), known for its active role in horizontal transfer of *lin* genes (3), and Ton-B-dependent receptor (COG1629), which mediates transport of iron siderophore complexes in Gram-negative bacteria (9), were detected in abundance, in the vicinity of the *lin* genes. Like *S. japonicum* UT26 (the HCH-degrading archetypal strain from which *lin* genes were first characterized and the genome was sequenced) (10), the B90A genome showed the presence of phenol- and pentachlorophenol-degrading gene clusters, but homogenitase and anthranilate degradation pathway genes were absent. The genome of B90A also showed two copies each of *lin*X, *lin*A, *lin*G, *lin*H, *lin*I, and *lin*J. Annotations by RAST revealed 392 subsystems with *S. japonicum* UT26 (score, 546), *Sphingomonas* sp. strain SKA58 (score, 530), *Sphingopyxis alaskensis* RB2256 (score, 492), and *Sphingomonas wittichii* RW1 (score, 443) as the closest neighbors of *S. indicum* B90A.

The availability of the genome sequence of *S. indicum* B90A coupled with metagenomic data from the HCH dumpsite (R. Lal, unpublished data) will act as an invaluable supplement to the ongoing research efforts toward understanding several unanswered questions associated with the degradation of HCH isomers and would thus aid in the development of *in situ* bioremediation technology in the future.

**Nucleotide sequence accession number.** The draft genome sequence has been deposited in GenBank under accession no. AJXQ00000000.

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**REFERENCES**


