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Draft Genome Sequence of *Sphingobium chinhatense* Strain IP26^T, Isolated from a Hexachlorocyclohexane Dumpsite

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***Sphingobium chinhatense* strain IP26^T is a conducive hexachlorocyclohexane (HCH) degrader isolated from a heavily contaminated (450 mg HCH/g soil) HCH dumpsite. IP26^T degrades α-, β-, γ-, and δ-HCH, which are highly persistent in the environment. Here we report the draft genome sequence (~5.8 Mbp) of this strain.**

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In order to study the evolution of hexachlorocyclohexane (HCH)-degrading phenotypes at intragenus level among sphingomonads, we have isolated several HCH-degrading and/or -tolerating genotypes, including *Sphingobium chinhatense* strain IP26^T from the HCH dumpsite (1) located at Chinhat, Lucknow (26°54′ N and 81°09′ E), India. Gas-liquid chromatography-based HCH isomer degradation analysis (time dependent) revealed that IP26^T is a faster degrader of HCH isomers than the prototype bacterium *Sphingobium indicum* strain B90A^T (2).

A draft genome sequence of *S. chinhatense* IP26^T was obtained by use of Illumina Genome Analyzer IIx and 454 GS FLX titanium platforms, which generated ~1.4 Gb (pair-end) and ~116 Mb (single-end) sequencing data with coverage of 131- and 20-fold, respectively. Raw data were assembled into contigs (n = 236, >500 bp) using the ABySS 1.3.3 assembler (3) set at a k-mer size of 61. The assembled genome had an N_{50} value of 142 kb and an average GC content of 64.1%. The draft genome was annotated using RAST version 4.0 (4) and NCBI Prokaryotic Genome Annotation Pipeline (PGAP) version 2.1 (http://www.ncbi.nlm.nih.gov/genomes/static/Pipeline.html), which identified 5,703 protein-coding genes and 10 pseudogenes. Eleven rRNA and 66 tRNA genes were also predicted using PGAP annotations. A contig of size 5,392 bp possessing similar coding sequences (CDS) to plasmid pUT2 (5,398 bp) of *S. japonicum* UT26 (5) was also identified. Whole-genome-based average nucleotide identity (ANI) (6) comparisons revealed that *Sphingobium indicum* B90A^T (97.98%), *Sphingobium japonicum* UT26S (97.79%), *Sphingobium chlorophenolicum* L-1 (90.55%), and *Sphingomonas* SKA58 (80.29%) are the closest phylogenetic neighbors of IP26^T.

The potential to metabolize HCH isomers and a wide range of aromatic hydrocarbons is predicted from the genome. For instance, HCH-degrading *lin* genes associated with IS*6100* elements were present in the genome assembly. IS*6100* elements (n = 19) were identified using ISFinder (7). A full-length (1 kb) IS*6100* element was observed with *linA*, *linB*, *linC*, and *linR* genes. In addition, a partial (~331 bp) IS*6100* element was also observed with *linF*, *linG*, *linH*, *linI*, and *linJ* genes. The presence of 30 transposases and 24 phage integrases indicates that the genome is subjected to ongoing genetic rearrangement. Furthermore, phenol/toluene and chlorophenol degradation pathways were observed in IP26^T. Unlike the genome of *S. indicum* B90A^T (2), the draft genome assembly of IP26^T was found to have a homogentisate degradation pathway. Genes encoding putative metal resistance/efflux proteins, including resistance proteins for lead, mercury, arsenic, copper, cobalt, cadmium, and zinc, were also identified.

Further analysis of this genome, coupled with the metagenomic data from the HCH dumpsite (8, 9), will be used to understand the possible mechanism of acquisition of *lin* genes and other catabolic genes in the sphingomonads, along with the highly diverse microbial community that has been reported from the HCH dumpsite (8, 9). In addition, sequencing and analysis of more HCH-degrading genotypes from the HCH dumpsite will augment the ongoing efforts to understand the pangenomic aspects of this widely distributed genus at the HCH dumpsite and will reveal the ambiguities that exist in the horizontal gene transfer (HGT) of *lin* genes and other catabolic genes involved in the biodegradation of aromatic compounds.

Nucleotide sequence accession numbers. The draft genome sequence of *S. chinhatense* IP26^T is available in GenBank database under accession number AUDA00000000. The version described in this paper is the first version, AUDA01000000.

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REFERENCES

1. **Dadhwal M, Jit S, Kumari H, Lal R.** 2009. *Sphingobium chinhatense* sp. nov., a hexachlorocyclohexane (HCH)-degrading bacterium isolated from an HCH dumpsite. Int. J. Syst. Evol. Microbiol. **59:**3140–3144. doi:10.1099/ijs.0.005553-0.
2. **Anand S, Sangwan N, Lata P, Kaur J, Dua A, Singh AK, Verma M, Kaur J, Khurana JP, Khurana P, Mathur S, Lal R.** 2012. Genome sequence of *Sphingobium indicum* B90A, a hexachlorocyclohexane-degrading bacterium. J. Bacteriol. **194:**4471–4472. doi:10.1128/JB.00901-12.
3. **Simpson JT, Wong K, Jackman SD, Schein JE, Jones SJ, Birol İ.** 2009. ABySS: a parallel assembler for short read sequence data. Genome Res. **19:**1117–1123. doi:10.1101/gr.089532.108.
4. **Aziz RK, Bartels D, Best AA, DeJongh M, Disz T, Edwards RA, Formsma K, Gerdes S, Glass EM, Kubal M, Meyer F, Olsen GJ, Olson R, Osterman AL, Overbeek RA, McNeil LK, Paarmann D, Paczian T, Parrello B, Pusch GD, Reich C, Stevens R, Vassieva O, Vonstein V, Wilke A, Zagnitko O.** 2008. The RAST server: rapid annotations using subsystems technology. BMC Genomics **9:**75. doi:10.1186/1471-2164-9-75.
5. **Nagata Y, Natsui S, Endo R, Ohtsubo Y, Ichikawa N, Ankai A, Oguchi A, Fukui S, Fujita N, Tsuda M.** 2011. Genomic organization and genomic structural rearrangements of *Sphingobium japonicum* UT26, an archetypal γ-hexachlorocyclohexane-degrading bacterium. Enzyme Microb. Technol. **49:**499–508. doi:10.1016/j.enzmictec.2011.10.005.
6. **Konstantinidis KT, Tiedje JM.** 2005. Towards a genome-based taxonomy for prokaryotes. J. Bacteriol. **187:**6258–6264. doi:10.1128/JB.187.18.6258-6264.2005.
7. **Siguier P, Perochon J, Lestrade L, Mahillon J, Chandler M.** 2006. ISfinder: the reference centre for bacterial insertion sequences. Nucleic Acids Res. **34:**D32–D36. doi:10.1093/nar/gkj014.
8. **Sangwan N, Lata P, Dwivedi V, Singh A, Niharika N, Kaur J, Anand S, Malhotra J, Jindal S, Nigam A, Lal D, Dua A, Saxena A, Garg N, Verma M, Kaur J, Mukherjee U, Gilbert JA, Dowd SE, Raman R, Khurana P, Khurana JP, Lal R.** 2012. Comparative metagenomic analysis of soil microbial communities across three hexachlorocyclohexane contamination levels. PLoS One **7:**e46219. doi:10.1371/journal.pone.0046219.
9. **Sangwan N, Verma H, Kumar R, Negi V, Lax S, Khurana P, Khurana JP, Gilbert JA, Lal R.** Reconstructing an ancestral genotype of two hexachlorocyclohexane degrading *Sphingobium* species using metagenomic sequence data. ISME J., in press.