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Genome analysis of *Sphingopyxis flava R11H*^{T}: An overview of genetic attributes

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A HCH tolerant strain, R11HT was isolated from the soil sample of HCH dumpsite located at Ummari village, Lucknow, Uttar Pradesh, India. On the basis of 16S rRNA gene similarity, the strain was identified as the member of genus *Sphingopyxis* with highest identity with *Sphingopyxis indica* DS15T (97.85%). In addition, three more strains were identified with similarity >97%. The pairwise DDH analysis revealed that the strain R11HT belongs to a separate species. Further biochemical and chemotaxonomic studies confirmed the novelty of the strain and thus designated as *Sphingopyxis flava* R11HT. Due to the HCH tolerance ability, strain R11HT was selected for genome sequencing using Illumina Hiseq technology. It has a genome size of 4.15 Mbp, with G+C content of 63.75% and 90.40% coding potential. The strain was found to code for 4185 protein coding sequences. The total number of RNA coded by the strain is equal to 58 with a single copy of 5S, 16S and 23S rRNA and 46 tRNAs. The pfam analysis revealed 3219 protein sequences engaged in variety of metabolic functions, dominated by amino acid transport and metabolism, energy production and conversion, lipid transport and metabolism, replication, transcription and translation. The strain was also found to harbor five biosynthetic gene clusters including terpene and ectoine. The KEGG pathway genes include degradation pathways for number of compounds including amino-benzoate, benzoate, bisphenol, caprolactlam, chloroalkene, chlorohexane but lin genes which are known for HCH degradation were not annotated in the genome. It will be interesting to further analyze the probable metabolic pathways of strain R11HT which helps the strain to withstand in such high concentration of HCH.

Recent Publications

- Verma H, Bajaj A, Kumar R, Kaur J, Anand S, Nayyar N, Puri A, Singh Y, Khurana JP, Lal R (2017) Genome organization of *Sphingobium indicum* B90A: an archetypal hexachlorocyclohexane (HCH) degrading genotype. Genome Biol Evol. DOI: 1093/gbe/evx133.
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Biography

Gauri Garg Dhingra is an Assistant Professor of Zoology at the University of Delhi, Kirori Mal College - Department of Zoology and has been involved in undergraduate teaching since past 13 years. She completed her PhD under supervision of Prof. Rup Lal, Department of Zoology in 2005 on Manipulations of Rifamycin Biosynthetic Gene Clusters in Amycolatopsis mediterranei. Presently she is working with Rup Lal's group focusing on metagenomic diversity of pesticide contaminated sites.

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