

# MICROBIOLOGY

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## Comparative genomic analysis reveals environment and habitat specific gene diversity within genus *Novosphingobium*

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The genus *Novosphingobium* is comprised of metabolically versatile bacteria within the family *sphingomonadaceae*. *Novosphingobium* species have been isolated from a wide range of ecological habitats and possess diverse physiological and biotechnological importance. In this study genomic attributes, phylogenetic relationships, the pan-genome and core genome content of 27 *Novosphingobium* strains were compared and analyzed. The study revealed a high level of variation in the genome size, coding potential and %GC content, suggesting the role of geographical location in shaping the genome of bacteria as they have different source of isolation. Interestingly, the phylogenetic analysis revealed that the impact of habitat on phylogeny was masked by overall genomic repertoire. The core genome and pan-genome analysis revealed the overall genomic trend of genus *Novosphingobium*. Thereafter, the strains were categorized based on their ecological habitats into four groups i.e., rhizosphere, contaminated soil, marine and freshwater. Out of 27 *Novosphingobium* strains, only 19 strains fall in this category. The habitat-based study revealed different modes of sulfur acquisition and metabolism across the four habitats with the presence of alkane sulfonate (ssuABCD) assimilation pathway in all the rhizospheric isolates. We also find that the genes/pathway for ectoine biosynthesis was present beyond the marine habitat, suggesting its relevance beyond the marine habitat. Further, the phage mediated acquisition appears to play a prominent role in adaptability of the members in their respective habitats. We also find that these *Novosphingobium* strains codes for numerous mono- and dioxygenases, responsible for their ability to metabolize several aromatic compounds. The current study provides the genetic basis for understanding their adaptability into their habitats and their vast potential to degrade a variety of aromatic compounds.

### Biography

Roshan Kumar has completed his PhD from University of Delhi, India. His work mostly comprised of comparative genomics, taxonomical studies of strains isolated from stressed niches such as hexachlorocyclohexane contaminated dumpsites. He has published more than 10 papers in reputed journals and has been serving as an Assistant Professor at the University of Delhi, India.

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