Draft Genome Sequence of *Novosphingobium nitrogenifigens* Y88T

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**Novosphingobium nitrogenifigens** was originally isolated from pulp and paper mill wastewater, a low-nitrogen, high-carbon environment. *N. nitrogenifigens* is the first known nitrogen-fixing, polyhydroxyalkanoate-accumulating sphingomonad, and we report the annotated draft genome sequence of the type strain Y88T here.

Sphingomonad bacteria are often found in high-carbon, low-nitrogen, environmentally degraded habitats and/or are capable of metabolizing various industrial pollutants as carbon sources (1, 5, 6, 9). Several of these species have also been found to produce polyhydroxyalkanoate (PHA) (1, 4, 6), which represents a class of polymers with properties comparable to those of petroleum-derived plastics (2). The potential of diazotrophic bacteria that can use waste-derived feedstocks to help lower the cost of PHA production is an active area of research (8). Sphingomonads can potentially serve as PHA production strains in nitrogen-poor waste stream substrates, based on their abilities to thrive in such environments.

*Novosphingobium nitrogenifigens* Y88T is a Gram-negative, obligate aerobe sphingomonad that was originally isolated from nickel-enriched pulp and paper mill wastewater (1). *N. nitrogenifigens* is capable of nitrogen fixation and production of poly-3-hydroxybutyrate (PHB). *N. nitrogenifigens* has also proven effective in the removal of Mn and Zn from model biorefinery effluent (A. Palumbo et al., submitted for publication). These metabolic properties led us to further explore the characteristics of this organism aided by its genome sequence.

The draft genome of *N. nitrogenifigens* Y88T (ICMP 16470T, DSM 19370T) was obtained via Roche 454 pyrosequencing (454 Life Sciences, Branford CT) combining 454 GS 20 and 454 GS FLX Titanium paired-end sequencing (1,151,296 quality reads). Using Newbler 2.3 (454 Life Sciences), these reads were assembled into 19 scaffolds comprising 77 contigs at 60-fold coverage, totaling 4.14 Mbp. G19 scaffolds comprising 77 contigs at 60-fold coverage, totaling 4.14 Mbp. G

1. **REFERENCES**


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