

Bacterial Strain of Thermodesulfobacteria

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Description

It has been proposed to divide members of class *Deltaproteobacteria* into four new strains, *Desulfobacterota*, *Myxococcota*, *Bdellovibrionota* and SAR324, and to classify *Thermodesulfobacteria* into a new strain, *Desulfobacterota*, along with some of the former members of *Deltaproteobacteria*. *Thermodesulfobacterium* is a Group II sulfate-reducing bacterium because it can be completely oxidized using acetate and other fatty acids. It also produces non-isoprenoid branched glycerol diether. Sulfated bacteria are classified into more than 20 genera and can be classified according to the type of substrate used. A convenient subdivision is the ability to use acetate as an electron source. Other Group II sulfate-reducing bacteria include *Desulfosarcina* and *Desulfobacter*.

The *Thermodesulfobacteria* commune expresses a unique type of catabolic sulfite reductase that is taxonomically different from the related genera or other hyperthermophilic sulfate reductases. Thermophilic, non-spore-forming, marine, sulfate-reducing bacteria, SL6T strains were isolated from deep-sea hydrothermal sulfides collected in the Guaymas basin. Gram-negative bacteria appeared as small, highly mobile rods, either individually or in pairs. The temperature range for growth was 50-80°C, with 75°C being optimal. The pH range for growth at 70°C was 6.36.8, with an optimal value of 6.5. The NaCl concentration range for growth was 555 g l (+1), with 30 g l (-1) being optimal. H₂ and CO₂ were the only substrates for growth and sulfate reduction.

However, growth was stimulated by some organic compounds. Sulfur, thiosulfate, sulfites, cystine, nitrates and fumarates were not used as electron acceptors. Pyruvate, lactate and malate did not support fermentative growth. Desulfovirdine was not detected. In addition, the R1Ha3 strain reduced nitrates and the JSP strain reduced sulfites. None of the strains were able to completely oxidize lactic acid to CO₂, and none of the strains contained desulfovirdine.

By the 16S rDNA sequence, the JSP strain was placed in the genus *Thermodesulfobacterium* and the R1Ha3 strain was placed in the genus *Thermomodesulfovibrio* DNA.

Based on DNA hybridization studies and morphological and physiologic differences from their closest relatives, the two new isolates were considered to be new species. The JSP strain is the R1Ha3 strain. A combination of coding potential prediction and similarity search was used to predict 2159 protein coding genes. Of these, 1458 genes with different generalizations and reliability were functionally assigned, but the function of the remaining 701 genes could not be predicted from the putative amino acid sequence. The characteristics and statistics of the genome are summarized. According to the membership of the *Thermodesulfobacteriaceae* strain, it shares more than half of the proteome with those of the closest relative with the sequenced genome. *Thermodesulfobacterium* commune. The molecular weight of the because it can be completely oxidized using acetate and other fatty acids. It also produces non-isoprenoid branched glycerol diether. Sulfated bacteria are classified into more than 20 genera and can be classified according to the type of substrate used.

A convenient subdivision is the ability to use acetate as an electron source. A new type of catabolic hydrogensulfite reductase, desulfofushidin, has been isolated from the non-spore-forming thermophilic sulfate-reducing microorganism, *Thermodesulfobacterium* commune. The molecular weight of the enzyme was estimated to be 167,000 by sedimentation equilibrium, and the protein was pure in both disk electrophoresis and ultracentrifugation.

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