Genome Sequence of the Halotolerant Marine Bacterium Myxococcus fulvus HW-1

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Myxococcus fulvus HW-1 (ATCC BAA-855) is a halotolerant marine myxobacterium. This strain exhibits complex social behaviors in the presence of low concentrations of seawater but adopts an asocial living pattern under oceanic conditions. The whole genome of M. fulvus HW-1 will enable us to further investigate the details of its evolution.

Myxobacteria are Gram-negative single-celled prokaryotes with complex social behaviors (14). Myxobacterial strains are commonly isolated from various terrestrial habitats and are thus regarded as soil-dwelling bacteria (3, 12), which are normally unable to grow with more than 1.0% salt concentration (13). However, some marine halophilic (4, 6, 7) and halotolerant (9) myxobacteria have recently been isolated. While the halophiles are phylogenetically distinct from soil-dwelling myxobacteria, the halotolerants are more closely related to their terrestrial relatives. The halotolerant myxobacteria exhibit complex social living patterns in the presence of low concentrations of saltwater, such as developing fruiting bodies and myxospores, in response to starvation on solid surfaces, similar to those exhibited by soil-dwelling myxobacteria, but they adopt a rather simple living pattern under oceanic conditions, for example, developing myxospores directly from vegetative cells without the formation of fruiting bodies (18). Further studies revealed that halotolerant strains enhance their S motility in high seawater concentrations (16), and salt tolerance is often closely associated with their social behaviors (10, 17). Even more, some horizontally transferred genes confer some advantages for their adaption to life in the ocean (11).

Myxococcus fulvus HW-1 (ATCC BAA-855) is a typical halotolerant strain, isolated from a coastal seawater sample (9). The strain is able to grow in medium containing a wide range of seawater concentrations, from 0% to 130% (corresponding salinity concentrations are 0% to 4.7%) (18). The whole genome of M. fulvus HW-1 was sequenced. The sequence data were obtained by a combination of the 454 method, with 23 paired-end libraries over 100 coverage depths. The Sanger method was employed for closing and validation of the complete genome. The genome of M. xanthus DK 1622 (5) was used as a reference. IslandViewer (8) identified 9 genomic islands in the genome. Compared to DK 1622, a global synteny with two large inversions is apparent. The overall average identity of the CDSs is 75.17% between the two genomes. Deep comparative genome analysis is under way. Sequencing of this model halotolerant Myxococcus enables us to get a full picture of the evolutionary trail recorded in the genome and further opens the way to understanding the molecular details of their two living patterns and oceanic adaptation evolution mechanisms.

Nucleotide sequence accession number. The whole-genome sequence was deposited in GenBank under accession number CP002830.

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REFERENCES


