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GENOME ANNOUNCEMENT

Genome Sequencing of Five *Shewanella baltica* Strains Recovered from the Oxic-Anoxic Interface of the Baltic Sea

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Here we describe five *Shewanella baltica* genomes recovered from the same sample, as well as 12 years apart from the same sampling station. These genomes expand the collection of previously sequenced *S. baltica* strains and represent a valuable resource for assessing the role of environmental settings on genome adaptation.

Five genomes were selected based on our observations from the four previously sequenced *Shewanella baltica* genomes and to cover the phylogenetic diversity among the 116 *S. baltica* strains in our collection (2, 3). The genomes are 5 to 5.4 Mb in size, show ~46% G+C and harbor between one to three plasmids. The genomes of OS117, BA175, and OS678 are closed, while those of OS183 and OS625 are at high-draft status (about 50 large contigs), with a single base call error rate comparable to that of a finished genome (1). The isolation conditions were described previously (3); we describe below the reasons for selecting each genome for sequencing.

Strains OS183 and BA175. Strains OS183 and BA175 belong to the same clade based on multilocus sequence analysis (MLSA) data and were isolated from the same depth and station (BY15, 120 m) 12 years apart (OS183 in 1986 and BA175 in 1998), providing an opportunity to assess genome evolution over tractable periods of time. Ninety-three percent of the total 3,985 single nucleotide polymorphisms (SNPs) detected between the two genomes are contained within six syntenic regions that have been apparently recombined with other, more divergent members of the *S. baltica* population, consistent with our previous findings of high intrapopulation recombination within the natural *S. baltica* population (2). Each genome carries about 100 genome-specific genes, which represent mainly hypothetical or mobile functions except for a block of approximately 12 distinct polysaccharide biosynthesis genes, which were likely acquired from *Vibrio* species.

Strains OS625 and OS117. Strain OS625 was isolated from the oxygenated zone just above the chemocline (80 m) and belongs to the OS195 MLSA clade dominated by strains isolated from deeper, low-oxygen to anoxic waters within the chemocline (2); conversely, OS117 belongs to the OS155 clade that is enriched in isolates recovered from above the chemocline and was isolated from the chemocline (130 m). Nonetheless, the genome-specific gene sets of these two genomes were not enriched in any obvious functions related to the redox potential or the physicochemical characteristics of the depth of isolation. These findings indicate that the redox-related, ecologically important genes may be hidden among the hypothetical genes or that most *S. baltica* strains differ in the regulation (not presence/absence) of their redox-related genes. More detailed studies are required to test these and alternative hypotheses such as vertical water mixing.

Strain OS678. Strain OS678 was isolated from the low-oxygen zone just above the chemocline (110 m) and belongs to the OS195 clade that is dominated by strains isolated from the chemocline, similarly to strain OS625 described above. Interestingly, the patterns of extensive homologous recombination observed previously between OS185 and OS195 (2) were also observed between OS185 and OS678, confirming that these two clades have been evolving sexually.

Nucleotide sequence accession numbers. The following genome sequences were deposited in GenBank: OS183 (NZ_AECY00000000, high-draft status), OS117 (CP002811.1, chromosome; CP002812.1, CP002813.1, and CP002814.1, plasmids), BA175 (CP002767.1, chromosome; CP002768.1 and CP002769.1, plasmids), OS678 (CP002383.1, chromosome; CP002384.1, plasmid), and OS625 (AGEX00000000).

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