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Genome Sequences of Eight Morphologically Diverse Alphaproteobacteria[∇]

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The *Alphaproteobacteria* comprise morphologically diverse bacteria, including many species of stalked bacteria. Here we announce the genome sequences of eight alphaproteobacteria, including the first genome sequences of species belonging to the genera *Asticcacaulis*, *Hirschia*, *Hyphomicrobium*, and *Rhodomicrobium*.

Prosthecae or stalks are found in a morphologically diverse group of Gram-negative bacteria belonging primarily to the class *Alphaproteobacteria*. The stalked *Alphaproteobacteria* typically have a characteristic dimorphic life cycle in which two dissimilar cell types are produced by asymmetric cell division (2, 4, 8–10, 17, 18). The swarmer progeny cells are motile and do not replicate DNA. The start of the new cell division cycle is coincident with the differentiation of the swarmer cell into a stalked cell. Stalks are true extensions of the cell body and are an integral part of the cell, bounded by both the cell membranes and the cell wall, and form a thin cylindrical extension of the cell surface layer (10). Stalks are essential for the reproduction of a subset of prosthecate bacteria, including *Rhodomicrobium* and *Hyphomicrobium*, which divide by budding, in which the daughter cell develops at and is later released from the tip of the stalk. The stalks of both budding and nonbudding prosthecate bacteria have been implicated in nutrient uptake and are likely to be particularly advantageous in oligotrophic habitats (5, 14–16, 18).

To facilitate an enhanced understanding of the function of stalks, the mechanism of budding, and regulation of dimorphic life cycles, the genomes of three nonbudding stalked bacteria, three budding stalked bacteria, and two closely related nonstalked bacteria were sequenced. The nonbudding stalked bacteria include *Brevundimonas subvibrioides*, *Asticcacaulis biprosthecum*, and *Asticcacaulis excentricus*. The budding stalked bacteria include *Hirschia baltica*, *Rhodomicrobium vannielii*, and *Hyphomicrobium denitrificans*. Finally, the nonstalked,

TABLE 1. Characteristics of genomes sequenced in this study

Organism	Reference	Genome analysis					GenBank accession no.
		Sequencing status[a]	Size (Mb)	No. of scaffolds	% GC	No. of CDS[b]	
Asticcacaulis biprosthecum C19	9	PD	5.30	6	60	4,712	NZ_ADUH00000000
Asticcacaulis excentricus CB48	10	F	2.59	4	59	2,330	Chromosome 1, NC_014816
			1.32		60	1,121	Chromosome 2, NC_014817
			0.24		59	172	pASTEX01 NC_014818
			0.16		57	140	pASTEX02 NC_014819
Brevundimonas diminuta ATCC 11568	13	PD	3.24	8	65	3,002	NZ_ADUI00000000
Brevundimonas subvibrioides ATCC 15264	1	F	3.45	1	68	3,327	NC_014375
Caulobacter segnis ATCC 21756	1	F	4.66	1	67	4,139	NC_014100
Hirschia baltica ATCC 49814	12	F	3.46	2	45	3119	Chromosome, NC_012982
			0.08		43	68	pHba101 NC_012983
Hyphomicrobium denitrificans ATCC 51888	11	F	3.64	1	60	3,512	NC_014313
Rhodomicrobium vannielii ATCC 17100	18	F	4.01	1	62	3,565	NC_014664

[a] F, finished; PD, permanent high-quality draft.
[b] Number of annotated protein coding sequences (CDS).

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nonbudding bacteria *Caulobacter segnis* and *Brevundimonas diminuta* were sequenced. Characteristics of the sequenced genomes are provided in Table 1.

Finished genomes were sequenced as part of the Department of Energy (DOE) Joint Genome Institute (JGI) Community Sequencing Program 2008 using a combination of Sanger, 454, and Illumina methods as described at the JGI website (http://www.jgi.doe.gov/sequencing/protocols/prots_production.html) and were annotated using the JGI-Oak Ridge National Laboratory annotation pipeline (7). Permanent draft genomes were sequenced by the Center for Genomics and Bioinformatics at Indiana University using standard 454 methods to obtain 17× coverage for *A. biprosthecum* and 58× coverage for *B. diminuta*. Permanent draft genomes were annotated using the Integrative Services for Genomic Analysis annotation pipeline (3). All genome annotations were loaded into the JGI Integrated Microbial Resource for analysis (6). Further analysis and comparisons of the genomes sequenced in this work are expected to provide insights into the generation of bacterial morphology, survival in oligotrophic environments, and the evolution of differing modes of bacterial cell growth.

Nucleotide sequence accession numbers. GenBank accession numbers for all of the chromosomes and plasmids sequenced in this study are shown in Table 1.

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