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Draft Genome Sequences of *Pseudomonas fluorescens* BS2 and *Pusillimonas noertemannii* BS8, Soil Bacteria That Cooperate To Degrade the Poly-γ-D-Glutamic Acid Anthrax Capsule

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A mixed culture of *Pseudomonas fluorescens* BS2 and *Pusillimonas noertemannii* BS8 degraded poly-γ-D-glutamic acid; when the 2 strains were cultured separately, no hydrolytic activity was apparent. Here we report the draft genome sequences of both soil isolates.

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Experimental infections caused by bacteria that elaborate a polysaccharide or polypeptide capsule can be resolved by administration of capsule hydrolases that strip away the protective capsular layer from the bacterial surface (1, 2). Anthrax is an excellent candidate for this approach: the inhalational form of the infection requires prompt therapy, and the causative agent, *Bacillus anthracis*, invariably expresses a unique poly-γ-D-glutamic acid (PDGA) capsule that is necessary for optimal pathogenesis (3). If successful, the capsule-stripping approach could confound attempts to render anthrax untreatable by the engineering of multidrug-resistant strains for unlawful dissemination. The poly-γ-glutamate-specific capsule depolymerase (CapD) produced by *B. anthracis* removes the capsule from the surface of the anthrax bacillus (4) and can protect against anthrax infection (5) but is markedly unstable (6) and therefore unlikely to be useful for therapeutic development.

We have recently obtained a highly stable PDGA-specific capsule depolymerase from bacterial cultures (unpublished data); soil enrichment techniques were employed to isolate bacteria with the capacity to degrade PDGA and to use the hydrolytic products as the sole source of carbon and energy. The most pronounced hydrolytic activity was associated with a strongly mutualistic consortium culture comprising two morphologically distinct colony types; when the two strains were cultured separately, no depolymerase activity was apparent in either culture. A 16S sequence identified these organisms as *Pseudomonas fluorescens* (s_ab score = 1) and *Pusillimonas noertemannii* (s_ab score = 0.996). The two isolates, *P. fluorescens* BS2 and *P. noertemannii* BS8, were sequenced in order to provide a database for the identification of the PDGA depolymerase and to provide a platform for elucidation of the basis of interstrain cooperation. Only one *Pusillimonas* species genome sequence, from an oil-degrading bacterium isolated from the Bohai Sea, is currently available (7).

Whole-genome sequencing was performed on the Illumina HiSeq 2000 platform using a single read (read 1) from a paired-end read library with read lengths of 100 bp. The short sequence reads were first processed with Trimmomatic (8) and quality assessed using FastQC (http://www.bioinformatics.babraham.ac.uk//projects/fastqc/) software. VelvetOptimiser (http://bioinformatics.net.au/software.velvetoptimiser.shtml) was used for optimization of the Velvet *de novo* assembly (9), resulting in 122 contigs with an N_{50} of 5,355 bp for *P. fluorescens* BS2, comprising in total 6,123,259 bp, and 121 contigs with an N_{50} of 15,214 bp for *P. noertemannii* BS8, comprising in total 3,916,977 bp. Automated gene prediction and annotation were performed using RAST (10), which predicted 5,539 and 3,633 coding sequences for *P. fluorescens* BS2 and *P. noertemannii* BS8, respectively. Interestingly, RAST indicated that the nearest neighbor to *P. fluorescens* BS2 was *P. fluorescens* SBW25 and to *P. noertemannii* BS8 was *Bordetella bronchiseptica* RB50.

Nucleotide sequence accession numbers. The *Pseudomonas fluorescens* BS2 and *Pusillimonas noertemannii* BS8 sequences have been deposited in NCBI under accession numbers AMZF00000000 and AMZG00000000. Short reads have been deposited in the SRA under accession number SRA058672.

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