Genome Sequence of the Polychlorinated-Biphenyl Degradar *Pseudomonas pseudoalcaligenes* KF707

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***Pseudomonas pseudoalcaligenes* KF707 is a soil polychlorinated biphenyl (PCB) degrader, able to grow both planktonically and as a biofilm in the presence of various toxic metals and metalloids. Here we report the genome sequence (5,957,359 bp) of *P. pseudoalcaligenes* KF707, which provides insights into metabolic degradation pathways, flagellar motility, and chemotaxis.**

Pseudomonas pseudoalcaligenes KF707 is a robust soil polychlorinated biphenyl (PCB) degrader (5) that is able to grow in the presence of various toxic metals and metalloids (6, 7) as a biofilm, and it has been found to be chemotactically attracted to biphenyl and PCBs (7).

Here we present the draft genome sequence of *P. pseudoalcaligenes* KF707, providing information on the genetic bases for the peculiar physiological aspects and environmental behaviors of this strain, such as chemotaxis, biofilm formation, and metabolic degradation properties.

Sequencing technologies used included the 454 Genome Sequencer FLX system (Roche) and HiSeq2000 (Illumina) (2). The 454 sequencing was performed at the National Research Council Plant Biotechnology Institute (Saskatoon, Canada), and it generated 231,206 reads, with a modal length of 370 bp. Output data were processed and assembled using Newbler software (3), producing 729 contigs covering approximately 6 Mbp. Illumina sequencing was performed at the Institute of Applied Genomics (Udine, Italy) and yielded ~110,000,000 paired-end reads of 100 bp in length, which were assembled using ABySS software (4). As expected, with Illumina paired-end technology, the fragmentation dramatically decreased: the resulting assembly consisted of 255 contigs of over 200 bp (N50, 81,842 bp; maximum contig size, 367,837 bp), yielding a genome reconstruction (i.e., the total number of assembled bases) of 6.53 Mb, in agreement with that obtained with 454 sequencing.

An optical map of the *P. pseudoalcaligenes* KF707 genome was constructed at the Canadian Food Inspection Agency (Lethbridge, Canada) with the BamHI restriction enzyme, yielding 650 ordered restriction fragments (average fragment size, 9.1 kb; maximum contig size, 64.8 kb). The *P. pseudoalcaligenes* KF707 genome size was estimated to be approximately 5.95 Mb, which was obtained from the sum of all restriction fragments of the map. The assembly was partially finished by scaffolding the contigs on the optical map, using the MapSolver software (OpGen). All the contigs longer than 40 kb (a suggested threshold value for reliable mapping) were placed on the map, thus confirming the consistency of the assembly. This scaffold, supported by the contig connectivity returned by ABySS software, was used to chain 33 contigs shorter than 50 kb, thus increasing the N50 of the assembly to 97,881 bp. The resulting scaffold accounted for a map coverage of 79.63%.

The RAST (rapid annotations based on subsystem technology)

Prokaryotic Genome Annotation server was used for annotation (1) (<http://www.nmpdr.org/FIG/wiki/pub/Main/HowToUseNMPDR/RASTworkshop3.pdf>).

The findings indicated that the KF707 genome comprises 5,957,359 bp, with a GC content of 64.24%. The RAST annotation software was used on the set of contigs longer than 200 bp, and it returned 6,620 genes (of which 48% are assigned to subsystems), among which were 6,512 CDSs (coding sequences), 81 tRNAs (representing all 20 amino acids), and 27 rRNAs. Analysis of the whole-genome shotgun sequence gave information for most of the KF707 biochemical pathways involved in biphenyl and PCB degradation (22 CDSs), phenol (7 CDSs), benzoate (54 CDSs), and chloroaromatic compound metabolism (13 CDSs). Additionally, 118 CDSs involved in flagellar motility and chemotaxis were identified. Furthermore, 55 CDSs were found to be involved in cobalt, zinc, cadmium, arsenic, or tellurium resistance.

Nucleotide sequence accession numbers. The results from this whole-genome project have been deposited at DDBJ/EMBL/GenBank under the accession number [AJMR000000000](#). The version described in this paper is the first version, [AJMR01000000](#).

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