



# The Complete Genome Sequence of *Proteus mirabilis* Strain BB2000 Reveals Differences from the *P. mirabilis* Reference Strain

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1 The complete genome sequence of strain BB2000 reveals differences from the *Proteus*  
2 *mirabilis* reference strain

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23 Running title: Complete genome sequence of *P. mirabilis* BB2000

24

24 Abstract

25           We announce the complete genome for *Proteus mirabilis* strain BB2000, a model  
26 system for self recognition. This opportunistic pathogen contains a single, circular  
27 chromosome (3,846,754 base pairs). Comparisons between this genome and that of strain  
28 HI4320 reveal genetic variations corresponding to previously unknown physiological and  
29 self-recognition differences.

30

30           The gut commensal bacterium *Proteus mirabilis* is the primary cause of urinary  
31 tract infections in patients with long-term indwelling catheters (1-4). Interestingly,  
32 migrating colonies of *P. mirabilis* cells can distinguish self from non-self: a visible  
33 boundary forms at the interface between two genetically distinct colonies, while two  
34 genetically identical populations merge together (5). The genetic determinants of this  
35 self-recognition behavior, first identified in *P. mirabilis* strain BB2000, included self-  
36 identity genes containing numerous inter-strain nucleotide polymorphisms and suggested  
37 that additional genetic differences between strains are likely (6). To date, only the  
38 genome of *P. mirabilis* strain HI4320 (NCBI NC\_010554) has been completed (7). Here  
39 we report a second closed genome, that of the genetically distinct strain, BB2000 (8).

40           BB2000 genomic DNA was isolated and sequenced using standard protocols.  
41 Briefly, DNA was isolated from cells cultured in modified LB broth using  
42 phenol/chloroform extraction and ethanol (9). Beckman Coulter Genomics (Danvers,  
43 MA) performed initial library preparation and sequencing using the Roche 454 platform.  
44 Illumina sequencing was used to confirm the 454 data and resolve stretches of unknown  
45 nucleotides; genomic DNA libraries were prepared according to the Illumina  
46 Multiplexing Sample Preparation protocol and sequenced by Harvard FAS Systems  
47 Biology Core using an Illumina HiSeq 2000. Illumina reads were assembled onto the 454  
48 genomic data using Galaxy software (10). Genome closure was accomplished by  
49 amplifying across gaps using polymerase chain reactions followed by Sanger sequencing  
50 performed by Genewiz Corporation (South Plainfield, NJ).

51           The *P. mirabilis* BB2000 genome consists of a single chromosome (3,846,754  
52 base pairs) with 38.6% G+C content. Potential coding sequences (CDSs) were identified

53 using the xBase annotation service, which predicted CDS regions using Glimmer (11),  
54 and assigned predicted protein products based on a direct comparison to the *P. mirabilis*  
55 HI4320 genome (12-16). CDSs absent in the HI4320 genome were assigned  
56 “hypothetical protein” as the predicted product. Twenty-eight genes related to self-  
57 recognition (6, 17) were annotated manually using blastx (12) and the HMMER web  
58 interface (18). Sequence assembly and annotation were completed using Artemis  
59 software (19). The BB2000 genome encodes 3,457 potential CDSs, of which 2,592 are  
60 assigned a putative function; the remaining 865 CDSs are classified as hypothetical  
61 proteins, with an additional 81 tRNA genes and 22 rRNA genes.

62 Comparison of the BB2000 genome to that of strain HI4320 (7) revealed 93%  
63 similarity between the chromosomes. The CDSs unique to each genome include genes  
64 related to phage, toxin elements, and self recognition. The HI4320 genome encodes iron  
65 acquisition proteins that are absent in BB2000. Strain HI4320 also contains a plasmid  
66 (NCBI NC\_010555.1) (7), and the HI4320 chromosome encodes a complete set of *tra*  
67 genes for conjugative transfer. No plasmid was identified in BB2000, nor does its  
68 genome encode *tra* genes or any HI4320 plasmid-encoded genes. Further analysis of  
69 variations between *P. mirabilis* isolates will advance our understanding of the genetic  
70 determinants of pathogenicity and self recognition.

71 **Nucleotide sequence accession number.** The *P. mirabilis* BB2000 genome  
72 sequence has been deposited in GenBank under the accession number BankIt1590180  
73 BB2000 CP004022.

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