Nucleotide sequence of the regulatory region of the gene *pbpB* of *Escherichia coli*

M.J.Gómez, B.Fluoret[1], J.van Heijenoort[1] and J.A.Ayala

Centro de Biología Molecular, U.A.M., Canto-Blanco, 28049 Madrid, Spain and [1]Laboratoire de Biochimie Moleculaire et Cellulaire, Bàt. 432-433, Université Paris-Sud, 91405 Orsay, France

A 1.2 Kbp HindIII-XmaI fragment from the Carbon and Clarke plasmid pLC26−6 has been cloned and sequenced. This fragment contains the region closely upstream of the gene *pbpB* of *Escherichia coli*. A 1041-bp open reading frame (termed *orfB*) has been revealed in this sequence overlapping 248-bp with the previously sequenced 2.6 Kbp XmaI-PvuII fragment (1). A 35 Kd polypeptide was found in a maxicell experiment using plasmid pHE5 (a pUC9 derivative containing the 7.6 Kbp HindIII-EcoRI fragment) but not in an equivalent experiment using plasmid pXE15 (a pUC9 derivative containing the 6.4 Kbp XmaI-EcoRI fragment). Then, the identified 346-aa reading frame might be the coding region of this 35 Kd polypeptide. Two new thermosensitive mutations with a lytic (*lts33*) and a filamentous (*fts36*) phenotype have been recently described in this region (2) and the overexpression of the genes in this region produces a decrease of the colony-forming abilities of different cell division mutants (3). So, this sequence can play some role in the regulation of cell division in *E. coli*.

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   1  AAGCTTTTCCTCAGCTCCGTAAACTCCTTTCAGTGGGAAATTGTGGGGCAAAGTGGGAAT    60
  61  AAGGGGTGAGGCTGGCATGTTCCGGGGAGCAACGTTAGTCAATCTCGACAGCAAAGGGCG   120
 121  CTTATCAGTGCCTACCCGTTATCGGGAACAGCTGCTTGAGAACGCTGCCGGTCAAATGGT   180
 181  TTGCACCATTGACATTTATCACCCGTGCCTGCTGCTTTACCCCCTGCCTGAATGGGAAAT   240
 241  TATCGAGCAAAAATTATCGCGTCTGTCGAGCATGAACCCGGTTGAGCGCCGTGTGCAGCG   300
 301  CCTACTGTTAGGTCATGCCAGCGAATGTCAGATGGATGGCGCAGGTCGATTGTTAATCGC   360
 361  GCCAGTACTGCGGCAACATGCCGGGCTGACAAAAGAAGTGATGCTGGTTGGACAGTTCAA   420
 421  CAAGTTTGAGCTGTGGGATGAAACAACCTGGCATCAACAGGTCAAGGAAGATATCGACGC   480
   1                   M  K  Q  P  G  I  N  R  S  R  K  I  S  T  Q    15
 481  AGAGCAGTTGGCTACCGGAGACTTATCGGAGCGACTGCAGGACTTGTCTCTATAAAATGA   540
  16   S  S  W  L  P  E  T  Y  R  S  D  C  R  T  C  L  Y  K  M  M    35
 541  TGGAAAACTATAAACATACTACGGTGCTGCTGGATGAAGCCGTTAATGGCCTCAATATCC   600
  36   E  N  Y  K  H  T  T  V  L  L  D  E  A  V  N  G  L  N  I  R    55
 601  GTCCTGATGGCATCTACATTGATGGGACTTTTGGTCGCGGTGGTCACTCACGTCTGATCG   660
  56   P  D  G  I  Y  I  D  G  T  F  G  R  G  G  H  S  R  L  I  L    75
 661  TCTCGCAGCTTGGCGAAGAGGGGCGTTTGCTGGCGATCGATCGCGACCCGCAGGCTATCG   720
  76   S  Q  L  G  E  E  G  R  L  L  A  I  D  R  D  P  Q  A  I  A    95
 721  CCGTTGCGAAGACTATTGATGATCCGCGCTTCTCCATCATCCACGGACCTTTCTCCGCGC   780
  96   V  A  K  T  I  D  D  P  R  F  S  I  I  H  G  P  F  S  A  L   115
 781  TGGGCGAATACGTTGCCGAGCGCGATCTTATCGGCAAGATCGACGGCATTCTCCTCGATC   840
 116   G  E  Y  V  A  E  R  D  L  I  G  K  I  D  G  I  L  L  D  L   135
 841  TTGGCCGTCTCTTCACCGCAACTTGATGATGCTGAACGTGGCTTTTCCTTTATGCGCGATG   900
 136   G  V  S  S  P  Q  L  D  D  A  E  R  G  F  S  F  M  R  D  G   155
 901  GTCCGCTGGACATGCGTATGGACCCAACCCGTGGGCAGTCAGCCGCTGAATGGCTACAAA   960
 156   P  L  D  M  R  M  D  P  T  R  G  Q  S  A  A  E  W  L  Q  T   175
 961  CCGCAGAAGAAGCCGATATCGCCTGGGTATTGAAAACCTATGGTGAAGAGCGTTTTGCCA  1020
 176   A  E  E  A  D  I  A  W  V  L  K  T  Y  G  E  E  R  F  A  K   195
1021  AACGCATTGCCCGCGCCATTGTCGAGCGTAACCGCGAACAGCCGATGACCCGCACCAAAG  1080
 196   R  I  A  R  A  I  V  E  R  N  R  E  Q  P  M  T  R  T  K  E   215
1081  AACTGGCGGAAGTCGTGGCTGCTGCAACGCCGGTGAAAGATAAGTTTAAACATCCCGCGA  1140
 216   L  A  E  V  V  A  A  A  T  P  V  K  D  K  F  K  H  P  A  T   235
1141  CCCGTACCTTCCAGGCGGTGCGCATTTGGGTAAACAGTGAACTGGAGGAGATAGAGCAGG  1200
 236   R  T  F  Q  A  V  R  I  W  V  N  S  E  L  E  E  I  E  Q  A   255
1201  CGCTAAAAAGCTCGCTCAACGTGCTGGCCCCGGGTGGGCGGCTTTCGATCATCAGCTTCC  1260
 256   L  K  S  S  L  N  V  L  A  P  G  G  R  L  S  I  I  S  F  H   275
1261  ACTCGCTGGAAGACCGTATTGTGAAACGTTTTATGCGTGAAAACAGCCGCGGTCCGCAAG  1320
 276   S  L  E  D  R  I  V  K  R  F  M  R  E  N  S  R  G  P  Q  V   295
1321  TTCCGGCAGGGTTACCGATGACTGAAGAGCAGCTCAAAAAACTGGGTGGCCGTCAGCTGC  1380
 296   P  A  G  L  P  M  T  E  E  Q  L  K  K  L  G  G  R  Q  L  R   315
1381  GAGCACTAGGCAAGTTAATGCCGGGCGAAGAAGAGGTGGCTGAGAACCCTCGTGCCCGTA  1440
 316   A  L  G  K  L  M  P  G  E  E  E  V  A  E  N  P  R  A  R  S   335
1441  GTTCAGTTCTGCGTATTGCAGAGAGGACGAATGCATGATCAGCAGAGTGACAGAAGCTCT  1500
 336   S  V  L  R  I  A  E  R  T  N  A                             346
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