Nucleotide sequence of the *recA* gene of *Proteus mirabilis*Eiko Akaboshi*, Man Lun R.Yip⁺ and Paul Howard-Flanders[§]

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We have determined the DNA sequence of the *recA* gene of *P. mirabilis* (1). In the 5'-non coding region a palindromic sequence homologous to the sequence of the SOS box in *E. coli* is found (underlined). The deduced polypeptide has a calculated M_r of 38176, which is very close to the previous experimental value (2).

The nucleotide sequence shows 73% and 62% identity with *E. coli* and *P. aeruginosa* *recA* genes, respectively (3-5). However, the similarity is localized to the amino- and central regions. The carboxy-terminal regions diverge among all three sequences.

A sequence hypothesized previously by Walker et al. (6) as an adenine nucleotide-binding fold, R-----G---SGKT, is found at codon position 61-74. Moreover, the amino acid sequence from 191 to 228 are identical among all three proteins; the nucleotide sequence varies at the third position of certain of these codons but the amino acid sequence is conserved. This region coincides with the ATP binding site suggested by Kawashima et al. (7). The ORF of these three *recA* gene are very similar in size (346, 353 and 355 codons), even though they diverge at the carboxy-terminal region.

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TTTCTCTTTAAATCAATTCTTAAAGAAATTATTAATAATTAACCTGTACTGTATGATTATACAGTATAATGAGTTTCAACAAGCAAAATCATATACGT  -51
TTTAAATGTTAGTACCCATCTTTATGCTTCACTGCCAGAGGAGATACATGGCTATTGATGAAAAACAAACAAAGCATTTGGCCGAGCAGCTTGGTCA  50
IEKQFGKGSGSIMRLGEDRSMNVETISTGSLSLDV
AATTGAAAGCAATTTGGTAAAGTTCTATCATGCGTCTGGGCGAAGACCGTTCCATGAACGTAGAACTATCTCTACAGGATCTTTATCATTAGACGTT
ALGAGGLPRGRIVEIYGPESSGKTTTLTLQVIAASA
GCTTTAGTGCAGGTGGATTGCCACGTGGCGTATTGTTGAAATCTATGGCCCTGAATCTCTGGTAAAAACACCTTGACTCTACAAGTTATTGGCTCTG  250
QREKGKICAFIDAEHAFIDAPIYAOKLGLVDIDNLLC
CTCAGCGTGAAGAAAAATTTGGCATTATTGATGCTGAACATGCATTAGACCCAATTATTGCTCAAAAGCTAGGTGTCGATATCGATATCTACTCTG
SQPDITGEGQALEICDALSRS GAVDVIVVDSVAAL
CTCTCACTGACACAGGTGAACAAGCTCTGGAATTTGTGATGCATTATCTCGCTCTGGTCCGTCGATGTTATTGCTGGAGCTCCGTGGCAGCATTA  450
TPKAEIEGEGIDSHVGLAARMMSQAMRKL LAGNLK
ACACCAAAGCTGAAATGAAGCTGAAATTTGATTCACACGTTGGTTTACCGCAGCTATGATGACCAAGCTATGCGTAAACTAGCGGGTAACCTTA
NSNTLLLIPIFINQIRMKIGVMFGNPEPTTTTGGGNALK
AAAACCTAATACACTGCTGATTTTCATTAAACAAATTCGTATGAAAAATCGTGTATGTTTGGTAAACCCAGAACCCAGCCGGTGGTAAATGCGCTTAA  650
FYASVRLDIRRIGSVKNGDEIVIGTSETRVVKVKN
ATTCTATGCTTCTGTTGCTGTTAGACATTCGTGCTTGGCTCTGCAAAATGGTGATGAAGTCATTGGTAGTGAGCTCGCGTTAAAGTTGTTAAAAAT
KVAAPFKQAIEFQIMYGEIGINTYGEELIDLGLVKHKL
AAAGTGGCTGCACCGTTTAAACAAGCTGAATTCCAAATATGATACGGTGAAGGTATTAACTATGCGGAACCTGATTGATTAGGTGTTAAACATAAGT  850
VEKAGAWAYS YNGEKKIGQGKANAATNYLKEHEPEMY
TAGTAGAGAAAGCAGGTGCTTGGTATAGCTACAATGGCGAAAAAATTTGGTCAAGTAAAGCTAACGCAACCAATTACTTTAAAGAACATCTCTGAAATGTA
NE LNTKLR EML LNH AG EFT S A A D F A G E E S D S D A
CAATGAGTTAAACATAAATTCGCTGAAATGTTGTTAAATCATGCTGCTGAATTCACAAGTCTGCGGATTTTGACAGTGAAGAGTCAGACAGCTGATGCT  1050
D D T K E
GACGACACAAAGAGTAATTAGCTGGTTGCTGCTGCTGTTTGTGTGAAAATAGACCTTAAATCATTTGGCTATTATCACGACAGCATCCCATAGAAATACTT

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References

1. Eitner, G., Solonin, A. S. and Tanyashin, V. I. (1981) *Gene* 14, 301-308.
2. West, S. C., Countryman, J. K. and Howard-Flanders, P. (1983) *J. Biol. Chem.* 258, 4648-4654.
3. Horii, T., Ogawa, T. and Ogawa, H. (1980) *Proc. Natl. Acad. Sci. USA* 77, 313-317.
4. Sancar, A., Stachelek, C., Konigsberg, W. and Rupp, W. D. (1980) *Proc. Natl. Acad. Sci. USA* 77, 2611-2615.
5. Sano, Y. and Kageyama, M. (1987) *Mol. gen. Genet.* 208, 412-419.
6. Walker, J. E., Saraste, M., Runswick, M. J. and Gay, N. J. (1982) *EMBO J.* 1, 945-951.
7. Kawashima, H., Horii, T., Ogawa, T. and Ogawa, H. (1984) *Mol. gen. Genet.* 193, 288-292.