

Location of *gyrA* on the Physical Map of the *Escherichia coli* Chromosome

GENE WEBB, KALPANA ROHATGI, AND JAMES B. COURTRIGHT*

Department of Biology, Marquette University, Milwaukee, Wisconsin 53233

Three oligonucleotide probes with sequences corresponding to either the coding sequence or the complementary sequence of *gyrA* (6, 7) at nucleotide positions 295, 343, and 524 were synthesized. These oligomers were separately labeled at their 5' ends with ^{32}P and hybridized to phage DNA prepared from the λ miniset phages 371 through 377 (4). Each of the three probes hybridized only to E13A5 (phage 376). pAW012, which contains an *EcoRV* genomic fragment containing the *gyrA* gene (7), hybridized to 4F12 (phage 375) as well as to E13A5. The pAW012 *Bam*HI-*Hind*III fragment, which contains only the first 692 nucleotides for the *gyrA* gene (6, 7), did not hybridize to 4F12. The *gyrA* gene contains restriction sites for *Hind*III, *Kpn*I, *Pst*I, and *Pvu*II but none for the other four enzymes used for defining sites in the recombinant phage collection (4). This combined information identifies the *Hind*III site at nucleotide 692 of *gyrA* with the leftmost *Hind*III site of the E13A5 insert. The fact that the oligonucleotides hybridized with this phage, whereas pAW012 also hybridized to phage strain 4F12, places the *gyrA* gene, map position 48.3 min (1), at coordinate 2350 (5) immediately to the left of *ubiG* and with an orientation the same as that of *ubiG* (2) but opposite that of the *atoDAB* (3) operon at coordinate 2334 (Fig. 1). There was no inconsistency in terms of restriction sites, and the sizes of cloned genes were in good agreement with the restriction map (4, 5).

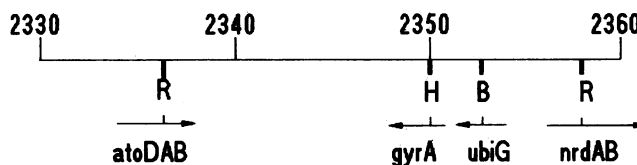


FIG. 1. Organization of the region encompassing coordinates 2330 to 2350 of the *Escherichia coli* chromosome. The coordinates of *atoDAB*, *gyrA*, *ubiG*, and *nrdAB* at *Bam*HI (B), *Eco*RI (R), and *Hind*III (H) sites are 2336.5, 2350, 2352.6, and 2357.68, respectively, on the basis of the corrected restriction map (5).

ACKNOWLEDGMENTS

This work was supported by Biomedical Research Support Grant to Marquette University and the Parke-Davis Pharmaceutical Research Division.

LITERATURE CITED

1. Bachmann, B. J. 1990. Linkage map of *Escherichia coli* K-12, edition 8. *Microbiol. Rev.* **54**:130-197.
2. Gfbert, I., M. Llagostera, and J. Barbé. 1988. Regulation of *ubiG* expression in *Escherichia coli*. *J. Bacteriol.* **170**:1346-1349.
3. Jenkins, L. S., and W. D. Nunn. 1987. Genetic and molecular characterization of the genes involved in short-chain fatty acid degradation in *Escherichia coli*: the *ato* system. *J. Bacteriol.* **169**:42-52.
4. Kohara, Y., K. Akiyama, and K. Isono. 1987. The physical map of the whole *E. coli* chromosome: application of a new strategy for rapid analysis and sorting of a large genomic library. *Cell* **50**:495-508.
5. Médigue, C., J. P. Bouché, A. Hénart, and A. Danchin. 1990. Mapping of sequenced genes (700kbp) in the restriction map of the *Escherichia coli* chromosome. *Mol. Microbiol.* **4**:169-187.
6. Swanberg, S. L., and J. C. Wang. 1987. Cloning and sequencing of the *Escherichia coli gyrA* gene coding for the A subunit of DNA gyrase. *J. Mol. Biol.* **197**:729-736.
7. Yoshida, H., Y. Kojima, J. Yamagishi, and S. Nakamura. 1988. Quinolone-resistant mutations of the *gyrA* gene of *Escherichia coli*. *Mol. Gen. Genet.* **211**:1-7.

* Corresponding author.