

## *E. COLI* MAP†

# A New Gene Located between *pss* and *rrnG* on the *Escherichia coli* Chromosome

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A 9-kilobase-pair (kb) fragment of *Escherichia coli* genomic DNA was cloned in the course of screening bacteriophage  $\lambda$ gt11 libraries for GTP-binding proteins. A previously unrecognized open reading frame was identified in the 9-kb clone by restriction mapping and by sequencing several different subclones. The new open reading frame is located downstream of the 3' end of the rRNA operon *rrnG* (W. Seol and A. J. Shatkin, *Nucleic Acids Res.*, in press) in a head-to-head orientation with respect to the phosphatidylserine synthase gene *pss* (the restriction sites of *pss* were kindly provided by W. Dowhan, Houston, Tex.). To confirm the location of the new gene, lambda bacteriophages 3F10 and 21D7 (2; obtained from M. Inouye, Piscataway, N.J.) were selected for hybridization studies on the basis of the mapping results. Both phage DNAs yielded positive bands of the expected sizes after digestion of 3F10 with *EcoRI*, *BglII*, *EcoRV*, and *PvuII* and of 21D7 with *PvuII*, followed by hybridization with a nick-translated 0.4-kb fragment of the new gene. The results indicate that this gene is located near 56.5 min on the *E. coli* chromosome. The physical maps of this region of the chromosome (2) and the 9-kb clone are identical. (An additional *BglII* restriction site at nucleotide positions 983 to 993 and the absence of a previously reported *EcoRV* site in the *rrnG* region have been confirmed by Y. Kohara [personal communication].)

The sequence of 432 amino acids deduced from the open reading frame suggests that the new gene (EMBL accession no. X53027) may encode a transporter. It has 50 to 58% sequence similarity and several characteristics common to the *E. coli* citrate and arabinose transporters and to the human glucose carrier protein (1, 3). Like the amino acid sequences of these defined transporters, the deduced amino acid sequence contains 12 hydrophobic segments which may span the membrane, a central hydrophilic region between hydrophobic segments 6 and 7, and a duplicated (R/K)XG(R/K)R motif between putative membrane-spanning domains (i) 2 and 3 and (ii) 8 and 9 (4). We have provisionally named the gene *witA* (for "what is transported?") and are attempting to identify the corresponding ligand.

### LITERATURE CITED

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† For information about this section, see the January 1990 issue of *ASM News* (56:6-7).