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The Dihydropteroate Synthase Gene, folP, Is Near the Leucine tRNA Gene, leuU, on the Escherichia coli Chromosome

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Dihydropteroate synthase (DHPS) (EC 2.5.1.15) is the target for the class of compounds known as sulfonamides (1, 4, 11, 16). We recently reported the cloning and sequencing of the DHPS gene, folP, from Escherichia coli (6). We used the cloned gene as a hybridization probe to determine which bacteriophages from the Kohara miniset phage collection carry folP (7). Two phages were found to be probe positive, 18H7 (520) and 14F11 (521), and inspection of the Kohara phage map revealed that they shared DNA fragments. Results from Southern hybridization analyses placed folP within 3 kb of the left end of phage 14F11 (521) (13). Therefore, oligonucleotide primers were synthesized and used to determine the DNA sequence between folP and the vector DNA, using phage DNA as a template (10). Using the new DNA sequence, a revised restriction map for the left end of phage 14F11 (521) was made and is presented in Fig. 1, which also shows the relative positions of folP and leuU, a leucine transfer RNA gene that had been previously mapped (8). The two genes are separated by about 2 kb and are transcribed in the same direction. An open reading frame (ORF) was identified between the two genes and could code for a protein with a compositional mass of 47,540 Da. The ORF would be transcribed in the same direction as that of folP and overlapped the end of folP by 5 bp. Using the nomenclature system proposed by K. Rudd (10a) that is analogous to the transposon mapping system reported by Chumley et al. (5), the ORF has tentatively been designated yhbF.

The function of the gene product coded by yhbF is not known. Maybe it is part of the folate biosynthetic pathway. In Bacillus subtilis and Streptococcus pneumoniae, some of the folate biosynthetic genes are contiguous (9, 12), while in Pneumocystis carinii, folK and folP are apparently joined and are expressed as a single protein with two enzymatic activities (15). However, folate biosynthetic pathway genes that have been mapped on the E. coli chromosome are scattered. The dihydrofolate reductase gene (folA) is at 1 min (3), the 7,8-dihydro-6-hydroxymethylpterin-pyrophosphokinase gene (folK) is at 3.6 min (14), the folylpoly-y-glutamate synthetase-dihydrofolate synthetase gene (folC) is at 50 min (2), and our work has mapped the DHPS gene (folP) to 71.5 min. Further work will be needed to characterize the product from yhbF.

Nucleotide sequence accession number. The new DNA sequence was combined with the folP sequence and has been submitted to GenBank under accession number L12968.

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![Diagram](http://jb.asm.org/)

**FIG. 1.** Physical and genetic map of the left end of phage 14F11 (521). Positions of restriction enzyme recognition sites were determined from the DNA sequence. Thick bars indicate recognition sites missing from previous restriction maps of this phage. The positions for three genes are shown beneath the physical map, with arrows indicating the direction of transcription.

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REFERENCES


10a. Rudd, K. Personal communication.


