Physical Map Location of the *Escherichia coli* Gene Encoding Phosphoglycerol Transferase I

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Membrane-derived oligosaccharides (MDO) are found as soluble components of the periplasmic compartment of *Escherichia coli* (15). They are a family of closely related oligosaccharides containing 6 to 10 glucose units joined by β-1,2 and β-1,6 linkages and are variably substituted with succinic acid O ester, phosphoethanolamine, and sn-1-phosphoglycerol (7, 14). The *mdoB* locus (4, 5) encodes phosphoglycerol transferase I, an enzyme which catalyzes the in vitro transfer of phosphoglycerol residues from phosphatidylglycerol to MDO or to the artificial substrate arbutin (p-hydroxyphenyl-β-D-glucoside) (6). Because this enzyme has its active site on the periplasmic side of the cytoplasmic membrane, it also catalyzes the in vivo transfer of phosphoglycerol to arbutin added to the medium (2), although arbutin cannot enter the cytoplasm.

Mutants defective at the *mdoB* locus cannot transfer phosphoglycerol residues to arbutin in vivo and synthesize MDO devoid of phosphoglycerol residues (5). One *mdoB::TnlO* mutation was found to be 56% cotransducible with *serB* and 36% cotransducible with *thr*, using phage P1, and the order *mdoB* serB thr was confirmed by three-factor crosses (5). Thus, the *mdoB* locus is localized near min 99 on the *E. coli* genetic map, probably around 4680 kb, between *dnaTC* and *serB* (1, 8, 11).

We have used two clones from the Kohara library (8) (clones 8D1 and 5C1) to fine map, subclone, and determine the nucleotide sequence of the *mdoB* locus. DNAs from these lambda phage clones were digested with various restriction endonucleases, and the resulting fragments were inserted in a multicopy vector. The recombinant plasmids were introduced by transformation in a *mdoB::TnlO* strain and tested for their abilities to complement the defect in phosphoglycerol transfer to MDO and to arbutin. Subcloning of the *mdoB* gene was obtained with a 7.1-kb *SalI* fragment (9). Analysis using restriction endonucleases indicated that the *mdoB* gene is located immediately adjacent to the *dnaTC*

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**FIG. 1.** Physical location of the *mdoB* gene on the *E. coli* chromosome. The scale at the top refers to position (in kilobases). The restriction map of Kohara library is shown (broken lines indicate that the restriction sites above them were unable to be read), as are the left ends of clones 8D1 and 5C1. Physical maps shown for the *tsr* and *dnaTC* region are from data deposited in the EMBL/GenBank DNA libraries and previously published (3, 10). Open boxes indicate regions whose nucleotide sequences are known, and shaded arrows indicate coding sequences. Letters below the horizontal line represent all the sites for the enzymes used by Kohara et al. (8) (B, *Bam*HI; D, *Hind*III; E, *Eco*RI; F, *Eco*RV; G, *Bgl*II; Q, *Kpn*I; S, *Pse*I; V, *Pvu*II). Letters above the horizontal line represent only the relevant sites for the *tsr, mdoB*, and *dnaTC* genes (M, *Mlu*I; L, *Sal*I).

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operon (Fig. 1). DNA sequencing around the KpnI site located in the middle of the SalI fragment confirmed its identity with the KpnI site present downstream from the dnaC gene, at 4679.4 kb (10).

This finding reopens the question of the location of the tsr gene (3), since controversial data have been published (11–13). On the basis of the restriction sites (VGFFFGV) present in the sequence deposited in the EMBL DNA library, Médigue et al. (11) placed tsr at the position actually occupied by mdoB (GVVFFVG). Miller (12) and Rudd et al. (13), using a different computer program, place tsr 6.4 kb to the left of dnaTC. Note that there is no information about the EcoRV sites (F in Fig. 1) in this region of the Kohara physical map (8). When the restriction sites surrounding the sequenced region (3) are considered, the best location of tsr is approximately 4670 kb (Fig. 1), as suggested previously by Miller (12) and Rudd et al. (13).

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