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E. COLI MAP†

Locations of the *zwf*, *edd*, and *eda* Genes on the *Escherichia coli* Physical Map

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The 40.5-min region of the *Escherichia coli* map contains the *zwf* gene, which encodes glucose-6-phosphate dehydrogenase, an enzyme of the pentose phosphate pathway, and the *edd* and *eda* genes, which encode 6-phosphogluconate dehydratase and 2-keto-3-deoxy-6-phosphogluconate aldolase, respectively, the key enzymes of the Entner-Doudoroff pathway (4). These three genes are tightly linked, and their order with respect to flanking genetic markers has been firmly established by fine-structure mapping (1, 3).

Some time ago the *zwf*, *edd*, and *eda* genes were shown to be present on two plasmids from the Clarke-Carbon gene library (8). Recently, the *zwf* gene was subcloned from pLC3-33 and its nucleotide sequence was determined (7). Likewise, the *edd* and *eda* genes were subcloned from pLC3-33 and pLC37-44, respectively, and their nucleotide sequences have been determined (2, 9). These sequence data cover the entire *zwf-eda* region and were used to computer generate a precise restriction map (2, 7, 9). This restriction map was confirmed by Southern analysis of *E. coli* W3110 genomic DNA with hybridization probes that were specific for each of the three genes (restriction fragments generated within the structural genes). In addition, conventional restriction mapping of pLC3-33 and pLC37-44 was used to establish the locations of some restriction sites that were not mapped by Southern analysis. The restriction map of the *zwf-eda* region is shown in Fig. 1.

It was not possible to align the restriction map of Fig. 1 with the 40.5-min region of the Kohara physical map (6).

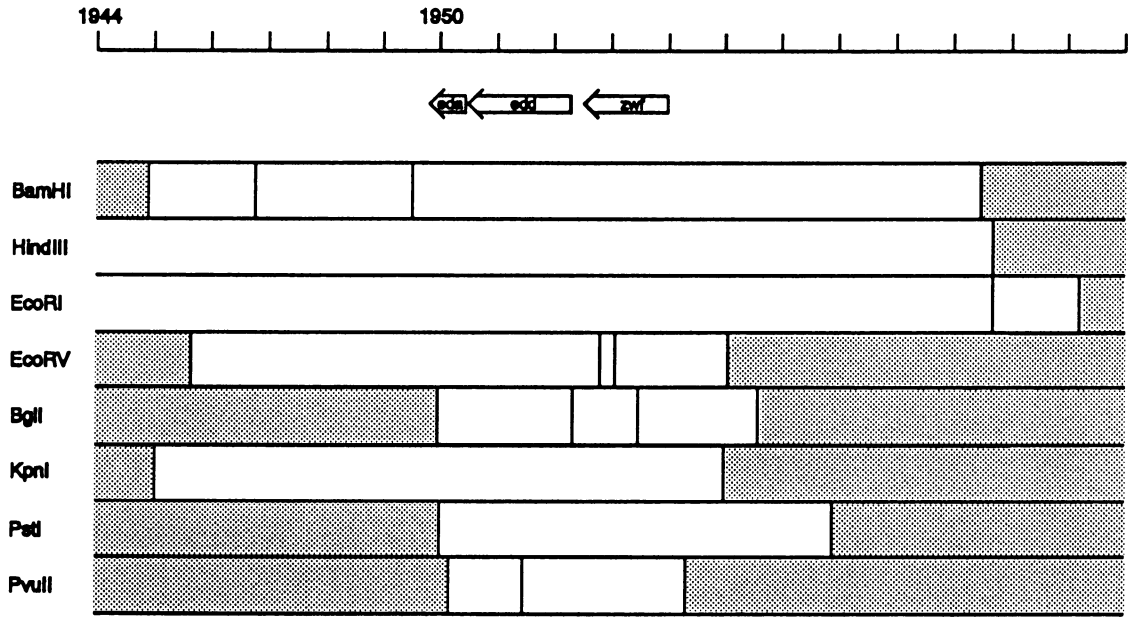

FIG. 1. DNA restriction map of the *zwf-eda* region of the *E. coli* W3110 genome. The open bars represent restriction fragments that were mapped by a combination of methods, including computer analysis of the nucleotide sequence of the region containing the three structural genes, Southern analysis using hybridization probes specific for each gene, and conventional mapping of pLC3-33 and pLC37-44. The shaded areas were not mapped further and extend into confirmed regions of the Kohara physical map (6). The positions of the *zwf*, *edd*, and *eda* genes are shown above the map. The numbers at the top correspond to the map positions (in kilobase pairs) on the Kohara physical map. This restriction map covers the 12-kb *tar* (41.6-min) gap. Therefore, the numbers above 1950 kb are not in register with the Kohara physical map.

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

This was due to a gap in the *tar* (41.6-min) region of the Kohara physical map that renders the locations of restriction sites in the region ambiguous. It was possible, however, to align the *Bam*HI, *Hin*dIII, and *Eco*RI restriction pattern of the *zwf-eda* region of *E. coli* W3110 genomic DNA to a region of the *E. coli* K-12 308 map that fills in the *tar* region gap of the Kohara physical map (5). Comparisons with both physical maps allowed placement of the *zwf-eda* gene cluster precisely within the *tar* region gap of the Kohara physical map. Furthermore, the *Pst*I site located within the downstream end of *eda* is identical to the *Pst*I site located at kb marker 1950 on the Kohara physical map. Thus, the data in Fig. 1 extend the Kohara physical map into the *tar* gap region, although the restriction map on the right side of the *zwf-eda* region remains to be completed.

The relative order of the genes on the *E. coli* W3110 physical map is *pabB*, *eda*, *edd*, *zwf*, *tar*, proceeding clockwise. This order is in keeping with the data of Fraenkel and Banerjee (3). Transcription of the *zwf*, *edd*, and *eda* genes is in the counterclockwise direction. The precise map location of the *zwf-eda* cluster is between 1950 kb (downstream end of *eda*) and 1954 kb (upstream end of *zwf*). This corresponds to 40.8 min for *eda* and 40.9 min for *zwf*, with respect to *pabB* (39.9 min).

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