We have recently cloned and sequenced both genes of the envCD operon (4, 5), which complement the phenotypic defects associated with a mutation in the envC gene of Escherichia coli PM61.

It was not possible to align the restriction map with the proposed 81.5-min region (2) of the Kohara physical map. Therefore, the sequence of the envCD locus, with a total length of 5,461 bp (Fig. 1), was run against the latest E. coli restriction map update, applying the computer software of Rudd and coworkers (8–10). The published nucleotide sequence (EMBL data base, accession number X57948) was used, omitting the IS2 insertion located upstream of the structural genes.

The program suggested that envCD maps at min 72.5 of the physical map. Because of the different scales and E. coli strains used, the restriction map predicted from the envCD sequence matches the physical consensus map of Kohara et al. (6) in the region of 73.8 min (3481 kb), the only exception being two closely spaced EcoRV sites, where the Kohara map resolved only one. In order to experimentally verify the locations of the envCD genes, we used a digoxigenin-labeled DNA fragment, isolated from plasmid pJK131 (5), to probe DNA from five lambda clones of the Kohara “miniset” library (6, 7) (Fig. 1C). Southern hybridization of the 926-bp HincII-EcoRI fragment, which covers the 3’ end of envC and the 5’ start of envD, was positive with clones 529 and 530, and a weak signal was obtained with clone 531, indicating that this clone contains only parts of the probe sequence. As expected, clones 528 and 532 did not hybridize. Thus, the envCD genes could be located on the Kohara physical map between kb 3481.5 and 3485.5, with the sequence reading left to right. The relative order of the genes on the E. coli W3110 physical map is mreB, fabE, panF, and envCD, as summarized in Table 1.

We thank Peter Rice for his generous help with the computer programs and for running the map search at EMBL Heidelberg and Y. Kohara for the phages of the clone bank.

FIG. 1. Alignment of the restriction map of the sequenced envCD region and the restriction maps of the inserts of lambda clones from the Kohara “miniset” library. (A) Transcriptional directions are indicated by arrows. The sequence contains no sites for PstI and PvuII. (B) The HincII-EcoRI fragment used as probe in hybridization experiments. (C) Inserts of lambda clones from the Kohara library (7). Only those insert parts corresponding to the sequenced envCD region are shown.

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TABLE 1. Map locations of envCD and neighboring genes

<table>
<thead>
<tr>
<th>Gene (reference)</th>
<th>Genetic map position (min)</th>
<th>W3110 physical map</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Rudd^a</td>
<td>Bachmann^b</td>
</tr>
<tr>
<td>mreB (11)</td>
<td>72.2</td>
<td>70.95</td>
</tr>
<tr>
<td>fabE (1)</td>
<td>72.3</td>
<td>71.0</td>
</tr>
<tr>
<td>panF (3)</td>
<td>72.4</td>
<td>71.1</td>
</tr>
<tr>
<td>envCD</td>
<td>72.5</td>
<td>81.5</td>
</tr>
</tbody>
</table>

^a Computer analysis (8).
^b From reference 2.
^c Values were calculated by dividing the physical coordinates (in kilobase pairs) by 47.5 (2).
^d From reference 6.
^e ND, not determined.

REFERENCES