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Locations of Genes in the *nar-adhE* Region of the *Escherichia coli* K-12 Chromosome

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The known genes in the *nar-adhE* region of the *Escherichia coli* K-12 chromosome (27 min) have been located on the physical map of Kohara et al. (7) (Table 1). We used the Kohara phage λ4D8 to clone the *adhE* gene. A restriction map of the cloned DNA was compared with restriction maps of other cloned genes in the region for correspondence to the physical map.

The restriction maps of the cloned genes were mostly in agreement with the physical map, except that one *Hin*dIII site centrally located and a *Pvu*II site located at the 5′ end in the *tyrT* clone (11) are absent from the physical map (7), whereas in comparison to *narL* clones (6, 12) an extra *Pvu*II site was noted (Fig. 1). These discrepancies may be due to imprecisions caused by the construction of the physical map (7), but they could also be the result of strain differences, as duplications in the *tyrT* region could promote genetic rearrangement.

A report of the cloning of the *bglY-galU* region has been published (8). *bglY* mutants with several alternate phenotypes have been isolated under different names. Recently, the gene *bglY*, referred to as *drdX* by Göransson et al. (5), has been cloned and sequenced. Because of incomplete restriction data, *galU* and the *drc*, *drs*, and *irk* sequences of Lejeune et al. (8) cannot be precisely placed, but they are located between 27.40 and 27.49 min on the *E. coli* chromosome (Table 1 and Fig. 1). The correlation of restriction data for individual clones to the physical map of Kohara strongly suggests the gene order *galU-drc-drs-irk-bglY-adhE* (Fig. 1). This conflicts with earlier cotransductional mapping by our laboratory which suggested the gene order *bglY-galU-adhE* (2). This disparity could result from the difficulty of screening for *bglY* (3). The gene for thymidine kinase (*tdk*) has been cotransductionally mapped between *tyrT* and *galU* (1). Because *tdk* has not been cloned or sequenced, precise placement is impossible and *tdk* has been omitted from Fig. 1.

Another point to note is the lack, in the clone of Goodlove et al. (4), of two *Hin*dIII sites 5′ of the *adhE* gene (i.e., counterclockwise) which are present on the physical map (Fig. 1). The clone lacking these sites did not exhibit anaerobic regulation (4). However, when cloned from λ4D8, the *adhE* gene retained the *Hin*dIII sites and was subject to anaerobic regulation (unpublished data). Umeda and Ohtsubo (15) identified the positions of insertion sequences on the physical map, and alignment of their data with our own places the insertion sequence IS*2C* 1.4 kb upstream (i.e., counterclockwise) of *adhE*. It is possible that an IS*2*-mediated deletion event led to the loss of both *adhE* regulation and the two *Hin*dIII sites in the previous clones (4).

The *ana* mutation has also been cotransductionally mapped to this region (1). Three-point crosses showed a greater than 95% cotransduction frequency between *ana* and *adhC* and confirmed the gene order *zch*::Tn*10*-(*ana*, *adhC*)-*galU* (unpublished results). This, coupled with the data that *adhE* clones complement the *ana* mutation (4), implies that

TABLE 1. Physical locations of genes in the *nar-adhE* region of the *E. coli* K-12 chromosome

Gene	Genetic map location (min)[a]	Physical map location[b]		Reference(s)	Comments
		min	kb		
narL	27.18	27.18	1291	6, 12	*nar* regulatory gene
narX	27.18	27.21	1292	12	*nar* regulatory gene
narK	27.18	27.22	1293	12	*nar* regulatory gene
narGHJI	27.26	27.27	1295	10, 13, 14	Nitrate reductase structural genes
tyrT	27.36	27.37	1300	11	$tRNA^{Tyr}$, *supF*, *supE*, *tyrV*
tdk	27.50	—[c]	—[c]	1	Thymidine kinase
galU	27.56	[27.43]	[1303]	8	Glucose-1-phosphate uridylyltransferase
drc, *drs*, *irk*	—[d]	[27.47]	[1305]	8	Decrease in chloramphenicol and L-serine resistance; increase in kanamycin resistance
bglY	27.43	27.49	1306	5, 8	H1 proteins
adhE	27.66	27.62	1312	4	Coenzyme A-linked acetaldehyde and alcohol dehydrogenases
IS*2C*	—[d]	27.68	1315	15	Insertion sequence *2C*

[a] From reference 1.
[b] Positions in minutes are derived from the exact physical position in kilobase pairs by dividing by 47.5 (1). Brackets indicate positions deduced for genes strongly suspected to lie close to physically mapped genes.
[c] Not noted on linkage map in reference 1.
[d] No physical data available to place gene.

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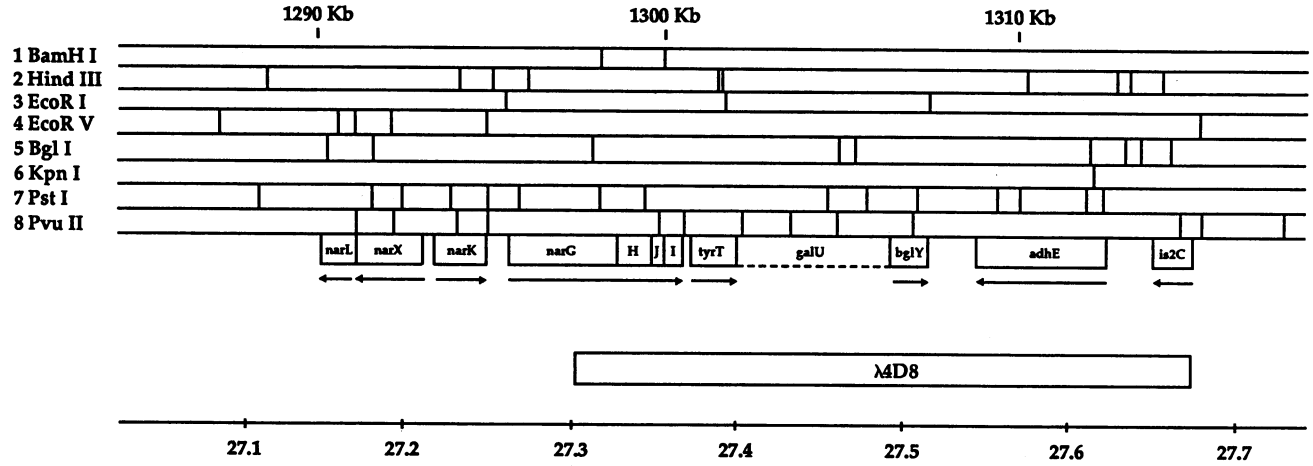

FIG. 1. Alignment of the genetic map of Bachmann (1) and the physical map of Kohara et al. (7). Data for gene alignment are from Leonardo and Clark (9) and references cited in Table 1. Arrows show transcriptional direction. The *Pvu*II site at 1300 kb and the first *Hin*dIII site at 1302 kb were absent from the Kohara map. The *Pvu*II site at 1291 kb is absent from the sequence of *narL* (12).

ana mutations are in the regulatory region of *adhE*, and therefore *ana* was omitted from Fig. 1.

Thus, the order of the genes in this region is *narL-narX-narK-narGHJI-tyrT-(tdk-galU-drc-drs-irk)-bglY-adhE-IS2C* in a clockwise direction. The direction of transcription is as indicated by arrows in Fig. 1.

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