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E. COLI MAP†

Physical Map Locations of Genes Encoding Components of the Aerobic Respiratory Chain of *Escherichia coli*

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The aerobic respiratory chain of *Escherichia coli* is composed of a number of membrane-bound, multisubunit enzymes located within the cytoplasmic membrane. Dehydrogenases such as succinate dehydrogenase or NADH dehydrogenase reduce ubiquinone-8 to ubiquinol-8 within the cytoplasmic membrane. Ubiquinol-8 then diffuses within the membrane bilayer and is oxidized by either of two quinol oxidase complexes: the cytochrome *o* complex or the cytochrome *d* complex (for a review, see reference 1). Mutations in the *cydC* gene reduce expression of cytochrome *d* oxidase. *cydC* may be involved in the synthesis of the heme *d* component of the cytochrome *d* complex (6).

For each of these five proteins, the genetic map positions (2) shown in Table 1 were used to approximate the locations of the corresponding genes on the physical map of Kohara et al. (8). For *cyoABCDE* (3) and *cydAB* (7), restriction maps calculated from the DNA sequences of the cloned genes correspond to the physical maps of the lambda clones listed in Table 1. The map position of *cydAB* is identical to the one previously identified by Rudd et al. (10). The restriction map calculated for *sdhCDAB* (5, 11) contains one more *Pvu*II site than does the physical map. This additional site is 185 bp from the one which appears in the physical map. Because the resolution of the physical map is roughly 500 bp (8, 9), the apparent discrepancy can be accounted for by the close proximity of the two sites. Medigue et al. made the same alignment of the *sdh* operon by using the contiguous DNA sequence of *gltA-sdhCDAB-sucABCD* (9).

The restriction map predicted from the DNA sequence of *ndh* (13) aligns well with lambda clone 15A8. However, the DNA sequence shows two *Pvu*II sites separated by 171 bp, whereas the physical map contains only one *Pvu*II site. As in the case of *sdh*, this discrepancy can be explained by the close proximity of the two sites. Using a computer analysis, Medigue et al. initially placed *ndh* in a different location on the physical map (1072 kbp) (9). We have confirmed that lambda clone 237 carries *ndh* DNA by demonstrating that this clone corrects the *ndh* mutation in strain IY12 (12). Additional computer analyses indicate that this position produces a better match than the one previously reported (4, 9).

To define the physical map location of *cydC*, the *cydC* mutant CG21 (6) was coinfected with lambda *c*I857 and one of 12 lambda clones ("Miniset" clones 206 to 217 [Table 1]). Clones 213 (1H1) and 214 (1F10) give rise to CydC$^+$ progeny, indicating that *cydC* is at least partially located within the 5-kbp overlap of these two clones.

TABLE 1. Physical locations of genes encoding components of the aerobic respiratory chain

Enzyme or function	Gene	Genetic map location[a]	Physical map location[b]	Phage(s) carrying gene[c]	Mutant strain[d]
Cytochrome *o* complex	*cyoABCDE*	10.2	458–464	147	
Cytochrome *d* complex	*cydAB*	16.6	785–788	177, 178	
Cytochrome *d* assembly	*cydC*	19.2	938–943	213, 214	CG21
NADH dehydrogenase	*ndh*	22.4	1184–1187	237	IY12
Succinate dehydrogenase	*sdhCDAB*	16.3	767–769	176	

[a] From reference 2.
[b] From restriction information and complementation/recombination results. For *cydC*, direct selection for aerobic growth was employed, as described in reference 6. For *ndh*, direct selection for growth on mannitol was as described in reference 12. Locations are in kilobase pairs as assigned in reference 8.
[c] Numbers (8a) refer to the "Miniset" available from Y. Kohara and described in reference 8.
[d] From laboratory stocks.

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