

## Physical Map Location of a Set of *Escherichia coli* Genes (*hde*) Whose Expression Is Affected by the Nucleoid Protein H-NS

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Results of extensive genetic studies on the *Escherichia coli* nucleoid (histone-like) protein H-NS revealed that this protein influences the regulation of a variety of unlinked genes (3). It was recently demonstrated that the expression of numerous *E. coli* proteins is greatly enhanced in an *hns* deletion background compared with their levels in wild-type cells (8). H-NS thus appears to function as a global DNA-binding transcriptional regulator (7). In a previous study, we purified a subset of proteins whose expression is affected by H-NS and cloned the genes coding for some of these proteins (9). During these studies, an *E. coli* DNA segment encoding two *hns*-dependent genes (encoding proteins named 10K-S and 10K-L) was cloned from  $\lambda$ D9 phage (number 607 in the sets of 476 selected *E. coli* genomic clones constructed by Kohara et al. [4]). The nucleotide sequences for these contiguous genes have been determined (9). Here, we report the complete nucleotide sequence for the adjacent third gene, whose expression is also affected by H-NS. The positions of these *hns*-dependent genes have been unambiguously mapped on the *E. coli* physical map (Fig. 1), proposed by Kohara et al. (4).

The restriction map of the *E. coli* genomic DNA carried on  $\lambda$ D9 is schematically presented in Fig. 1. The physical map of the sequenced region was confirmed by Southern hybridization

with appropriate DNA probes. In this *EcoRI*-*PvuII* region (corresponding to 77.3 min of the *E. coli* genetic map [1, 5]), three complete open reading frames (*orf-a* for 10K-S, *orf-b* for 10K-L, and *orf-d*) were identified, in addition to two partial open reading frames (*orf-c* and *orf-e*). It should be emphasized that the expression of *orf-a*, *orf-b*, and *orf-d* is greatly derepressed in an *hns* deletion background (9). Thus, we tentatively propose the name *hde* (*hns*-dependent expression) for these genes (*hdeA*, *hdeB*, and *hdeD*, respectively [Fig. 1]). The *hdeA* and *hdeB* genes seem to constitute a operon (9), although this must be verified. Sequence similarity search against the sequence banks (GenBank, EMBL, and DDBJ) revealed no significant sequence homology with these sequences. However, it is worth mentioning that the homology search revealed that the N-terminal amino acid sequence predicted for *orf-c* is highly homologous to that of Mg<sup>2+</sup> transport ATPase protein C (MgtC), reported previously for *Salmonella typhimurium* (6), i.e., 49 amino acids within the N-terminal 114-amino-acid sequence of ORF-C and MgtC are identical.

Finally, it should be noted that very few genetic loci have been mapped in the region covered by  $\lambda$ D9 (1, 5). According to the compilation of *E. coli* DNA sequences of Kröger et al. (5), the DNA sequence specifying the *gor* gene, ECOGOR

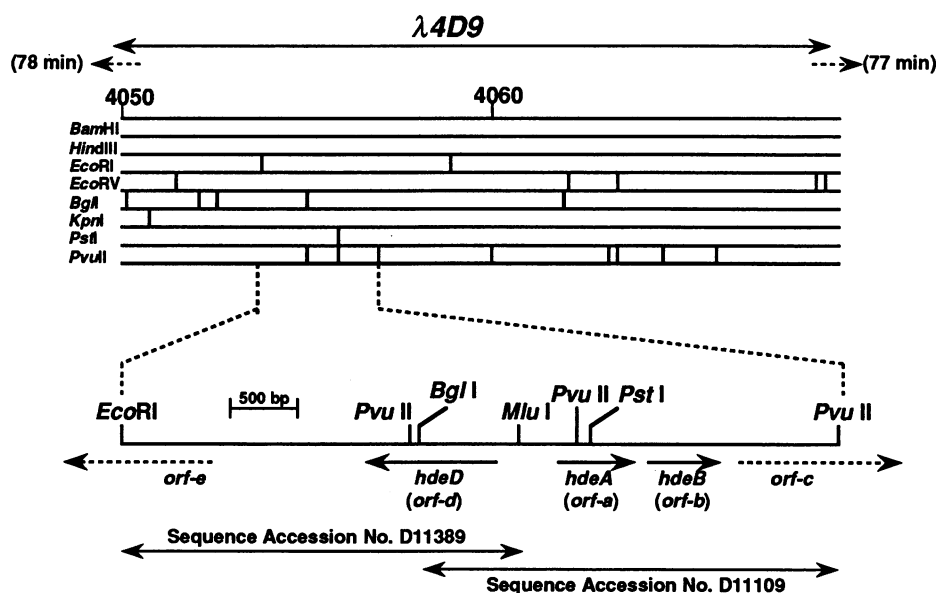


FIG. 1. Restriction map showing the region carried on  $\lambda$ D9. Restriction endonuclease cleavage sites, around coordinates 4050 to 4060 (in kilobase pairs) are depicted in the format of Kohara et al. (4). The region characterized in this study is enlarged. The positions of five open reading frames including *hdeA*, *hdeB*, and *hdeD* were identified. The arrows indicate the exact locations of the *hde* sequences as well as their directions of transcription (5' to 3'). Note that the sequences for the 3' proximal regions of *orf-c* and *orf-e* have not yet been determined.

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(GenBank), is likely to be located in this particular region, but our sequence does not overlap the *gor* sequence (2). Thus, the precise location of the *gor* gene could not be assigned.

**Nucleotide sequence accession number.** The DNA sequences of the *hdeA*, *hdeB*, and *hdeD* genes have been assigned GenBank, EMBL, and DDBJ accession numbers D11109 and D11389, as shown in Fig. 1.

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