The endonuclease I of *Escherichia coli* is an RNA-inhibitable DNase which is located in the periplasmic space of the *E. coli* cell (3); it cleaves native DNA into oligonucleotides (7). It is assumed that in the uninhibited, RNA-free state the enzyme introduces nucleotide sequence-independent double-strand breaks into DNA (2, 9), whereas the inhibited, RNA-complexed enzyme probably causes only nicking of DNA in the presence of high concentrations of salt (5). The enzyme is not essential for the cell, and its physiological role is unknown. Endonuclease I-deficient mutants resemble the wild type in growth rate, ability to propagate phage, and conjugal properties (4). The endA mutations were mapped near 64 min on the genetic map of the *E. coli* chromosome (1). We report the location of this gene on the physical map of *E. coli* and the direction of its transcription.

We devised an improved method to locate genes which determine a nonselectable phenotype on \( \lambda \) clones of the Kohara library of *E. coli* (6). Cells of an endA mutant (AB1806 endA; strain H520, obtained from H. Hoffmann-Berling) were coinfected with one of the Kohara \( \lambda \) clones and \( \lambda \) cI857 helper phage carrying a partially deleted Tn10 insertion with a functional tetracycline resistance gene (11). Phage suspensions (10\(^7\) PFU/ml) of the Kohara clones and the helper were mixed in a 2:1 ratio, and 10 \( \mu \)l of the mixture was spotted on the top agar of a Luria-Bertani agar plate seeded with 10\(^6\) stationary-phase H520 cells. After incubation of the plate for 24 h at 30\( ^\circ \)C, cells from the lysis zone were suspended and grown at 30\( ^\circ \)C overnight on LB plates containing 15 \( \mu \)g of tetracycline per ml. The colonies obtained were repotted to filter paper and stained with methyl green by the method of Wright (13). Green colonies are endA\(^-\); colorless colonies are endA\(^+\). Among the tetracycline-resistant colonies, about 3\% were EndA\(^+\) when the coinfected phage was \( \lambda \)474 and about 2\% were EndA\(^+\) when the coinfected phage was \( \lambda \)475, indicating that they carry the endA gene. No EndA\(^+\) clones were obtained with the flanking Kohara \( \lambda \) clones 471, 472, 473, 476, 477, 478, and 479. Selecting lysogens in this way avoids the necessity of screening \( \lambda \)-resistant clones, which normally constitute more than 90\% of the survivors in the lysis zones.

The inserts in Kohara \( \lambda \) clones 474 and 475 overlap by about 10 kb (Fig. 1). The approximately 1.3-kb HindIII fragment of the \( \lambda \)475 insert (6) was subcloned into a pBluescript vector. The resultant plasmid complements the endA mutation in the methyl green staining assay (13). Sequencing of the HindIII fragment and identification of the endA gene indicate that transcription occurs in a clockwise direction on the standard *E. coli* map (5a). Thus, the endA gene is located at position 3104 of the physical map (6), between genes metK and mutY near 63.6 min of the genetic map (1), as shown in Fig. 1.

We have constructed endA::Km and endA::Tc insertion mutants which will be reported elsewhere. These null mutants are available for strain construction on request.

**Nucleotide sequence accession number.** The nucleotide sequence of the endA gene has been assigned EMBL accession number X65169.

**REFERENCES**