In vitro synthesis of selenocysteinyl-tRNA_{UCA} from seryl-tRNA_{UCA}: Involvement and characterization of the *selD* gene product

(selenocysteine biosynthesis/SelD protein/selenium donor)

W. LEINFELDER, K. FORCHHAMMER, B. VEPREK, E. ZEHELEIN, AND A. BÖCK*

Lehrstuhl für Mikrobiologie der Universität München, Maria-Ward-Strasse 1a, D-8000 Munich 19, Federal Republic of Germany

Communicated by Thressa C. Stadtman, October 9, 1989 (received for review September 18, 1989)

ABSTRACT The selD gene from Escherichia coli, whose product is involved in selenium metabolism, has been cloned and sequenced. selD codes for a protein of 347 amino acids with a calculated molecular weight of 36,687. Analysis of the selD gene product through expression of the gene in the phage T7 promoter/polymerase system confirmed the predicted molecular weight of the protein. Gene disruption experiments demonstrated that the SelD protein is required both for the incorporation of selenium into the modified nucleoside 5methylaminomethyl-2-selenouridine of tRNA and for the biosynthesis of selenocysteine from an L-serine residue esterbonded to tRNA^{Ser}_{UCA}. tRNA^{Ser}_{UCA} has been purified, aminoacylated with L-serine, and used as a substrate for the development of an in vitro system for selenocysteine biosynthesis. Efficient formation of selenocysteinyl-tRNA^{Ser}_{UCA} was achieved by using extracts in which both the selD and the selA gene products were overproduced. The results demonstrate that selenocysteine is synthesized from L-serine bound to tRNA_{UCA} and they are in accord with SelD functioning as a donor of reduced selenium.

In Escherichia coli, selenium is inserted in the form of selenocysteine into the 80-kDa and 110-kDa subunits of formate dehydrogenases H and N (FDH_H and FDH_N), respectively, and into the modified nucleoside 5-methylaminomethyl-2-selenouridine (mnm ${}^{5}Se^{2}U$) (1–3). Mutants have been described that are either specifically deficient in selenoprotein synthesis (selA, selB, and selC genes) or unable to selenate both protein and tRNA (selD gene) (for review see ref. 4). The selC gene product has been shown to be a tRNA species (tRNA_{UCA}) that is aminoacylated with L-serine in vivo and that carries selenocysteine (5, 6). On the basis of these data it has been proposed that selenocysteine biosynthesis occurs from an L-serine residue charged to tRNAUCA (5). A putative role for the *selA* and *selD* gene products in this conversion process has been postulated. The selB gene product (SelB), on the other hand, is not essential for selenocysteinyl-tRNA formation in vivo (6). Recent results have shown that SelB is a guanine nucleotide-binding protein acting as a specific translation factor for selenocysteine insertion (34).

Mutants in *selD* are unique in that they are blocked in the incorporation of selenium both into FDH and into tRNA (7). They had originally been isolated as strains pleiotropically defective in FDH_H and FDH_N activity (8) and their additional defect in mnm⁵Se²U formation was detected only subsequently, when it was found that pleiotropic FDH mutants actually have a lesion in selenium metabolism (7). As an initial step toward identifying the biochemical function of the *selD* gene product, we have cloned and sequenced the *selD* gene from *E. coli* and devised an *in vitro* selenocysteine

biosynthesis system with the aid of extracts from cells in which the *selD* and *selA* gene products are overproduced.[†]

MATERIALS AND METHODS

Strains, Media, and Growth Conditions. The *E. coli* strains used in this study are listed in Table 1. Unless indicated otherwise, bacteria were grown in LB medium (13). When required, antibiotics were added to the following final concentrations: ampicillin, 50 μ g/ml; chloramphenicol, 20 μ g/ml; kanamycin sulfate, 50 μ g/ml.

Genetic Techniques. Basic genetic techniques were as described by Miller (13). recA mutations were transferred by P1kc-mediated transduction with JC10289(pKY102) as donor (10). Recombinant DNA methods were performed according to Maniatis *et al.* (14). DNA sequencing was carried out with the method of Maxam and Gilbert (15) as modified by Gray *et al.* (16) or with the dideoxy chain-termination method (17, 18).

Cloning and Subcloning of the selD Gene. A cosmid bank of genomic DNA from E. coli MC4100 (7) was screened for complementation (19, 20) of the lesion of strain MN30; DNA from a complementing clone obtained was partially digested with Sau3A1 and the fragments were ligated into the BamHI site of vector pACYC184 (21) to yield the complementing plasmid pMN302 (see Fig. 1) with a 3.8-kilobase (kb) Sau3A1 insert. The 1.2-kb BstEII fragment of pMN302 was then ligated into the Cla I site of plasmid pBR322 (22) to yield plasmid pMN330 and into the Sma I site of vector pT7-6 (23) to give plasmid pMN340. For selA overexpression, the 1.7-kb Sal I-Cla I insert of plasmid pWL171 (7) was ligated into Sal I/Cla I-cut vector pT7-6 to result in plasmid pWL187. Formation of the SelD protein was followed by [35S]methionine incorporation (23) by strain K38 transformed with pT7-6 or pMN340.

Construction of Strains WL400 and WL60153. The chromosomal *selD* gene was inactivated by inserting a 1.2-kb *Hin*PI fragment of pACYC184 carrying the *cat* gene into the *Cla* I site of pMN330 and by subsequent homologous recombination (11, 24) to yield strain WL400 (*selD204::cat*). Strain WL60153 (Δ *selAB*, *selD204::cat*) was constructed by transducing *selD::cat* from WL400 into strain WL30153 (Δ *selAB*) (7).

Preparation of Extracts for the Enzymatic Conversion of Seryl-tRNA_{UCA} to Selenocysteinyl-tRNA_{UCA}. Plasmids pWL187 and pMN340 were used to overexpress *selA* and *selD*, respectively, in the T7 polymerase system (23) using strain WL60153 as host. Supernatants were prepared by

The publication costs of this article were defrayed in part by page charge payment. This article must therefore be hereby marked "*advertisement*" in accordance with 18 U.S.C. \$1734 solely to indicate this fact.

Abbreviations: FDH, formate dehydrogenase; mnm^5Se^2U , 5-methylaminomethyl-2-selenouridine.

^{*}To whom reprint requests should be addressed.

[†]The sequence reported in this paper has been deposited in the GenBank data base (accession no. M30184).

Table 1. E. coli strains used

Strain	Relevant genotype	Reference or derivation
MC4100	sel ⁺	9
WL400	MC4100, selD204::cat ⁺	This work
WL30153	MC4100, $\Delta(selAB)$	7
WL60153	WL30153, selD204::cat ⁺	This work
JC10289	Δ(<i>srl-recA</i>)306::Tn10	10
CES200	recB21 recC22 sbcB15	11
MB08	selD165	6-8
MN30	MB08, Δ(<i>srl-recA</i>)306::Tn10	This work
K38	HfrC phoA4 pit-10 tonA22 ompF627 relA1 λ^+	12

centrifugation at 100,000 \times g and desalted by gel filtration through a Sephadex G-25 column. The resulting extract (termed S100/G25) was portioned, quick-frozen, and stored at -70° C under a N₂ atmosphere. Protein was determined by the method of Lowry *et al.* (25) with bovine serum albumin as a standard.

Purification and Aminoacylation of tRNA_{UCA} and of Cognate Serine Isoacceptors. Sixty milligrams of bulk tRNA, prepared from *E. coli* strain FM420 carrying plasmid pMN81 (5) was applied to a BD-cellulose column (Serva) (20×120 mm) equilibrated with buffer 1 (50 mM NaOAc, pH 5.0) containing 0.4 M NaCl and the column was developed with 600 ml of a linear gradient of 0.4 M NaCl to 1.1 M NaCl in buffer 1. On completion of the gradient, the strongly adsorbed material was eluted with 1.5 M NaCl/50 mM NaOAc, pH 5.0/14% (vol/vol) ethanol (26). Fractions containing tRNA_{UCA}, as monitored by gel electrophoresis (15), were pooled, and the tRNA was precipitated by the addition of 2 volumes of ethanol and finally dissolved in 2.5 ml of buffer 2 (10 mM NaOAc, pH 4.5/10 mM MgCl₂/1 mM dithiothreitol/1 mM EDTA) containing 1.3 M (NH₄)₂SO₄.

The tRNA was applied to a Sepharose 4B column $(12 \times 100 \text{ mm})$ equilibrated with buffer 2 containing 1.3 M $(NH_4)_2SO_4$ (27). The column was developed with 300 ml of a gradient decreasing from 1.3 M $(NH_4)_2SO_4$ to 0.3 M $(NH_4)_2SO_4$ in buffer 2. Fractions containing purified tRNA_{UCA} were pooled and dialyzed against three changes (2 liters each) of 10 mM NaOAc (pH 4.5), and the tRNA was collected by precipitation. The tRNA was charged with L-[¹⁴C]serine (170 μ Ci/ μ mol; 1 μ Ci = 37 kBq) as described (5).

Enzymatic Conversion of Seryl-tRNA_{UCA} to SelenocysteinyltRNA_{UCA}. The complete reaction mixture (50 μ l) for conversion of seryl-tRNA_{UCA} to selenocysteinyl-tRNA_{UCA} contained 100 mM Hepes (pH 7.5), 10 mM Mg(OAc)₂, 70 pmol of L-[¹⁴C]seryl-tRNA (171 μ Ci/ μ mol), 450 pmol of Na₂Se, 0.5 mM dithiothreitol, and S100/G25 extract to give a final protein content of 100 μ g. The reaction mixture was incubated at 30°C for 30 min. After 1 volume of 0.1 M NaOAc (pH 4.6) was added to the mixture, the aminoacylated tRNA was extracted with phenol, precipitated from the aqueous phase with ethanol, and dried *in vacuo*.

Hydrolysis of the aminoacyl-tRNA ester bond was carried out by incubation for 40 min at 40°C in 150 mM NH₄HCO₃ (pH 8.8). All procedures described were conducted in an anaerobic chamber under an atmosphere of 96% N₂ and 4% H₂. After hydrolysis of the aminoacyl-tRNA ester bond, 1 μ g of authentic DL-selenocysteine was added. The selenocysteine was then oxidized to the diselenide, selenocystine, by exposure to air (6). The solution was lyophilized and redissolved in water. Compounds were then analyzed by thinlayer chromatography under aerobic conditions (6). Authentic selenocystine was detected with the ninhydrin reagent.

RESULTS

Cloning, Nucleotide Sequence, and Expression of *selD.* Mutant MB08 from *E. coli* has been described as a strain that is pleiotropically defective in both FDH_H and FDH_N activity (8). A subsequent analysis revealed that it is deficient in the incorporation of selenium into both protein and tRNA (7). Cloning of the respective gene, *selD* (7), delivered plasmid pMN302, which carries a 3.8-kb chromosomal *Sau*3A1 fragment; its restriction map is given in Fig. 1. To narrow down the complementing region within the insert of pMN302, the plasmid was cut with *Mlu* I, the protruding ends were filled in with DNA polymerase Klenow fragment, and the linearized plasmid was religated. The mutant derivative had lost its complementation capacity, indicating that the *Mlu* I site is situated within the *selD* coding region (data not shown).

The Mlu I site, therefore, could be conveniently used for determining the nucleotide sequence in both directions by employing the strategy detailed in Fig. 1. The sequence (Fig. 2) contained an open reading frame coding for a putative gene product of 347 amino acids with a calculated molecular weight of 36,687.

Analysis of the sequence for restriction sites suitable for subcloning revealed that a *Bst*EII site borders the coding region at the 5' and 3' ends. To test whether the gene could be expressed and the putative gene product synthesized, the 1.2-kb *Bst*EII fragment was isolated and cloned into the expression vector pT7-6 to yield plasmid pMN340; it carries the open reading frame under the control of the phage T7 ϕ 10 promoter (23). In an [³⁵S]methionine-labeling experiment, bacteria carrying pMN340 synthesized a protein of the size expected from the deduced amino acid sequence (Fig. 3).

The selD Gene Product Has a Role in Selenium Insertion into Both Protein and tRNA. The deficiency of mutant MB08 in the incorporation of selenium into selenopolypeptides and into the modified nucleotides of tRNA could be due to two independent mutations, only one of which (that responsible for incorporation into protein) is complementable by the cloned gene. To test this possibility, we disrupted the open reading frame and replaced the chromosomal gene by the plasmid-encoded, disrupted gene. The resulting strain, WL400, is an MC4100 derivative with a cat gene cartridge inserted in the selD open reading frame. It is evident that the insertional inactivation of selD causes the loss of the capacity to incorporate selenium into the 80-kDa and 110-kDa selenopolypeptides of FDH_H and FDH_N, respectively, and into the modified nucleosides of tRNA (Fig. 4). Transformation of WL400 with plasmid pMN330 (selD⁺) restores the capacity for selenation of these macromolecules.

In Vitro Conversion of L-Seryl-tRNA_{UCA} to SelenocysteinyltRNA_{UCA}. An *in vitro* system was established to assess the role of *sel* gene products, in particular that of the *selD* gene, in selenocysteine biosynthesis. To this end, strain WL60153 was



FIG. 1. Restriction map of the DNA fragment of the 3.8-kb insert of pMN302 coding for the *selD* gene. The arrow above the restriction map signifies the transcriptional orientation of the *selD* gene. The arrows below give the sequencing strategy: \triangle , 5' labeling; \bigcirc , 3' labeling; \bigcirc , DNA sequenced by the dideoxy chain-termination method. B, *Bst*Ell; E, *Eco*Rl; C, *Cla* I; M, *Mlu* I; N, *Nco* I; Su, *Sau*3A1.

-37

GGTTACC ATACCOGGAT TGCATTGACA GGAGATGTCC

ATG AGC GAG AAC TOG ATT OGT TTG AGC CAA TAC AGC CAC GGA GCT GGT TGC GGC TGT AAA ATT TGC CCA AAA GTG TTG GAA AGC Met Ser Glu Asn Ser Ile Arg Leu Thr Gln Tyr Ser His Gly Ala Gly Cys Gly Cys Lys Ile Ser Pro Lys Val Leu Glu Thr ATC CTG CAT AGT GAG CAG GOG AAG TTT GTT GAT COG AAT TTG CTT GTG GGT AAT GAA ACC COC GAC GAT GOG GOG GTG TAC GAT 29 Ile Leu His Ser Glu Gln Ala Lys Phe Val Asp Pro Asn Leu Leu Val Gly Asn Glu Thr Arg Asp Asp Ala Ala Val Tyr Asp CTG GGC AAT GGC AGC AGC GTT ATC AGT AGC AGC GAC TTC TTT ATG CGG ATC GTT GAT AAT CCT TTC GAT TTT GGC CGC ATT GGG Leu Gly Asn Gly Thr Ser Val Ile Ser Thr Thr Asp Phe Phe Met Pro Ile Val Asp Asn Pro Phe Asp Phe Gly Arg Ile Ala 169 57 GOG ACT AAC GOC ATC AGC GAT ATC TTC GOG ATG GOG GOC AAA COG ATT ATG GOG ATT GOG ATC CTC GOC TGG COG ATT AAC AAA Ala Thr Asn Ala Ile Ser Asp Ile Phe Ala Met Gly Gly Lys Pro Ile Met Ala Ile Ala Ile Leu Gly Trp Pro Ile Asn Lys 253 CTT TOC OCA GAA ATT GOC OGC GAA GTG ACC GAA GGT GGA OGC TAT GCA TGT CGT CAG GOG GGT ATT GOG CTG GCC GGC GGT CAC 337 113 Leu Ser Pro Glu Ile Ala Arg Glu Val Thr Glu Gly Gly Arg Tyr Ala Cys Arg Gln Ala Gly Ile Ala Leu Ala Gly Gly His TOC ATC GAT GOG COG GAG COG ATT TITT GGT CTG GOG GTA AOG GOG ATC GTA COG ACC GAG COG GTG AAG AAA AAC AGT AOC GCA Ser Ile Asp Ala Pro Glu Pro Ile Phe Gly Leu Ala Val Thr Gly Ile Val Pro Thr Glu Arg Val Lys Lys Asn Ser Thr Ala 421 141 505 CAA GOC GGA TGC AMA CTG TTC CTG ACG AMA CCG CTG GGG ATC GGC GTT CTT ACC ACG GCT GAG AMA AMA TCA CTG TTG AMA CCA Gln Ala Gly Cys Lys Leu Phe Leu Thr Lys Pro Leu Gly Ile Gly Val Leu Thr Thr Ala Glu Lys Lys Ser Leu Leu Lys Pro 169 GAA CAT CAG GGA CTG GOG AOG GAA GTG ATG TOC COG ATG AAC ATC GCA GOC GOG TOC TTT GOC AAC ATC GAA GOC GTA AAA GOG Glu His Gln Gly Leu Ala Thr Glu Val Met Cys Arg Met Asn Ile Ala Gly Ala Ser Phe Ala Asn Ile Glu Gly Val Lys Ala 197 ATG ACC GAC GTT ACG GCC TTT GGT CTG CTG GCC CAC TTG ACC GAA ATG TGT CAG GCG GCT GGT GTG CAG GCA CGC GCC GAC TAT Met Thr Asp Val Thr Gly Phe Gly Leu Leu Gly His Leu Ser Glu Met Cys Gln Gly Ala Gly Val Gln Ala Arg Val Asp Tyr 673 225 GAA GOG ATC OOG AAA CTC OOC GGT GTT GAA GAG TAC ATT AAG TTG GGC GCA GTA OCT GGC GGC ACT GAA OGT AAC TTT GOC AGC Glu Ala Ile Pro Lys Leu Pro Gly Val Glu Glu Tyr Ile Lys Leu Gly Ala Val Pro Gly Gly Thr Glu Arg Asn Phe Ala Ser TAC GET CAT CTG ATG GET GAA ATG COG CET GAA GTG COC GAT CTG CTG TET GAT COG CAA ACT TCT GGC GET TTG CTG CTG COG 281 Tyr Gly His Leu Met Gly Glu Met Pro Arg Glu Val Arg Asp Leu Leu Cys Asp Pro Gln Thr Ser Gly Gly Leu Leu Ala GTC ATG CCG GAA GCA GAA AAT GAG GTC AAA GCT ACA GCC GCC GAG TTT GGC ATT GAA CTG ACG GCA ATT GGC GAA CTG GTG CCA Val Met Pro Glu Ala Glu Asn Glu Val Lys Ala Thr Ala Ala Glu Phe Gly Ile Glu Leu Thr Ala Ile Gly Glu Leu Val Pro 925 309 GOG GGC GGC GGT GGT GCC ANG GTT GAG ATT CGT TAA TICAANGOGG TIGITITATIG COGAAAAACC GAGICIGGOG GOGGCCATIG CIGATGIC Ala Arg Gly Gly Arg Ala Met Val Glu Ile Arg *** 337

1102 CT GOCCAAACCG CACCEGAAAG GOGATGECTT TATOGASTIC GETAATGETC AGETGETGAC C

FIG. 2. Nucleotide sequence and derived amino acid sequence of the *selD* gene from *E. coli* MC4100. The sequence of the noncoding, RNA-like strand is given 5' to 3'; the adenosine of the putative ATG initiation codon is taken as +1. The putative ribosome binding sequence is underlined and the termination codon TAA is indicated by stars.

constructed, which carries a deletion of the *selAB* genes plus an insertionally inactivated *selD* gene. It was transformed with either plasmid pWL187 (*selA*⁺) or pMN340 (*selD*⁺); after induction of expression of *selA* and *selD*, crude extracts were prepared. tRNA_{UCA}, purified by the procedure given in Fig. 5, charged with L-[¹⁴C]serine was used as substrate. The seryltRNA_{UCA}, as well as serine-inserting seryl-tRNA (as control), were incubated with extracts from strain WL60135 in which either the *selA* or *selD* gene had been overexpressed. The extracts were used either singly or in combination, and in the



presence or absence of sodium selenide. The products of the reaction were subjected to thin-layer chromatography and visualized by autoradiography (Fig. 6). L-Serine was converted to selenocysteine only when the reaction mixture



FIG. 4. ⁷⁵Se incorporation by wild-type *E. coli* MC4100 and by the *selD*::*cat* mutant WL400. An autoradiograph of a NaDodSO₄/ 10% polyacrylamide gel is shown in which denatured lysates of labeled cells (1) were electrophoretically fractionated. The migration positions of the 80- and 110-kDa selenopolypeptides of FDH_H and FDH_N, respectively, and of selenated tRNA are indicated. Lanes: 1 and 2, *E. coli* MC4100 (wild type); 3 and 4, WL400 (*selD*::*cat*); 5 and 6, WL400 carrying pBR322; 7 and 8, WL400 carrying pMN330. Cells were grown anaerobically in the absence (lanes 1, 3, 5, and 7) or presence (lanes 2, 4, 6, and 8) of nitrate (0.5%, wt/vol).

FIG. 3. Expression of the *selD* gene product from plasmid pMN340 in the T7 system, monitored by $[^{35}S]$ methionine labeling and NaDodSO₄/PAGE (23). Lanes: 1 and 2, vector pT7-6; 3 and 4, pMN340 (*selD*⁺). Cells were induced in the presence (lanes 1 and 3) or absence (lanes 2 and 4) of rifampicin.



FIG. 5. Purification of tRNA_{UCA} and cognate serine-inserting tRNA. (A) Chromatography of bulk tRNA on BD-cellulose. \blacktriangle , Serine acceptor activity. Pool a, tRNA_{UCA}; pool b, the serine-inserting isoacceptor species. (B) Chromatography of partially purified tRNA_{UCA}, corresponding to pool a in A, on Sepharose 4B using a decreasing salt gradient. \blacktriangle , Serine acceptor activity. Pool c contains essentially pure tRNA_{UCA}.

contained extracts with overproduced *selA* and *selD* gene products as well as sodium selenide. L-Serine charged to serine-inserting tRNA was not recognized as a substrate.

DISCUSSION

The proposed pathway of selenocysteine biosynthesis in E. coli, as suggested by previous work (5, 6) and by the results presented above, is depicted in Fig. 7. Biosynthesis starts with an L-serine residue aminoacylated to the *selC* gene



FIG. 6. Conversion of seryl-tRNA_{UCA} to selenocysteinyl-tRNA_{UCA}. Autoradiograph of a thin-layer chromatogram of the deacylation products from tRNA_{UCA} (lanes 1-5) and from cognate serine isoacceptor tRNA (lane 6). Seryl-tRNA[®]_{CA} (lanes 1-5) was incubated with the following: lane 1, 450 pmol of Na₂Se; lane 2, S100/G-25 extracts of WL60153/pGP1-2/pWL187 (*selA*⁺) and WL60153/pGP1-2/pMN340 (*selD*⁺) (50 μ g of protein from each extract); lane 3, as in lane 2 plus 450 pmol of Na₂Se; lane 4, 100 μ g of an S100/G-25 extract of WL60153/pGP1-2/pWL187 (*selA*⁺) plus 450 pmol of Na₂Se; lane 5, 100 μ g of a S100/G-25 extract of WL60153/pGP1-2/pWL187 (*selA*⁺) plus 450 pmol of Na₂Se; lane 6, seryl-tRNA^{Ser} (serine-inserting) was incubated as indicated for lane 3. The migration positions of serine (Ser) and selenocysteine (Sc) are indicated. X denotes an unidentified compound formed by SelA-containing extracts in the absence of SelD protein.

product, tRNA $\frac{VC}{VCA}$. After activation at the hydroxyl group, the leaving group is replaced by a selenol moiety to yield selenocysteinyl-tRNA $\frac{VCA}{VCA}$. In eukaryotes, it has been unequivocally demonstrated that the active serine derivative is O^3 -phosphoseryl-tRNA (28, 29); the evidence presented by Mizutani *et al.* (30) that *E. coli* selenocysteine formation also involves O-phosphorylation of L-serine is less compelling. Experiments have yet to be presented which show that (*i*) the *in vitro* phosphorylation reaction is dependent on the presence of the *selC*-encoded tRNA and (*ii*) the phosphorylated product is identical with *O*-phosphoserine ester-bonded to tRNA (30).

Mutant studies (5, 6) had suggested that the *selA* gene product is specifically involved in the conversion of L-serine into selenocysteine. SelA might be the first enzyme to act on seryl-tRNA_{UCA}, since L-serine was consumed and an as yet unidentified compound appeared (Fig. 6, lanes 2 and 4) when the extracts in the *in vitro* conversion system contained overexpressed SelA and lacked SelD protein. Our conversion system did not contain ATP and the extracts employed were purified by gel filtration to remove low molecular weight compounds. Some carryover of ATP from the charging reaction or its resynthesis, however, cannot be ruled out completely. A detailed analysis of the serine-activation step, therefore, must await the purification of the SelA protein.

In contrast to SelA, the SelD protein is required for incorporating selenium both into selenocysteine and into



Selenocysteinyl-tRNA UCA

FIG. 7. Pathway of selenocysteine biosynthesis and suggested role of the *selD* gene product. mnm^5S^2U , 5-methylaminomethyl-2-thiouridine; X-O-seryl-, serine residue activated at the hydroxyl group; *serS*, structural gene for serine-tRNA ligase.

mnm⁵Se²U (7). Kramer and Ames (31) have described a mutant ("selA1") from Salmonella typhimurium that exhibits a phenotype identical to that of E. coli MB08. Its defect could be complemented by plasmid pMN330, which carries the E. coli selD gene (32). The selA1 locus of S. typhimurium, therefore, is functionally equivalent to the E. coli selD locus, although these loci are situated at different sites on the chromosomes of these closely related organisms (8, 31). Interestingly, the Salmonella selA1 and the E. coli selD mutant effectively took up selenite from the medium and incorporated selenium nonspecifically into protein, as both selenocysteine and selenomethione (32). These facts preclude that the selD gene has a function in selenite uptake or in its intracellular reduction to selenide (32). Rather, the in vitro results have demonstrated that SelD is required for the enzymatic conversion of L-seryl-tRNA_{UCA} to selenocysteinvl-tRNA; therefore, an analogous role in tRNA selenation also seems obvious. From a purely theoretical basis, it seems implausible to assume that the SelD protein recognizes both substrates for selenation, the 2-thiouridine precursor of mnm⁵Se²U (33) and X-O-seryl-tRNA_{UCA}. In accordance with previous arguments (32) we therefore propose that SelD has a function in delivering reduced selenium to two specific enzymes catalyzing the individual reactions. If this is the case, we have to postulate the existence of at least two additional sel gene products, one specific for selenating the X-O-serine residue and another for the sulfur/selenium exchange at the modified uridine. As yet, no specific mutants are available that are blocked in either of these reactions.

The extracts used in the *in vitro* synthesis of selenocysteine contained overexpressed SelA and SelD but, due to a *selB* deletion mutation in strain WL60153, lacked SelB protein. This provides evidence that SelB is not required for selenocysteinyl-tRNA formation. Indeed, recent experiments have shown that SelB is a translation factor specific for the insertion of selenocysteine into protein (34).

We thank T. C. Stadtman for many stimulating discussions on selenium biochemistry, especially on the role of SelD. We are greatly indebted to M.-A. Mandrand-Berthelot for providing mutant MB08, to H. Nöth for the synthesis of sodium selenide, and to R. Leberman for the donation of purified seryl-tRNA ligase. We are obliged to G. Sawers for suggestions and for reading and improving the manuscript. This work was supported by grants from the Bundesministerium für Forschung und Technologie (Genzentrum, Munich) and the Fonds der Chemischen Industrie.

- Cox, J. C., Edwards, E. S. & DeMoss, J. A. (1981) J. Bacteriol. 145, 1317–1324.
- Zinoni, F., Birkmann, A., Stadtman, T. C. & Böck, A. (1986) Proc. Natl. Acad. Sci. USA 83, 4650–4654.
- Wittwer, A. J., Tsai, L., Ching, W.-M. & Stadtman, T. C. (1984) Biochemistry 23, 4650–4655.
- 4. Böck, A. & Stadtman, T. C. (1988) Biofactors 1, 245-250.

- Leinfelder, W., Zehelein, E., Mandrand-Berthelot, M.-A. & Böck, A. (1988) Nature (London) 331, 723-725.
- Leinfelder, W., Stadtman, T. C. & Böck, A. (1989) J. Biol. Chem. 264, 9720-9723.
- Leinfelder, W., Forchhammer, K., Zinoni, F., Sawers, G., Mandrand-Berthelot, M.-A. & Böck, A. (1988) J. Bacteriol. 170, 540-546.
- Haddock, B. A. & Mandrand-Berthelot, M.-A. (1982) Biochem. Soc. Trans. 10, 478-480.
- Casadaban, M. & Cohen, S. N. (1979) Proc. Natl. Acad. Sci. USA 76, 4530–4533.
- Ihara, M., Yoshimitsu, O. & Yamamoto, K. (1985) FEMS Microbiol. Lett. 30, 33-35.
- 11. Nader, W. F., Edlind, T. D., Huetterman, A. & Sauer, H. W. (1985) Proc. Natl. Acad. Sci. USA 82, 2698–2702.
- 12. Lyons, L. B. & Zinder, N. D. (1972) Virology 49, 45-60.
- 13. Miller, J. H. (1972) *Experiments in Molecular Genetics* (Cold Spring Harbor Lab., Cold Spring Harbor, NY).
- 14. Maniatis, T., Fritsch, E. F. & Sambrook, J. (1982) Molecular Cloning: A Laboratory Manual (Cold Spring Harbor Lab., Cold Spring Harbor, NY).
- 15. Maxam, A. M. & Gilbert, W. (1980) Methods Enzymol. 65, 499-561.
- Gray, C. P., Sommer, R., Polke, C., Beck, E. & Schaller, H. (1978) Proc. Natl. Acad. Sci. USA 75, 50–53.
- 17. Sanger, F., Nicklen, S. & Coulson, A. R. (1977) Proc. Natl. Acad. Sci. USA 74, 5463-5467.
- 18. Chen, E. J. & Seeburg, P. H. (1985) DNA 4, 165-170.
- Barrett, E. L., Jackson, C. E., Fukumoto, H. T. & Chang, G. W. (1979) Mol. Gen. Genet. 177, 95-101.
- Pecher, A., Zinoni, F. & Böck, A. (1985) Arch. Microbiol. 141, 359-363.
- 21. Chang, A. C. Y. & Cohen, S. N. (1978) J. Bacteriol. 134, 1141-1156.
- Bolivar, F., Rodriguez, R. L., Greene, P. I., Betlach, M. C., Heyneker, H. L., Boyer, H. W., Crosa, J. H. & Falkow, S. (1977) Gene 2, 95-113.
- 23. Tabor, S. & Richardson, C. C. (1985) Proc. Natl. Acad. Sci. USA 82, 1074–1078.
- Winans, S. C., Elledge, S. J., Krueger, J. H. & Walker, G. C. (1985) J. Bacteriol. 161, 1219–1221.
- Lowry, O. H., Rosebrough, N. J., Farr, A. L. & Randall, R. J. (1951) J. Biol. Chem. 193, 265–275.
- 26. Roy, K. L. & Söll, D. (1970) J. Biol. Chem. 245, 1394-1400.
- Holmes, W. M., Hurd, R. E., Reid, B. R., Rimerman, R. A. & Hatfield, G. W. (1975) Proc. Natl. Acad. Sci. USA 72, 1068– 1071.
- Lee, B. J., Warland, P. J., Davies, J. N., Stadtman, T. C. & Hatfield, D. L. (1989) J. Biol. Chem. 264, 9724–9727.
- 29. Mizutani, T. (1989) FEBS Lett. 250, 142-146.
- Mizutani, T., Maruyama, N., Hitaka, T. & Sukenaga, Y. (1989) FEBS Lett. 247, 345-348.
- 31. Kramer, G. F. & Ames, B. N. (1988) J. Bacteriol. 170, 736-743.
- Stadtman, T. C., Davis, J. N., Zehelein, E. & Böck, A. (1989) Biofactors 2, 35-44.
- Wittwer, A. J. & Stadtman, T. C. (1986) Arch. Biochem. Biophys. 248, 540-550.
- 34. Forchhammer, K., Leinfelder, W. & Böck, A. (1989) Nature (London), in press.