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**TITLE: Relationship of the Superoxide Dismutase Genes,
sodA and sodB, to the Iron Uptake (*fur*) Regulon
in *Escherichia coli* K-12**

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RELATIONSHIP OF THE SUPEROXIDE DISMUTASE GENES,
sodA AND *sodB*, TO THE IRON UPTAKE (*fur*) REGULON IN
ESCHERICHIA COLI K-12¹

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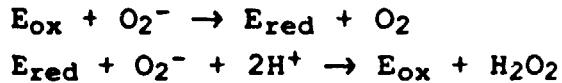
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ABSTRACT Expression of *sodA*, as indicated by MnSod activity is normal in *fur* mutants. This suggests that *sodA* is not a member of the *fur* regulon and that the putative Fe-binding, regulatory protein of *sodA*, suggested by Moody and Hassan (1984 J Biol Chem 259:12821), is not the Fur protein. By contrast, expression of *sodB*, as indicated by FeSod activity, is completely blocked in *fur* mutants and the effect is restored by transformation with a plasmid having a normal *fur* locus. The observations suggest that Fur, either directly or indirectly, controls SodB biosynthesis. Additional observations are described which indicate that SodB and Fur act together in a complicated fashion to control the biosynthesis of enterobactin.

INTRODUCTION

Metalloproteins that catalyze the disproportionation of superoxide anion are denoted superoxide dismutases (EC 1.15.1.1) (1-3), which function by the following catalytic cycle.

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There are three forms: an iron-requiring protein (FeSod) found in bacteria and plants, a manganese-containing protein (MnSod) present in bacteria and mitochondria, and a copper-zinc protein (CuZnSod) found in the cytosol of eukaryotic cells. In *Escherichia coli*, the 38.7-kDa FeSod and 45.8-kDa MnSod are dimeric structures with one iron or manganese atom bound to each subunit; the bacterial enzymes have remarkably similar structures (4). Their common physical structures and catalytic properties have suggested a common biological function, namely protection against oxygen toxicity through superoxide dismutation. This idea has been criticized by Fee (5).

The regulation of Sod activities in *E. coli* is remarkably complex. Expression of the *sodA* gene, which codes for the Mn-protein, is apparently coupled to respiration. Thus, *sodA* is expressed during respiratory growth with dioxygen, nitrate, trimethylamine oxide, dimethyl sulfoxide, and ferricyanide acting as electron acceptors (6-10); during either aerobic or anaerobic respiration, MnSod is induced by added methyl-viologen (11). Contrary to previous claims (11), *sodA* expression is not dependent on O_2^- (12). The work of Moody and Hassan (13) suggested that *sodA* expression was enhanced by removing Fe^{2+} from the culture medium. By contrast, expression of *sodB* appears to be enhanced with increased levels of Fe^{2+} in the medium (14, and references in 15). Thus, both genes may be responsive to Fe in the environment.

In this work we present evidence that *sodB* is closely related to the iron uptake systems of *E. coli*. Iron is required for growth of the cell and is available through several genetically unlinked uptake systems (16-18). These include the siderophores; enterobactin, aerobactin, and ferrichrome; the ferric citrate transport system; and a low-affinity, iron transport apparatus. The ferric ion uptake regulatory locus (*fur*) negatively

controls expression of these systems through the Fur protein (19). *In vivo*, the Fur protein binds, as a Fe²⁺-containing dimer, to a specific sequence of DNA (20), denoted the "iron box" (GATAATGATAATCATTACT), which is in the promoter regions of genes coding for iron uptake. An apparent "iron box" can be found in the *sodA* promoter region (21) suggesting the possibility that *sodA* may interact with Fur. By contrast, the *sodB* promoter region does not contain this iron-regulatory element (15).

Recognition of the "iron box" in *sodA* prompted us to examine *sodA* and *sodB* regulation in *fur* mutants. We predicted that *sodA* would be constitutively expressed in *fur* mutants while *sodB* would be unchanged (wild-type phenotype) in *fur* mutants. Our predictions were completely wrong.

METHODS

Some of the *E. coli* K-12 strains and the multicopy plasmids used in this work are listed in Table 1. Cells were grown in LB medium supplemented with glucose (0.2%) and the appropriate antibiotics. Cultures were induced with 100 μM methylviologen. Anaerobic cultures were grown in sealed flasks. Minimal medium consisted of Chelex-treated M9, glucose, thiamine, amino acids, MgCl₂, CaCl₂, FeCl₂, and the appropriate antibiotics. Catechol production was assayed by the Arnow method (22).

Saturated cultures were harvested, washed twice with 50 mM KPi, 0.5 mM EDTA, 1 mM MnCl₂, pH 8.0 buffer, lysed with lysozyme, treated with p-toluenesulfonyl fluoride, sonicated at 4°C for 90 s, and centrifuged at 10 000 × g for 10 min to remove cell debris. Protein concentrations were determined by the BCA method (23); bovine gamma globulin served as the calibration standard. Proteins were analyzed on 10% polyacrylamide gels (24). The gels were stained for protein with 26% isopropanol, 11% glacial acetic acid, and 0.1% Coomassie blue R, and destained with 10%

isopropanol and 10% glacial acetic acid, or stained for Sod activity with nitro blue tetrazolium (25).

TABLE 1
Strains And Plasmids

Strains	Genotype	Source or Reference
GC4468	<i>F</i> ⁻ Δ lac4169 <i>rps L</i>	D. Touati
QC774	GC4468 Φ (<i>sodA-lacZ</i>)49	D. Touati
	Φ (<i>sodB-Km</i>)1- Δ 2 <i>Cm</i> ^R <i>Km</i> ^R	
AB1157	<i>his arg thr</i>	G. Walker
BN402	P1 <i>lac</i> Δ U169 \times AB1157 <i>galK</i> ⁻	J. Neilands
BN407	P1 <i>lac</i> Δ U169 \times AB1157 <i>galK</i> ⁻	J. Neilands
	<i>pColVA3:Tn10 Tc</i> ^R	
BN4020	P1 <i>lac</i> Δ U169 \times AB1157 <i>galK</i> ⁻	J. Neilands
	<i>fur:Tn5 Km</i> ^R	
BN4023	P1 <i>lac</i> Δ U169 \times AB1157 <i>galK</i> ⁻	J. Neilands
	<i>fur:Tn5 Km</i> ^R	
	<i>pColVA3:Tn10 Tc</i> ^R	
EN3	P1 QC774 \times EN407 <i>Km</i> ^R	J. A. Fee
EN5	P1 QC774 \times BN402 <i>Km</i> ^R	J. A. Fee
EN9	P1 QC774 \times BN402 <i>Cm</i> ^R	J. A. Fee
EN13	P1 QC774 \times BN4020 <i>Cm</i> ^R	J. A. Fee
<u>Plasmids</u>		
pHS1-4	<i>sodB</i> ⁺ <i>Tc</i> ^R	D. Touati
pJM19	<i>sodB</i> ⁺ <i>Am</i> ^R	J. A. Fee
pABN203	<i>fur</i> ⁺ <i>Tc</i> ^R	J. Neilands

The xanthine-xanthine oxidase coupled reduction of cytochrome c was used to quantify soluble Sod activity (26).

RESULTS

As determined by PAGE using the assay of Beauchamp and Fridovich (24) (not shown), strains BN402 (wild-type) and BN 4020 (*fur*⁻) showed the normal phenotype for MnSod activity. No MnSod was produced under anaerobic growth, but O₂ and methylviologen induced MnSod activity. The FeSod activity was present in BN402, but FeSod activity was not detected in BN4020. Transformation of BN4020 with pABN203 (*fur*⁺) restores the wild-type levels of FeSod activity. The plasmid pHs1-4 (*sodB*⁺) produced large amounts of FeSod activity in BN402 but barely detectable levels of FeSod activity in BN4020.

Both MnSod and FeSod contribute to the total activity in cell extracts. In *sodA* mutants, the cytosolic activity is due only to FeSod; specific activities for *sodA* mutants appear in Table 2. The values directly parallel the observation made in the PAGE analysis and provide a quantitative base for our conclusions (see below).

TABLE 2
Specific Iron Superoxide Dismutase Activities^a For
sodA Mutants

No O ₂	<i>fur</i> ⁺			<i>fur</i> ⁻		
	BN402	pABN203	pHS1-4 ^b	BN4020 ^c	pABN203	pHS1-4
No O ₂	15	40	1700	<2	38	36
O ₂	29	170	1800	<2	29	36
O ₂ + PQ ²⁺	56	41	1700	<7	12	49

^a Sod activity measured by the xanthine-xanthine oxidase coupled cytochrome c method (26); units/mg protein; 5-28 µg protein/mL in assay

^b 0.2 µg protein/mL in assay

^c 50-250 µg protein/mL in assay

Enterobactin production assayed by the method of Arnow (22) indicates total catechol content of the sample. Selective strains were tested and the results appear in Table 3. As expected, *fur⁺* strains did not produce catechol in iron sufficient conditions while *fur* mutant strains excreted catechol independently of iron in the medium. Unexpectedly, interruption of the *sodB* gene led to an apparent *fur* phenotype, and this was not restored by transformation of *sodB* strains with pJM19 *sodB⁺*. Indeed, multiple copies of either *fur⁺* (pABN203) or *sodB⁺* (pJM19) led to the apparently complete suppression of enterobactin biosynthesis in all strains tested.

TABLE 3
Production of Catechols^a by Selected Strains

Strain Genotype	-Fe	+Fe	Phenotype
<i>fur⁺</i>	+	-	wt
<i>fur⁻</i>	+	++	<i>fur</i>
<i>fur⁻</i> pABN203 <i>fur⁺</i>	-	-	
<i>fur⁺</i> <i>sodB⁻</i>	+	++	<i>fur</i>
<i>fur⁺</i> <i>sodB⁻</i> pJM19 <i>sodB⁺</i>	-	-	
<i>fur⁺</i> pJM19 <i>sodB⁺</i>	-	-	

^a Ref. (22); + indicates a wild-type level of catechol production, ++ indicates an obvious increase in catechol production, - indicates that no catechol was present.

DISCUSSION

Three general conclusions can be drawn from our observations: First, expression of *sodA* is not affected by mutation in the *fur* locus. Second, *sodB* expression is directly or indirectly controlled by the *fur* locus. Finally, *sodB* (or downstream cistrons) is somehow controlling

expression of enzymes involved with enterobactin biosynthesis.

Based on the observation that *E. coli* expresses MnSod under anaerobic conditions in iron-depleted media, Moody and Hassan (13) postulated the existence of an Fe-binding protein that acts as a repressor of *sodA*. To account for the apparent "oxidative" induction of MnSod activity, it was further speculated that oxidation of Fe^{2+} to Fe^{3+} relieved repression of *sodA* (8). The recognition of a nearly perfect "iron box" in the -35 region of *sodA* prompted us to test the idea that *sodA* was part of the *fur* regulon. The data indicate that *sodA* is not regulated by *fur*; it is possible that another iron-binding protein is involved.

In contrast to *sodA*, *sodB* expression is dramatically influenced by the *fur* locus. Thus, the *sodB* gene product, FeSod, is absent in *fur* mutants and is restored when supplemented with pABN203 *fur*⁺. The return of FeSod activity parallels the appearance of protein (not shown) indicating that *sodB* regulation by *fur* involves synthesis of new enzyme rather than activation of incompetent enzyme. Assuming regulation of transcription, our observations indicate that *fur* through its product Fur, is acting in trans to control *sodB* expression. The question of whether this is a direct activation of *sodB* by Fur or an indirect activation through some other loci, is presently under experimental consideration..

The *ent* operon, responsible for the biosynthesis of enterobactin, is central to *E. coli*'s strategy for obtaining Fe from its environment (18). It has been known for some time that expression of *ent* is controlled by the *fur* locus whose gene product, in combination with Fe^{2+} , acts as a repressor of *ent*. As shown in Table 3, our observations confirm this basic hypothesis and extend it to include a role for *sodB* (or downstream cistrons). Excess *fur* in the cell, as obtains in the presence of the multicopy plasmid, pABN203 *fur*⁺, suppresses enterobactin biosynthesis even in iron poor medium. Similarly, the multicopy

plasmid, pJM19, bearing *sodB*⁺ also suppresses enterobactin biosynthesis. Broadly speaking, cells lacking either Fur or SodB appear to sense iron starvation and the ent operon is turned on, while cells having excess Fur or SodB sense iron sufficiency and expression of the ent operon is shut down. We are currently exploring the genetic and molecular basis of *sodB* in these regulatory processes.

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