

A *Bacillus subtilis* Malate Dehydrogenase Gene

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A *Bacillus subtilis* gene for malate dehydrogenase (*citH*) was found downstream of genes for citrate synthase and isocitrate dehydrogenase. Disruption of *citH* caused partial auxotrophy for aspartate and a requirement for aspartate during sporulation. In the absence of aspartate, *citH* mutant cells were blocked at a late stage of spore formation.

Enzymes of the Krebs citric acid cycle are known to play critical roles in the growth and differentiation of *Bacillus subtilis* (4, 8, 10, 15, 16, 25). Mutations in genes for Krebs cycle enzymes typically cause auxotrophy for amino acids and vitamins derived from Krebs cycle intermediates and a failure to metabolize substrates that cannot pass through the glycolytic pathway. Moreover, in most cases studied, mutations in Krebs cycle genes have been shown to cause a significant defect in spore formation even when cells are supplied with nutrients derived from the cycle (8, 10, 25).

With the exception of the genes for succinate thiokinase and malate dehydrogenase (MDH), the isolation of all *B. subtilis* Krebs cycle genes has been reported (12, 16), and the phenotypes of mutants defective in the various gene products have been analyzed (12, 16). In the course of studying citrate synthase genes, we found that the gene for the major citrate synthase (*citZ*) is located upstream of and is cotranscribed with the gene for isocitrate dehydrogenase (*citC*) (16, 17). Just downstream of *citC* we found a DNA sequence that could encode part of an MDH-like enzyme. Since the physical location of this cluster was consistent with prior mapping studies of the MDH gene (*citH*) and since Hulett and colleagues had found that an insertion mutation in this region (14) causes partial aspartate auxotrophy (13), we undertook completion of the sequencing and determination of whether the cloned DNA truly encodes MDH.

The 1.85-kb insert of *B. subtilis* DNA in plasmid pCS54 (Fig. 1) contains the 3' end of the *citC* gene and the 5' end of the *phoP* gene (19), surrounding a region of about 1 kb that was not previously reported. The sequence of this region was determined on both strands by using Sequenase version 2.0 and Taqsequence enzymes (U.S. Biochemicals) with double- or single-stranded DNAs of pCS54 and pMJB4 (Fig. 1) as templates. Analysis of the sequence (Fig. 2), using the University of Wisconsin Genetics Computer Group programs (7), revealed that an open reading frame (ORF) of 312 codons, preceded by an apparent ribosome binding site, lies downstream of *citC*. By comparison with sequences in the EMBL-GenBank collection, we found that the putative product of this ORF is similar to proteins described as lactate dehydrogenases (LDHs) and

MDHs. The greatest similarity (35 to 38% identity) was found to LDHs from *Bacillus* and *Lactococcus* spp. The only MDH in the same range of similarity (37% identity) was from *Haloarcula marismortui* (a halophilic archaeobacterium) (5).

LDH and MDH catalyze analogous chemical reactions (2). While the product of the *B. subtilis* ORF appears to be more similar to LDHs than to MDHs, it seemed likely that a cluster of Krebs cycle genes would include a gene for MDH rather than one for LDH. In fact, a conserved residue (Arg-87 in the *B. subtilis* ORF) involved in substrate specificity for both types of enzymes (5, 11, 24) is always arginine in MDH enzymes but is glutamine in LDHs (5) (Fig. 3). Moreover, two residues in the same region of the protein, Met-91 and Asp-94 in the *B. subtilis* ORF, are often Met and Asp in MDHs but are invariably Glu and Leu in LDHs (Fig. 3). On the other hand, a region between residues 127 and 158 in the *B. subtilis* ORF is much more similar to the corresponding region in LDHs than in MDHs (except for MDH of *H. marismortui*) (Fig. 3). Cendrin et al. (5) have noted that the sequence of *H. marismortui* MDH is sufficiently different from those of most eubacterial MDHs and LDHs to cause it to be placed on a distinct branch of the evolutionary tree; the product of the *B. subtilis* ORF may belong on the same branch.

To establish the function of the *B. subtilis* ORF unambiguously, we cloned a spectinomycin resistance cassette (18) between the *HincII* and *StyI* sites within *citH* in pCS60, creating pCS77 (Fig. 1), and integrated this insertion-deletion mutation into the *B. subtilis* chromosome by double-crossover recombination. Southern blot hybridization of restriction enzyme-digested chromosomal DNA of the resultant strain, SJB238, verified that the expected recombination event had occurred. Strain SJB238 and its isogenic *citH*⁺ parent, JH642 (22), were grown in nutrient broth sporulation (DS) medium (9) until early stationary phase (Krebs cycle enzymes are usually at their peak specific activity at this time). Extracts of cells were tested for MDH and LDH activities. As shown in Table 1, wild-type cells had both MDH and LDH activities; strain SJB238 had nearly normal LDH activity but a very low level of MDH activity. We conclude that the *B. subtilis* ORF encodes MDH. Since, in prior work, a mutation causing a deficiency in MDH activity was mapped to the *phoP* region of the chromosome and called *citH* (1), we assume that the same genetic locus is affected in strain SJB238. Repeated attempts to acquire and culture the original *citH* mutant strain have been unsuccessful.

The *citH::spc* mutation had only a slight effect on cell growth in minimal medium (and no effect in DS medium). In minimal-glucose-salts medium, the mutant had a doubling time of about 116 min, while the wild-type strain doubled every 94 min.

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Region 1

	R
Pig MDH	PDCLKGCDDVVVIPAGVPRKPGMTRDDL
Mus MDH	PDCLKGCDDVVVIPAGVPRKPGMTRDDL
Soy MDH	EDALIGMDLVIIPAGVPRKPGMTRDDL
Sce MDHp	ENTLSNAQVVLIPAGVPRKPGMTRDDL
Pho MDH	TPALEGADVLLISAGVARKPGMDRSDL
Eco MDH	TPALEGADVLLISAGVRRKPGMDRSDL
Sty MDH	TPALEGADVLLISAGVARKPGMDRSDL
Hma MDH	YEDTAGSDVVVITAGIPRQPGQTRIDLA
Bsu MDH	⁷⁰ YEDTAGSDIVVITAGIARKPGMSRDDL ⁹⁷
Bsu LDH	YEDCKDADIVCICAGANQKPGETRLDLV
Bps LDHp	YSDCKDADIVCICAGANQKPGETRLDLV
Bst LDH	YDDCRDADLVVICAGANQKPGETRLDLV
Bca LDH	YDDCRDADLVVICAGANQKPGETRLDLV
Bct LDH	YDDCRDADLVVICAGANQKPGETRLDLV
Bme LDH	YKDCADLAVITAGANQAPGETRLDLV
Lca LDH	YSDAKDADLVVITAGAPQKPGETRLDLV
Sth LDH	YEDCADADLVVITAGAPQKPGETRLDLV
Tma LDH	YADLKGSDVVIVAAGVQKPGETRLQLL
Mus LDH	YCVTANSKLVIIITAGARQQEGESRLNLV
Rat LDH	YSVTANSKLVIIITAGARQQEGESRLNLV
Hum LDH	YNVTANSKLVIIITAGARQQEGESRLNLV

Q E L

Region 2

Pig MDH	VNSTIPITAEVFKKHGVYVNPKNKIFGV	TTLDIVRAN
Mus MDH	VNSTIPITAEVFKKHGVYVNPKNKIFGV	TTLDIVRAN
Soy MDH	VNSTVPIAAEVFKRAGTYDPKRLG	TMLDVVRAN
Sce MDHp	VNSLVPIAVETLKKMGKFKPGNVMGV	TNLDLVRAN
Pho MDH	VNTTVAIAADVLLKAGVYDKRRLFGI	TTLDIIRSE
Eco MDH	VNTTVAIAAEVLKAGVYDKRRLG	TTLDIIRSN
Sty MDH	VNTTVAIAAEVLKAGVYDKRRLFGV	TTLDIIRSN
Hma MDH	VD LLNRHLYEAGDRSREQVIGFGRLDSARFR	
Bsu MDH	¹²⁷ VD AMTYAVYKESGFP KERVIGQSGVLD ¹⁵⁸ TARFR	
Bsu LDH	VD ILTYATWKFSGLP KERVIGSGTILDSARFR	
Bps LDHp	VD ILTYATWKFSGLP KERIIGSGTILDTGRFR	
Bst LDH	VD ILTYATWKFSGLP HERVIGSGTILDTARFR	
Bca LDH	VD ILTYATWKFSGLP HERVIGSGTILDTARFR	
Bct LDH	VD ILTYATWKFSGLP QERVIGSGTILDTARFR	
Bme LDH	VD ILAHTVQKVSGLP NGRVIGSGTILDTARFR	
Lca LDH	VD ILTYATWKLISGFP KNRVIGSGTSLDTARFR	
Sth LDH	VD VLTYSVWKFSGFP KERVIGSGTSLDSARFR	
Tma LDH	VD VLTYYFLLKESGMD PRKVFVSGTSLDTARLR	
Mus LDH	VD ILTYVAWKISGFP KNRVIGSGCNLDSARFR	
Rat LDH	VD ILTYVAWKISGFP KNRVIGSGCNLDSARFR	
Hum LDH	VD ILTYVAWKISGFP KNRVIGSGCNLDSARFR	

FIG. 3. Alignments of protein sequences for MDH and LDH from various organisms. Two conserved regions are compared, and selected highly conserved residues in region 1 are indicated above and below the sequence. The accession numbers for the sequences cited are as follows: pig mitochondrial MDH, P00346; mouse mitochondrial (Mus) MDH, M16229; soybean glyoxysomal (Soy) MDH, L01628; *Saccharomyces cerevisiae* (Sce) MDHp, the peroxisomal enzyme, P32419; *Photobacterium* sp. (Pho) MDH, L13319; *Escherichia coli* (Eco) MDH, P06994; *Salmonella typhimurium* (Sty) MDH, P25077; *H. marismortui* (Hma) MDH, M97218; *Bacillus subtilis* (Bsu) MDH, U05257; *B. subtilis* (Bsu) LDH, P13714; *Bacillus psychrosaccharolyticus* (Bps) LDHp, one of two LDH isozymes in this organism, P14561; *Bacillus stearothermophilus* (Bst) LDH, A91726; *Bacillus caldolyticus* (Bca) LDH, B29704; *Bacillus caldolenax* (Bct) LDH, S00019; *Bacillus megaterium* (Bme) LDH, P00345; *Lactobacillus casei* (Lca) LDH, A43944; *Streptococcus thermophilus* (Sth) LDH, D13405; *Thermotoga maritima* (Tma) LDH, S36863; mouse (Mus) LDH M chain, S06290; rat LDH M chain, P04642; and human (Hum) LDH M chain, A00347.

upstream genes should decrease *citH* expression. In fact, *spc* insertions in *citZ* or *citC* reduced MDH activity by about 70% (Table 1). Since the *spc* cassette is expected to block transcriptional read-through, such a result is consistent with partial

TABLE 1. L-MDH and L-LDH activities^a

Strain	Relevant genotype	Sp act ^b	
		MDH	LDH
JH642	<i>cit</i> ⁺	1.00	1.00
SJB194	Δ <i>citZ::spc</i>	0.28	ND
SJB219	Δ <i>citC::spc</i>	0.35	0.72
SJB238	Δ <i>citH::spc</i>	0.02	0.86

^a Cell cultures were grown in DS medium to approximately 1.5 h after exponential phase. Crude extracts were prepared as described previously (16) in a buffer containing 0.1 M Tris (pH 7.5), 2 mM EDTA, 0.2 M dithiothreitol, and 10% (vol/vol) glycerol.

^b Enzyme-specific activities of the wild-type strain were normalized to 1.00, and the ratios of enzyme activities in mutant strains to those in the wild-type strain are reported. Actual specific activities in the wild-type strain were as follows: MDH, 63.1 U/mg; LDH, 61.2 U/mg. One unit of enzyme activity produced 1 μ mol of NADH per min at 25°C. Enzyme assay solution contained 50 mM Tris (pH 7.5 [for MDH] or pH 8.8 [for LDH]), 2 mM NAD⁺, and 50 mM L-malate or 100 mM L-lactate. ND, not determined.

cotranscription. To test whether *citH* has its own promoter, we integrated into the *B. subtilis* chromosome a plasmid, pCS79, carrying the 3' end of *citC* and the 5' end of *citH* (Fig. 1). (This construction does not disrupt either the *citC* gene or the *citH* gene per se but separates the *citH* coding sequence from any promoter that lies upstream of the *Hind*III site within *citC*.) The resultant strain, SJB258, had no defect in cell growth (data not shown) and sporulated more efficiently than did the *citH::spc* strain (Table 2), suggesting that a promoter for *citH* lies within the cloned segment. (The vector does not supply a promoter for read-through transcription in the orientation used.) Strain SJB258 still sporulated less efficiently than did the wild-type strain, however, unless the medium was supplemented with aspartate. Taken together, these results suggest that *citH* has its own promoter but that this promoter is not able to achieve a rate of MDH accumulation adequate for sporulation. Read-through transcription from the *citZ* or *citC* promoter may be needed to provide the level of MDH expression needed for efficient sporulation.

The less-than-total blockage of sporulation caused by a *citH* null mutation might be explained by the presence of a second MDH-encoding gene in *B. subtilis*. E. M. Bryan and C. P. Moran, Jr. (3), have isolated a σ^E -dependent gene whose putative product is similar to a minority class of MDHs and LDHs (distinct from those listed in Fig. 3).

Nucleotide sequence accession number. The nucleotide sequence reported here has been given GenBank accession number U05257.

TABLE 2. Sporulation frequencies of *B. subtilis* strains with or without 0.2% aspartate^a

Strain	Relevant genotype	Addition to medium	Heat-resistant CFU at 17.5 h	Relative sporulation frequency
JH642	<i>cit</i> ⁺		2.6 \times 10 ⁸	1.00
SJB258	<i>'citC citH::neo</i>		3.7 \times 10 ⁷	0.14
SJB238	Δ <i>citH::spc</i>		3.0 \times 10 ⁵	1.15 \times 10 ⁻³
JH642	<i>cit</i> ⁺	Aspartate	4.6 \times 10 ⁸	1.00
SJB258	<i>'citC citH::neo</i>	Aspartate	3.4 \times 10 ⁸	0.74
SJB238	Δ <i>citH::spc</i>	Aspartate	5.0 \times 10 ⁷	0.11

^a Cell cultures were grown in DS medium (9) with or without the addition of 0.2% aspartate. All cultures grew to approximately the same cell density (4 \times 10⁸ to 5 \times 10⁸ cells per ml). Spore formation was assayed by heating a sample of each culture to 80°C for 10 min and then plating each on DS medium. Samples were taken 17.5 h after the end of the exponential growth phase.

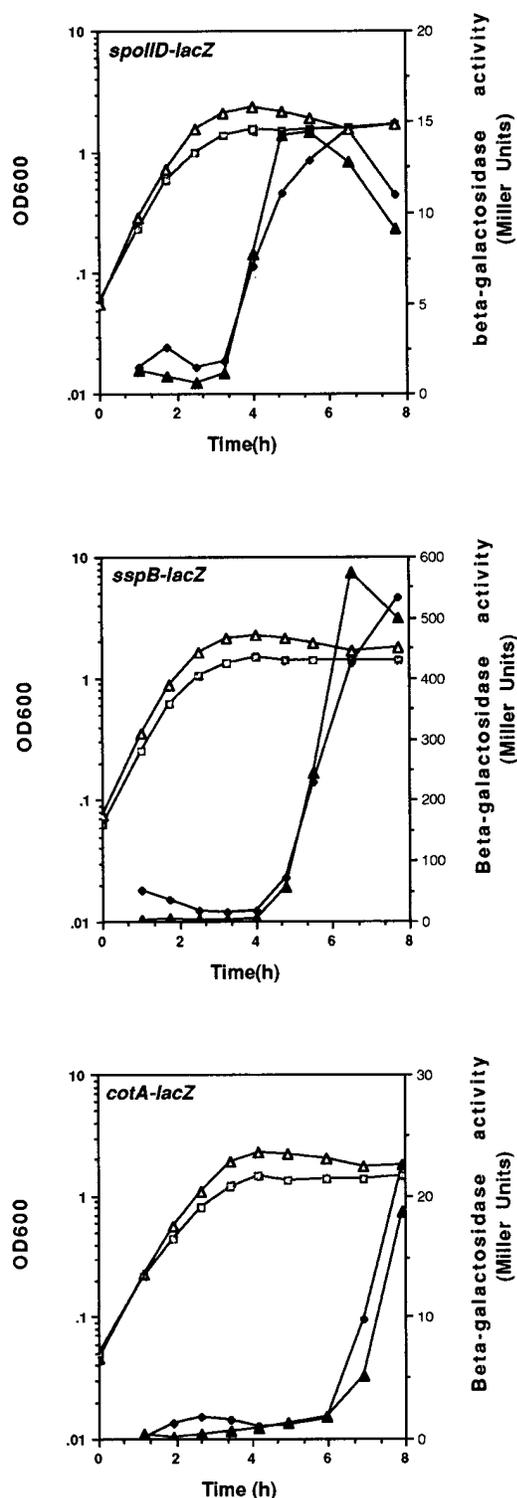


FIG. 4. β -Galactosidase activity in *B. subtilis* strains carrying fusions of sporulation gene promoter sites to *lacZ*. In each case, a *citH*⁺ and an isogenic *citH::spc* mutant strain were compared. The isogenic strains were constructed by transformation with DNA isolated from strain SR10 (23) for the *spoIID-lacZ* fusion, plasmid pJF751 (20) for the *sspB-lacZ* fusion, and DNA from strain SC432 (6) for the *cotA-lacZ* fusion. Cells were harvested, made permeable by exposure to toluene, and assayed for β -galactosidase activity as described previously (17). Open symbols indicate culture turbidity (optical density at 600 nm [OD600]); closed symbols indicate β -galactosidase activity. The triangles reflect data obtained with the *citH*⁺ strain; the squares and diamonds indicate data for the Δ *citH* strain.

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