Identification of Genes Encoding the Folate- and Thiamine-Binding Membrane Proteins in Firmicutes
Eudes, Aymerick; Erkens, Guus B.; Slotboom, Dirk; Rodionov, Dmitry A.; Naponelli, Valeria; Hanson, Andrew D.

Published in:
Journal of Bacteriology

DOI:
10.1128/JB.01070-08

IMPORTANT NOTE: You are advised to consult the publisher’s version (publisher’s PDF) if you wish to cite from it. Please check the document version below.

Document Version
Publisher’s PDF, also known as Version of record

Publication date:
2008

Link to publication in University of Groningen/UMCG research database

Citation for published version (APA):

Copyright
Other than for strictly personal use, it is not permitted to download or to forward/distribute the text or part of it without the consent of the author(s) and/or copyright holder(s), unless the work is under an open content license (like Creative Commons).

Take-down policy
If you believe that this document breaches copyright please contact us providing details, and we will remove access to the work immediately and investigate your claim.

Downloaded from the University of Groningen/UMCG research database (Pure): http://www.rug.nl/research/portal. For technical reasons the number of authors shown on this cover page is limited to 10 maximum.
Identification of Genes Encoding the Folate- and Thiamine-Binding Membrane Proteins in Firmicutes

Aymeric Eudes,1† Guus B. Erkens,2† Dirk J. Slotboom,2 Dmitry A. Rodionov,3,4 Valeria Naponelli,3 and Andrew D. Hanson1* 

Horticultural Sciences Department, University of Florida, Gainesville, Florida 326111; Department of Biochemistry, University of Groningen, Groningen Biomolecular Science and Biotechnology Institute, Nijenborgh 4, 9747 AG Groningen, The Netherlands2; Burnham Institute for Medical Research, La Jolla, California 920373; Institute for Information Transmission Problems RAS, Moscow 127994, Russia; and Food Science and Human Nutrition Department, University of Florida, Gainesville, Florida 326115

Received 30 July 2008/Accepted 27 August 2008

Genes encoding high-affinity folate- and thiamine-binding proteins (FolT, ThiT) were identified in the Lactobacillus casei genome, expressed in Lactococcus lactis, and functionally characterized. Similar genes occur in many Firmicutes, sometimes next to folate or thiamine salvage genes. Most thiT genes are preceded by a thiomodulin riboswitch.

The folate and thiamine transport systems of Lactobacillus casei were partially characterized 30 years ago by Henderson and colleagues (8, 9, 11, 12). These systems were shown to involve two small membrane proteins for specific substrate binding—one for folate and the other for thiamine—as well as an uncharacterized component shared by both systems.

To identify genes encoding the binding proteins (FolT and ThiT), we used the AACompIdent tool on the ExPASy server (27) to search the L. casei (strain ATCC 334) genome for open reading frames with amino acid compositions and molecular masses matching those published for FolT and ThiT (9, 12). The best match for FolT was LSEI_2252, a 19.0-kDa protein with five predicted transmembrane domains (Fig. 1A). LSEI_2252 has homologs in other Firmicutes, and in some cases, the corresponding genes are adjacent to folC (Fig. 1B). FolC is a salvage enzyme that mediates polyglutamylation of folates (2). The best match for ThiT was LSEI_1757, a 21.2-kDa protein with six predicted transmembrane domains, which belongs to the YuaJ family (InterPro accession number IPR012651) of predicted, uncharacterized thiamine transporters in the Bacillus/Clostridium group (20). LSEI_1757 is 32% identical to Bacillus subtilis YuaJ (Fig. 1C). In several Firmicutes, the thiT gene forms a putative operon with the thiamine pyrophosphokinase thiN gene (Fig. 1D). Like FolC, ThiN is a salvage enzyme that converts thiamine to its active pyrophosphate form (15).

To investigate whether folT and thiT indeed code for vitamin-binding proteins, the folT and thiT genes were PCR amplified from L. casei genomic DNA, cloned between the NcoI and SstI sites of pNZ8048, a vector carrying the nisin-inducible promoter (14), and introduced into membrane vesicles prepared by differential centrifugation (23) and expressed in L. casei cells (22). In all cases, vitamin binding approached a plateau within 5 s and was rapidly reversed by adding an excess of unlabeled substrate. The observed vitamin acquisition, thus, has the characteristics of a binding process rather than those of an uptake process.

For further characterization, FolT and ThiT were tagged with N-terminal His sequences. FolT-His and ThiT-His were produced in L. lactis as described above, except that cells were cultured in chemically defined medium (17, 19) without folic acid (for FolT-His) or thiamine (for ThiT-His) and harvested 3 h after induction. Membrane vesicles were prepared (24), and proteins were solubilized with dodecyl-β-maltoside (DDM) and purified to homogeneity by using nickel-Sepharose and gel filtration chromatography (3) (Fig. 3A and B). Vitamin binding was measured via quenching of intrinsic tryptophan fluorrescence, using a Spex Fluorolog 322 spectrophluorometer (Jobin Yvon) and a 1-ml stirred cuvette at 25°C. The FolT-His and ThiT-His concentrations were 100 to 17 pmol/mg protein, and those expressing ThiT bound a similar amount of [3H]thiamine. Adding a polyglutamyl tail of 2 to 4 residues to [3H]thiamine (16) markedly reduced binding, indicating that polyglutamyl folates are poor substrates for FolT, which is consistent with results from experiments using L. casei cells (22).

Published ahead of print on 5 September 2008.
The proteins bind their substrates with high affinity. The binding stoichiometries calculated from these data were far lower than 1:1 (0.17:1 for ThiT and 0.08:1 for FolT), compared to those calculated from the data for FolT and ThiT purified from L. casei. A likely explanation is that the substrates copurified with the binding proteins, thereby obscuring binding sites, as occurred with the purified high-affinity riboflavin-binding protein RibU (3). Absorption spectra of purified FolT confirmed that substrate had indeed been copurified (not shown).

Analysis of prokaryotic genomes using the SEED comparative genomics resource (18) revealed that ThiT and FolT homologs occur commonly and almost exclusively in Firmicutes, many of which are pathogens. The multiple sequence alignments and maximum-likelihood phylogenetic trees for the FolT and ThiT protein families are shown in Fig. S1 to S3 in the supplemental material. The FolT family is substantially more diverse; while the majority of FolT proteins have five predicted transmembrane domains, two subgroups have insertions that add two more such domains, and a third subgroup has a C-terminal extension similar to aspartyl-tRNA amidotransferase subunit C (see Fig. S1A in the supplemental material). Folate-binding activity was verified experimentally for FolT proteins from three pathogens (Mycoplasma capricolum, Clostridium novyi, and Streptococcus mutans) by expression in L. lactis cells and by measuring [3H]folic acid binding as above (Fig. 4). Two of these bacteria, C. novyi and S. mutans, have complete folate biosynthesis pathways (2), as do various other pathogenic Firmicutes with folT genes, including Bacillus anthracis and Clostridium botulinum. It is likely that such organisms can both make and take up folates and that their folate transport capacity—which was hitherto unsuspected—confers intrinsic resistance to antibiotics targeting the folate pathway, as in malaria parasites (26).

Most of the genes encoding ThiT proteins, including that of L. casei, were found to be preceded by a thiamine pyrophosphate (TPP) riboswitch (see Fig. S1B in the supplemental material), and indeed, the ThiT/YuaJ family was previously predicted to participate in thiamine transport based on computational identification of these riboswitches (20). A marked feature of L. casei ThiT is its almost total repression by high levels of thiamine in the medium (8). TPP riboswitches located in 3′ noncoding gene regions attenuate expression of downstream genes upon binding TPP (20, 28), which readily suggests a mechanism for the observed repression.

The identification of the genes encoding the folate- and thiamine-binding proteins of L. casei and other Firmicutes opens the way for dissection of the corresponding transport systems at the molecular level. These systems are undoubtedly novel, as FolT and ThiT are integral membrane proteins without characterized homologs. In terms of size and hydrophobicity (but not sequence), they resemble an emerging group of integral membrane proteins implicated in vitamin and trace metal uptake. These include the following: RibU of L. casei and Mycoplasma capricolum, a component of a biotin uptake system (5); and CbiM and NikM, involved in uptake of cobalt and nickel (21). The latter three systems all include a characteristic transmembrane protein (e.g., BioN) and an ATPase similar to those of ABC-type transporters (e.g., BioM), both encoded by genes adjacent on the chromosome to genes encoding the FolT/ThiT-like component. Although there are no bioN- and bioM-related genes linked to folT or thiT, it is reasonable to infer that they lie elsewhere in the genome, given the evidence that L. casei FolT and ThiT require other, shared components to form an active transport system and that the energy source is ATP hydrolysis (10, 11). And indeed, the
The L. casei genome contains a gene cluster encoding homologs of BioN (LSEI_2472) and BioM (LSEI_2473 and LSEI_2474), which are thus candidates for shared components of the folate and thiamine transporters.

**FIG. 2.** Functional expression of L. casei FolT and ThiT in L. lactis. (A) SDS-PAGE (12% gel) of membrane fractions from L. lactis harboring pNZ8048 alone (lane 1; 50 μg protein), or containing FolT (lane 2; 25 μg protein) or ThiT (lane 3; 25 μg protein). Staining was with Coomassie brilliant blue. The arrows indicate FolT and ThiT bands. Positions of molecular mass markers (kDa) are shown. (B to E) Binding of [3H]-labeled folates or thiamine to L. lactis cells harboring pNZ8048 alone (open squares) or expressing FolT or ThiT (filled squares). Assays (total volume, 1 ml) were performed in phosphate-buffered saline (PBS), pH 7.4, at 30°C with stirring. Cells were washed and resuspended (optical density at 600 nm, 20), and 0.5-ml aliquots were pretreated for 5 min with 2-deoxyglucose (25 mM final concentration). Assays were started by adding 0.5 ml of PBS containing [3H]-labeled vitamin (final concentration, 12.6 to 14.5 nM). At various times, cells (100 μl) were harvested by vacuum filtration on a cellulose nitrate membrane (0.45 μm). Filters were washed twice with 2 ml of ice-cold PBS, and their 3H content was determined by scintillation counting. The arrows show when unlabeled vitamin was added to give a final concentration of 50 nM. Cells expressing FolT were incubated with (6S)-[3',5',7,9-[3H(N)]folinic acid diammonium salt (Moravek; 10 Ci/mmol) (E) and folic acid (F).

**FIG. 3.** Purification and characterization of His-tagged L. casei ThiT and FolT. (A and B) SDS-PAGE of purified ThiT-His and FolT-His, as in Fig. 2A. (C) Fluorescence spectrum of ThiT-His (320 nM in 50 mM K phosphate, 200 mM KCl, 0.05% [wt/vol] DDM, pH 7.0) in the absence of thiamine (uppermost trace) and in the presence of successively higher concentrations of thiamine (up to 400 nM). (D) Fluorescence titration of ThiT-His with thiamine. (E and F) Fluorescence titration of FolT-His (210 nM in 50 mM K phosphate, 200 mM KCl, 0.05% [wt/vol] DDM, pH 7.0) with (6S)-folinic acid (E) and folic acid (F).
FIG. 4. Folate-binding by FoHT homologs from pathogenic Firmicutes expressed in L. lactis. The foHT genes from Clostridium novyi and Streptococcus mutans were obtained by PCR from genomic DNA; that of Mycoplasma capricolum was synthesized by GenScript (Piscataway, NJ). Cells harboring pNZ8048 alone (empty squares) or containing FoHT homologs (filled squares) were assayed for binding of (6S)-[3H]folinic acid (final concentration, 13.5 nM) as in Fig. 2. The arrows show when unlabeled folinic acid was added to give a final concentration of 50 μM.

We thank Robert Burne (University of Florida) for Streptococcus mutans genomic DNA and Shbin Zhou (Johns Hopkins University School of Medicine) for Clostridium novyi genomic DNA.

This project was supported by National Institutes of Health grant R01 GM071382 (to A.D.H.), by The Netherlands Organization for Scientific Research (vidi grant to D.J.S.), and by an endowment from R01 GM071382 (to A.D.H.), by The Netherlands Organization for Health Research and Development, by the C.V. Griffin, Sr. Foundation.

REFERENCES