The glucitol permease of *Escherichia coli*: a tripartite permease of the phosphotransferase system

In 1987, a report from this laboratory described the primary structure of the glucitol permease of *Escherichia coli* (5). This permease (GenBank accession no. J02708; SWISS-PROT identifier P05705) appeared to be unique in its domain structure since in contrast to all of the phospho-transferases (PTS), it appeared to have its IIB domain sandwiched in between the two halves of the IIC domain in a single polypeptide chain (3). The gene encoding this protein was designated *gutA* (5). The IIA domain was a distinct polypeptide chain encoded by a distinct gene, *gutB*.

Recently, two glucitol PTS permeases have been sequenced, one from the close *E. coli* relative *Erwinia amylovora* (accession no. Y14603; 1) and the other from the Gram-positive bacterium *Clostridium beijerinckii* (accession number AJ002527; 4). Both of these permeases were found to consist of three, rather than two polypeptide chains. Aldridge et al. (1) referred to the two genes encoding the equivalent of the putative GutA protein of *E. coli* as the *srlA* and *srlE* genes, whereas the gene encoding the IIA domain was referred to as *srlB*.

Recently, Blattner et al. (2) and Yamamoto et al. (7) reported the sequence of the *E. coli* glucitol operon as part of the *E. coli* genome sequencing projects (accession numbers AE000354 and D90892, respectively). Their results reveal the probable presence of a glucitol permease in the mannitol Enzyme I1 of *E. coli* (5). In contrast to all other sugar-specific PTS permeases, this permease has the same tripartite polypeptide structure as those from *E. amylovora* and *C. beijerinckii.* Thus, *gutA* encodes a hydrophobic protein (187 residues) with four putative transmembrane α-helical spanners (TMS); *gutE* encodes a larger protein (319 residues) that includes the hydrophilic IIB domain fused to a hydrophilic putative 4 TMS domain; and *gutB* encodes the hydrophilic IIA domain (3). We note that no other sugar-specific PTS permease is known to possess an IIA domain which is encoded by two distinct genes.

An average hydropathy plot and an average amphipathy plot (with the angle set at 100° for α-helix) of the *gutA* and *gutE* gene products revealed the presence of striking peaks of amphipathy preceding both hydrophilic domains (T. Le, T.-T. Tseng & M.H. Saier, Jr, unpublished). As previous results have clearly suggested that the corresponding amphipathic helical structure in the mannnitol Enzyme II of *E. coli* is required for proper insertion of the protein in the membrane (6), we suggest that the *gutA* and *gutE* gene products are independently inserted into the membrane using the same insertion machinery, dependent on an amphipathic α-helical structure preceding the first hydrophobic TMS. The revised sequences have been submitted to the GenBank/EMBL and SWISS-PROT databases.

This work was supported by NIH grants GM55434 and AI14176 to M.H.S.

Jonathan Reizer, Aila Reizer, Mamoru Yamada* and Milton H. Saier, Jr*++

1Department of Biology, University of California at San Diego, La Jolla, CA 92093-0116, USA.
2Department of Biological Chemistry, Faculty of Agriculture, Yamaguchi University, Yamaguchi 753, Japan.
*Correspondence. Tel: +1 619 534 4084. Fax: +1 619 534 7108. e-mail: msai@ucsd.edu
++For correspondence. Tel: +1 619 534 4084. Fax: +1 619 534 7108. e-mail: msai@ucsd.edu


GUIDELINES

Communications should be in the form of letters and should be brief and to the point. A single small Table or Figure may be included, as may a limited number of references (cited in the text by numbers, and listed in alphabetical order at the end of the letter). A short title (fewer than 50 characters) should be provided.

Approval for publication rests with the Editor-in-Chief, who reserves the right to edit letters and/or to make a brief reply. Other interested persons may also be invited to reply. The Editors of *Microbiology* do not necessarily agree with the views expressed in *Microbiology Comment*.

Contributions should be addressed to the Editor-in-Chief via the Editorial Office.

