A Phosphoenolpyruvate-Dependent Phosphotransferase System Is the Principal Maltose Transporter in *Streptococcus mutans*[▽]

Alexander J. Webb, Karen A. Homer, and Arthur H. F. Hosie*

Microbiology, King's College London Dental Institute, London, United Kingdom

Received 20 October 2006/Accepted 26 January 2007

We report that a phosphoenolpyruvate-dependent phosphotransferase system, MalT, is the principal maltose transporter for *Streptococcus mutans*. MalT also contributes to maltotriose uptake. Since maltose and maltodextrins are products of starch degradation found in saliva, the ability to take up and ferment these carbohydrates may contribute to dental caries.

The fermentation of carbohydrates by bacteria, such as *Streptococcus mutans*, and the corresponding production of organic acids are central to dental caries in humans (7). Analysis of the completed genome sequence of an *S. mutans* strain suggested that this bacterium has the capacity to transport and metabolize a wide range of carbohydrates (2). However, the precise role of many gene products is unknown, and many aspects of *S. mutans* physiology and carbohydrate metabolism are still incompletely understood. For example, although *S. mutans* can ferment maltose and utilize it as a sole carbon source (19), it is not known how maltose is taken up by this bacterium.

Maltose and maltodextrins are carbohydrates which are present in the oral cavity as dietary starch is broken down by α -amylase, an abundant enzyme in saliva (8). Therefore, fermentation of these carbohydrates by *S. mutans* may contribute to the competitiveness of *S. mutans* and to dental caries. BLAST (3) searches indicate that there are two members of the ATP-binding cassette (ABC) transporter superfamily in *S. mutans* which are similar to the well-characterized *Escherichia coli* maltose permease (Mal) (5). It was reported that the uptake of melibiose by one of these, the multiple sugar metabolism transporter (Msm), was inhibited by maltose (20), indicating that maltose may also be transported by this permease. Furthermore, the second of these Mal-like ABC transporters in *S. mutans*, encoded by *malX*, *malF*, *malG*, and SMU.1571, has been annotated as a putative maltose/maltodextrin transporter. However, as far as we know, no experimental evidence exists to support this designation. During the course of related research, we noted that *S. mutans* strains that lacked both a functional Msm permease and a Mal-like ABC transporter were still able to ferment maltose and use it as a sole carbon source, in a previously described minimal medium (22), to support growth (Fig. 1). Therefore, it is apparent that there is an unidentified maltose transporter in *S. mutans* and that this may be the principal maltose/maltodextrin permease in this species.

In addition to the Msm and Mal-like ABC transporters, there are 14 phosphoenolpyruvate-dependent phosphotransferase transport systems (PTS) in *S. mutans* (2). Such transporters are also involved in transporting a range of carbohydrates (21). There is biochemical evidence that some oral streptococci encode a maltose PTS, including strain OMZ176, which, although originally described as *S. mutans*, is now reclassified as *Streptococcus sobrinus* (23). However, the identities of streptococcal genes encoding such a maltose PTS are unknown. Therefore, we proposed that one of the *S. mutans* PTS transporters is the unidentified maltose transporter and sought to examine this hypothesis.

A number of maltose-specific PTS have been found in other bacterial species. In *E. coli* strains lacking a functional Mal ABC transporter, overexpression of *malX*, which in *E. coli* encodes a PTS transporter, restored the ability to grow on maltose, indicating that this PTS could transport maltose (12). However, it was proposed that MalX transports maltose by facilitated diffusion and that maltose is not the natural substrate of this transporter (12). In contrast, it is apparent that maltose is a principal substrate of *Enterococcus faecalis* MalT, since inactivation of the gene encoding this PTS decreased [¹⁴C]maltose uptake by 97% and markedly impaired growth of *E. faecalis* on maltose (9). Similarly, in *Bacillus subtilis* maltose is taken up by a maltose-specific PTS, MalP (17).

Each of the previously characterized maltose PTS belongs to the PTS glucose-glucoside family (transport classification no. 4.A.1.1) (14). Therefore, we compared the EII components of the members of this family present in *S. mutans* with the characterized maltose PTS transporters and related glucose PTS that belong to the same transporter classification subfamily (Fig. 2). Only 4 of the 14 PTS present in *S. mutans* UA159 belong to the glucose-glucoside family. These are BglP (a β -glucoside-specific PTS [6]), ScrA (a sucrose-specific PTS [16]), PttB (a putative trehalose-specific PTS), and the uncharacterized SMU.2047 protein. Only one of the *S. mutans* proteins had particular similarity to a characterized maltose system. The gene encoding this PTS (SMU.2047) was originally named *ptsG* by the genome annotators. However, the encoded protein is only 33% identical to *B. subtilis* PtsG. In contrast, *S. mutans* PtsG is 64% identical to *E. faecalis* MalT, a PTS that was characterized after the *S. mutans* genome was annotated (9). Therefore, we propose that rather than being a glucose-

* Corresponding author. Mailing address: Microbiology, King's College London Dental Institute, Floor 28, Guy's Tower, King's College London, Guy's Campus, London SE1 9RT, United Kingdom. Phone: 44 (0)20 7188 1825. Fax: 44 (0)20 7188 3871. E-mail: arthur.hosie@kcl.ac.uk.

[▽] Published ahead of print on 2 February 2007.

FIG. 1. Growth of *S. mutans* UA159 (solid lines), the isogenic *msmK::aphA3* mutant (KCL57; dotted lines), the SMU.1571::*aphA3* mutant (KCL48; dashed line), and the *msmK::aphA3* SMU.1571::*ery* double mutant (KCL82; dash-dot-dot line) in minimal medium containing 10 mM maltose as the sole carbon source. Data shown are means from at least three independent experiments.

specific PTS, *S. mutans* PtsG is an orthologue of *E. faecalis* MalT, and as such it should be renamed MalT or EII^{mal}. As with *E. faecalis* MalT (9), *S. mutans* MalT is a complex protein containing fused EIIA, EIIB, and EIIC domains.

Although *S. mutans* MalT (PtsG) has identity with *E. faecalis* MalT, the genetic context of the genes encoding this permease

in these two species is different. Of particular note is the absence in *S. mutans* of any apparent orthologue of *E. faecalis* *malP*, which encodes a maltose phosphate phosphorylase. There is no evidence that any of the genes surrounding *S. mutans* *malT* are associated with maltose metabolism. However, the product of SMU.2046c does have similarity to metal-dependent hydrolases (COG3568). Therefore, it is possible that this gene encodes a maltose-6-phosphate hydrolase and is required for metabolism of maltose transported into the cell by MalT, but this requires experimental confirmation.

To confirm that *S. mutans* MalT (PtsG) is a functional orthologue of *E. faecalis* MalT, we adopted a targeted mutagenesis approach. It was previously reported that inactivation of *S. mutans* *malT* (*ptsG*) did not alter sugar metabolism (1). However, maltose and maltodextrins were not included in this study. Therefore, we inactivated *malT*, using standard genetic manipulation techniques (15) and the cloning strategy outlined in Table 1, using the primers described in Table 2, before transforming *S. mutans*, as previously described (11), with the *malT::Spec^r* DNA from pKCL163, generating a *malT* mutant, KCL93. Reverse transcription-PCR (RT-PCR) analysis, with the primers listed in Table 2, confirmed that the insertion into *malT* did not disrupt the transcription of any adjacent genes, including SMU.2046c (primers P275 and P276) and *relA* (SMU.2045; primers P277 and P278). An internal fragment of *malT* was amplified by RT-PCR using primers P273 and P274, and the size of this product was consistent with insertion of the *Spec^r* gene. This RT-PCR analysis also indicated that *malT* is cotranscribed with SMU.2046c (primers P281 and P282), *relA*

FIG. 2. Phylogenetic tree indicating the relationship between *S. mutans* MalT (PtsG) and related permeases. A phylogenetic tree was constructed from the amino acid sequences of *S. mutans* MalT (PtsG) and a number of related EII components that are members of a subclass of PTS (glucose-glucoside family; transport classification no. 4.A.1.1) using Vector NTI Suite (version 10), which uses the ClustalW algorithm, and Treeview (Win32). Protein designations and accession numbers are as follows: bsMalP, *Bacillus subtilis* MalP (NP_388701); bsPtsG, *B. subtilis* PtsG (NP_389272); ecPtsG, *Escherichia coli* PtsG (NP_415619); ecMalX, *E. coli* MalX (P19642); efMalT, *Enterococcus faecalis* MalT (NP_814695); SMU.2047 PtsG/MalT, *S. mutans* PtsG/MalT (NP_722340); SMU.980 BglP, *S. mutans* BglP (NP_721375); SMU.1841 ScrA, *S. mutans* ScrA (NP_722158); SMU.2038 PttB, *S. mutans* PttB (NP_722334).

TABLE 1. Strains and plasmids used in this study

Strain or plasmid	Description	Source or reference
Strains		
UA159	<i>S. mutans</i> ATCC 700610	ATCC
KCL48	<i>S. mutans</i> UA159 SMU.1571::aphA3	This study
KCL57	<i>S. mutans</i> UA159 <i>msmK</i> ::aphA3	This study
KCL82	<i>S. mutans</i> UA159 <i>msmK</i> ::aphA3 SMU.1571::Em ^r	This study
KCL93	<i>S. mutans</i> UA159 <i>malT</i> (<i>ptsG</i>)::Spec ^r	This study
KCL103	KCL93 pKCL166	This study
KCL104	KCL93 pVA838	This study
Plasmids		
pCR2.1-TOPO	Cloning vector for PCR products; Km ^r Amp ^r	Invitrogen Life Technologies
pCR4-TOPO	Cloning vector for PCR products; Km ^r Amp ^r	Invitrogen Life Technologies
pNE1gfp	pDL278 shuttle vector with <i>gfpmut2</i> cloned into EcoRI site	4
pVA838	<i>E. coli-Streptococcus</i> species shuttle vector; Cm ^r Em ^r	10
pALH124	pALH123 carrying nonpolar <i>aphA3</i> (Km ^r) cassette	A. L. Honeyman
pKCL134	pALH124 containing <i>ery</i> (Em ^r), amplified from pVA838 with primers P184 and P185, replacing <i>aphA3</i> between HindIII sites	This study
pKCL55	pCR4-TOPO containing SMU.1571 from UA159, amplified using primers P84 and P85	This study
pKCL63	pCR4-TOPO containing <i>msmK</i> from UA159, amplified using primers P96 and P99	This study
pKCL90	pUC19 containing <i>msmK</i> cloned from pKCL63 as 1.5-kb SphI/SacI fragment	This study
pKCL96	pUC19 containing SMU.1571 cloned from pKCL55 as 1.9-kb EcoRI fragment	This study
pKCL98	pKCL90 with <i>aphA3</i> from pALH124 cloned into EcoRV site in <i>msmK</i>	This study
pKCL103	pKCL96 with <i>aphA3</i> from pALH124 cloned into HpaI site in SMU.1571	This study
pKCL148	pKCL96 with <i>ery</i> from pKCL134 cloned into HpaI site in SMU.1571	This study
pKCL154	pCR2.1-TOPO containing <i>malT</i> (<i>ptsG</i>) (SMU.2047) from UA159 amplified using primers P228 and P229	This study
pKCL156	pCR2.1-TOPO containing spectinomycin resistance gene from pNE1gfp, amplified using primers P232 and P233	This study
pKCL163	<i>malT</i> (<i>ptsG</i>)::Spec ^r , i.e., spectinomycin resistance gene from pKCL156, inserted between HpaI sites in <i>malT</i> in pKCL154, deleting 165 bp	This study
pKCL161	pCR4-TOPO containing <i>malT</i> (<i>ptsG</i>) (SMU.2047) from UA159, amplified using primers P235 and P236	This study
pKCL166	pVA838 containing <i>malT</i> (<i>ptsG</i>) from pKCL161 inserted into unique SalI site	This study

TABLE 2. Oligonucleotide primers used in this study

Primer function and name	Sequence
Cloning	
P84	GCATGCGTACTGATCGCCATTCCAATC
P85	GCTTTGGCAGCTGCTGTT
P96	GCATGCATCAAATTAATTCAACTTAC
P99	GAGCTCTTATCGAATGGCTGCTTCC
P184	AAGCTTAAAGAGGAAGGAAATAATAA ATGAACAAAAATATAATAA
P185	AAGCTTCTATTTCCTCCGTTAAATA ATAG
P228	CAATCAAGAAAAGGAGCGGAATC
P229	GAAAAAGATGTTTGCTGGGAGGT
P232	CCCGGGAAAAGAGGAAGGAAATAATAA GTGAGGAGGATATATTTGAA
P233	CCCGGGCTATTATAATTTTTTAATCTGT
P235	GTCGACTTAAAGTTCTACTTTGGCGA
P236	GTCGACGTTTGCGGAGCTTCTTA
RT-PCR analysis	
P273	GTATGTGGATTGCTTCTTCACAA
P274	AACCTTGAACACAGCGTAAAC
P275	ATGATGTTATTTGCGTTCAAGAGG
P276	GCTTGATACCCTTCATTTTCATAAG
P277	TGGTGTCACAAAGCTAGGGA
P278	GCATGGCATAAACATCACTTTG
P279	GGTAATGCAGGATTTGATTTTC
P280	GCAGGCATAACAGCAATAACA
P281	GATGGTTTCGCTGTTGAGC
P282	GCAGTTTCTGAATGCAAAAG
P283	CTTTTAATGGGGGATTTTAACAACC
P284	CTAAAATTCCTGCAACCTGAATAG

(SMU.2045; primers P238 and P284), and the putative gene annotated as SMU.2048 (primers P279 and P280). Coexpression with SMU.2048 was not expected, since it is transcribed divergently from *malT*. However, on closer inspection of the sequence annotated as SMU.2048, we doubt whether this is an actual gene, since it has only 152 nucleotides, it lacks an obvious initiation codon, and it has no significant similarity to known genes.

The abilities of wild-type *S. mutans* UA159 and the isogenic *malT* (*ptsG*) mutant to utilize maltose and maltodextrins as a sole carbon source were determined by observing growth in a semidefined medium (Fig. 3). This semidefined medium was described in a previous publication (22). Growth was determined by incubating inoculated 96-well microtiter plates, previously equilibrated and sealed under anaerobic conditions (80% N₂, 10% H₂, 10% CO₂), at 37°C in a microtiter plate reader (Labsystems iEMS reader MF; Thermo Life Sciences) and recording the optical density (620 nm) at 15-min intervals after shaking.

Although the *malT* mutant was able to grow on maltose as a sole carbon source, it did so only at a much reduced rate compared to growth of *S. mutans* UA159 (Fig. 3A). There was also a reduction in its ability to utilize maltotetraose and maltotriose (Fig. 3B and C). In contrast, there was no difference between the wild-type and the *malT* mutant when glucose (Fig. 3D) or isomaltose (data not shown) was the sole carbon source. Growth analysis of the complemented *malT* mutant,

FIG. 3. Growth of *S. mutans* UA159 (solid lines), the isogenic *malT* mutant (KCL93; dotted lines), the complemented *malT* mutant (KCL103; dashed lines), and the noncomplemented *malT* mutant plasmid control (KCL104; dash-dot-dot-dash line) in minimal medium containing 10 mM maltose (A), 10 mM maltotetraose (B), 10 mM maltotriose (C), or 20 mM glucose (D) as the sole carbon source. Data shown are means from at least three independent experiments.

KCL103, confirmed that the observed phenotype was due to the mutation of this gene and not any secondary mutation (Fig. 3). These data support the hypothesis that MalT is the principal transporter of maltose in *S. mutans* and not, as originally supposed, a glucose-specific PTS. Thus, *S. mutans* MalT is an orthologue of *E. faecalis* MalT.

The slight decrease in growth observed in maltotetraose and maltotriose (Fig. 3) indicates that these maltodextrins may also be substrates of MalT, but alternative transporters of these carbohydrates must be present in *S. mutans*. It has previously been reported that the principal transporter of isomaltose in *S. mutans* is the Msm transporter (13, 20). It is possible that maltotetraose or maltotriose is also transported by this or the related Mal-like ABC transporter, but further studies are required to confirm this.

The presented growth data are strong evidence that MalT is involved in maltose uptake. Nonetheless, to confirm this, we performed a series of radioactive uptake assays using [^{14}C]maltose (Amersham GE Healthcare). *S. mutans* strains were grown in a semidefined medium (described previously

[22]) with 20 mM glucose, 10 mM maltose, or 5 mM glucose plus 10 mM maltose as sole carbon sources. Exponentially growing *S. mutans* cells were harvested by centrifugation when the optical density (620 nm) was approximately 0.5, and uptake of [^{14}C]maltose was assayed by the rapid filtration method described previously, with a final concentration of 25 μM and 0.125 μCi [^{14}C]maltose (22). The *S. mutans* strains which lacked active *malT* (KCL93 and KCL104) were unable to accumulate [^{14}C]maltose, whereas the wild-type strain (UA159) and the complemented mutant (KCL103) did so at a rapid rate (Fig. 4). This confirms that MalT is the principal maltose transporter in *S. mutans*.

The rate of [^{14}C]maltose uptake was slightly enhanced by the inclusion of maltose in the growth medium rather than glucose (Fig. 4), indicating that the presence of this substrate increased expression of *malT*. However, the high rate of [^{14}C]maltose uptake observed for *S. mutans* grown on glucose as a sole carbon source (Fig. 4) indicates that *malT* is expressed under these conditions and it is not subject to significant catabolite repression.

FIG. 4. Uptake of $[U-^{14}C]$ maltose by *S. mutans* UA159 (A) (filled symbols), KCL93, the isogenic *malT* mutant (A) (open symbols), KCL103, the complemented *malT* mutant (B) (closed symbols), and KCL104, the noncomplemented *malT* mutant plasmid control (B) (open symbols) grown in minimal medium containing 20 mM glucose (squares), 10 mM maltose (triangles) (UA159 and KCL103 only, since the *malT* mutant cannot grow on maltose as a sole carbon source), or 5 mM glucose plus 10 mM maltose (circles). Data shown are means from at least three independent experiments.

To obtain an indication of the range of solutes transported by MalT, $[U-^{14}C]$ maltose uptake was carried out in the presence of 1 mM (40-fold excess) competing solutes (Fig. 5). None of the substrates tested inhibited uptake to the same extent as an excess of unlabeled maltose, which reduced uptake to only 5% of the control rate. Therefore, it is likely that MalT has greatest affinity for maltose. However, maltotriose, mannose, galactose, and fructose each inhibit $[U-^{14}C]$ maltose uptake by 60 to 72%, and maltotetraose, glucose, sucrose, and raffinose inhibit it by 28 to 42%. It is thus possible that these are substrates of MalT, with the latter group being lower-affinity substrates, although it is also possible that some are not actual substrates for this transporter but merely inhibit uptake of maltose. Nevertheless, it is apparent that MalT is at least not the sole transporter in *S. mutans* for some of these substrates. As discussed above, our growth data (Fig. 3) indicate there are other

FIG. 5. Inhibition of $[U-^{14}C]$ maltose uptake by competing solutes. The rate of $[U-^{14}C]$ maltose uptake by *S. mutans* UA159 grown in minimal medium containing 20 mM glucose was determined over the initial minute of uptake. Competing solutes were added to a final concentration of 1 mM, 5 s before the addition of 25 μ M (0.06 μ Ci) $[U-^{14}C]$ maltose.

transporters for maltotriose and maltotetraose. Furthermore, Abranches et al. (1) report that a *malT* mutant, which they refer to as a *ptsG* mutant, had no altered glucose, fructose, and mannose PTS activity compared to the wild-type strain. It is therefore unlikely that MalT is the dominant transporter of these carbohydrates.

Orthologues of *S. mutans* MalT are apparent, as a result of BLAST (3) searches, in the genomes of other *Streptococcus* species, including *Streptococcus pneumoniae* TIGR4 and R6, *Streptococcus pyogenes* MGAS5005, *Streptococcus agalactiae* 2603V/R, and *Streptococcus suis* 89/1591. Therefore, MalT orthologues may also play an important role in maltose and maltodextrin uptake in these important pathogens. It has been proposed that maltodextrin transport is a key component for the initial colonization of the oropharynx by *S. pyogenes* (18). In contrast to our observations with *S. mutans*, mutation of the gene encoding a single ABC transporter component in *S. pyogenes*, *malE* (which is similar to the genes encoding the solute binding proteins of *S. mutans* Msm and Mal-like ABC transporters), significantly impaired growth on maltose as a sole carbon source (18). We speculate that the MalT orthologue enables the residual growth on maltose in this *malE* mutant. However, it is clear that MalT alone cannot support optimum growth on maltose for *S. pyogenes*. Therefore, there are apparent differences in the relative contribution of MalT to maltose transport in *S. pyogenes* compared to that in *S. mutans*. Further research is required to determine whether the MalT orthologue in *S. pyogenes* contributes to colonization.

This work was funded by King's College London Dental Institute and The University of London Central Research Fund.

We thank A. L. Honeyman for providing us with plasmid pALH124.

REFERENCES

1. Abranches, J., M. M. Candella, Z. Z. T. Wen, H. V. Baker, and R. A. Burne. 2006. Different roles of EIIAB^{Man} and EIIA^{Glc} in regulation of energy me-

- tabolism, biofilm development, and competence in *Streptococcus mutans*. J. Bacteriol. **188**:3748–3756.
2. Ajdic, D., W. M. McShan, R. E. McLaughlin, G. Savic, J. Chang, M. B. Carson, C. Primeaux, R. Y. Tian, S. Kenton, H. G. Jia, S. P. Lin, Y. D. Qian, S. L. Li, H. Zhu, F. Najjar, H. S. Lai, J. White, B. A. Roe, and J. J. Ferretti. 2002. Genome sequence of *Streptococcus mutans* UA159, a cariogenic dental pathogen. Proc. Natl. Acad. Sci. USA **99**:14434–14439.
 3. Altschul, S. F., T. L. Madden, A. A. Schaffer, J. H. Zhang, Z. Zhang, W. Miller, and D. J. Lipman. 1997. Gapped BLAST and PSI-BLAST: a new generation of protein database search programs. Nucleic Acids Res. **25**:3389–3402.
 4. Bartilson, M., A. Marra, J. Christine, J. S. Asundi, W. P. Schneider, and A. E. Hromockyj. 2001. Differential fluorescence induction reveals *Streptococcus pneumoniae* loci regulated by competence stimulatory peptide. Mol. Microbiol. **39**:126–135.
 5. Boos, W., and H. Shuman. 1998. Maltose/maltodextrin system of *Escherichia coli*: transport, metabolism, and regulation. Microbiol. Mol. Biol. Rev. **62**: 204–229.
 6. Cote, C. K., D. Cvitkovitch, A. S. Bleiweis, and A. L. Honeyman. 2000. A novel beta-glucoside-specific PTS locus from *Streptococcus mutans* that is not inhibited by glucose. Microbiology **146**:1555–1563.
 7. Hamada, S., and H. D. Slade. 1980. Biology, immunology, and cariogenicity of *Streptococcus mutans*. Microbiol. Rev. **44**:331–384.
 8. Humphrey, S. P., and R. T. Williamson. 2001. A review of saliva: normal composition, flow, and function. J. Prosthet. Dent. **85**:162–169.
 9. Le Breton, Y., V. Pichereau, N. Sauvageot, Y. Auffray, and A. Rince. 2005. Maltose utilization in *Enterococcus faecalis*. J. Appl. Microbiol. **98**:806–813.
 10. Macrina, F. L., J. A. Tobian, K. R. Jones, R. P. Evans, and D. B. Clewell. 1982. A cloning vector able to replicate in *Escherichia coli* and *Streptococcus sanguis*. Gene **19**:345–353.
 11. Murchison, H. H., J. F. Barrett, G. A. Cardineau, and R. Curtiss. 1986. Transformation of *Streptococcus mutans* with chromosomal and shuttle plasmid (pYA629) DNAs. Infect. Immun. **54**:273–282.
 12. Reidl, J., and W. Boos. 1991. The *malX-malY* operon of *Escherichia coli* encodes a novel enzyme II of the phosphotransferase system recognizing glucose and maltose and an enzyme abolishing the endogenous induction of the maltose system. J. Bacteriol. **173**:4862–4876.
 13. Russell, R. R. B., J. Aduseopoku, I. C. Sutcliffe, L. Tao, and J. J. Ferretti. 1992. A binding protein-dependent transport system in *Streptococcus mutans* responsible for multiple sugar metabolism. J. Biol. Chem. **267**:4631–4637.
 14. Saier, M. H. 2000. A functional-phylogenetic classification system for transmembrane solute transporters. Microbiol. Mol. Biol. Rev. **64**:354–411.
 15. Sambrook, J., and D. W. Russell. 2001. Molecular cloning: a laboratory manual, 3rd ed. Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY.
 16. Sato, Y., F. Poy, G. R. Jacobson, and H. K. Kuramitsu. 1989. Characterization and sequence analysis of the *scrA* gene encoding enzyme-II^{scr} of the *Streptococcus mutans* phosphoenolpyruvate-dependent sucrose phosphotransferase system. J. Bacteriol. **171**:263–271.
 17. Schonert, S., S. Seitz, H. Kraft, E.-A. Feuerbaum, I. Andernach, G. Witz, and M. K. Dahl. 2006. Maltose and maltodextrin utilization by *Bacillus subtilis*. J. Bacteriol. **188**:3911–3922.
 18. Shelburne, S. A., P. Sumby, I. Sitkiewicz, N. Okorafor, C. Granville, P. Patel, J. Voyich, R. Hull, F. R. Deleo, and J. M. Musser. 2006. Maltodextrin utilization plays a key role in the ability of group A *Streptococcus* to colonize the oropharynx. Infect. Immun. **74**:4605–4614.
 19. Simpson, C. L., and R. R. B. Russell. 1998. Intracellular α -amylase of *Streptococcus mutans*. J. Bacteriol. **180**:4711–4717.
 20. Tao, L., I. C. Sutcliffe, R. R. B. Russell, and J. J. Ferretti. 1993. Transport of sugars, including sucrose, by the Msm transport system of *Streptococcus mutans*. J. Dent. Res. **72**:1386–1390.
 21. Vadeboncoeur, C., and M. Pelletier. 1997. The phosphoenolpyruvate:sugar phosphotransferase system of oral streptococci and its role in the control of sugar metabolism. FEMS Microbiol. Rev. **19**:187–207.
 22. Webb, A. J., and A. H. F. Hosie. 2006. A member of the second carbohydrate uptake subfamily of ATP-binding cassette transporters is responsible for ribonucleoside uptake in *Streptococcus mutans*. J. Bacteriol. **188**:8005–8012.
 23. Wursch, P., and B. Koellreutter. 1985. Maltotriitol inhibition of maltose metabolism in *Streptococcus mutans* via maltose transport, amylomaltase and phospho- α -glucosidase activities. Caries Res. **19**:439–449.