Identification of TlpC, a novel 62 kDa MCP-like protein from *Bacillus subtilis*

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We report the sequence and characterization of the *Bacillus subtilis* tlpC gene. tlpC encodes a 61.8 kDa polypeptide (TlpC) which exhibits 30% amino acid identity with the *Escherichia coli* methyl-accepting chemotaxis proteins (MCPs) and 38% identity with *B. subtilis* MCPs within the C-terminal domain. The putative methylation sites parallel those of the *B. subtilis* MCPs, rather than those of the *E. coli* receptors. TlpC is methylated both in vivo and in vitro although the level of methylation is poor. In addition, the *E. coli* anti-Trg antibody is shown to cross-react with this membrane protein. Inactivation of the tlpC gene confirms that TlpC is not one of the previously characterized MCPs from *B. subtilis*. Capillary assays were performed using a variety of chemoeffectors, which included all 20 amino acids, several sugars, and several compounds previously classified as repellents. However, no chemotactic defect was observed for any of the chemoeffectors tested. We suggest that TlpC is similar to an evolutionary intermediate from which the major chemotactic transducers from *B. subtilis* arose.

Keywords: chemotaxis, *Bacillus subtilis*, MCP, DNA sequence, methylation

INTRODUCTION

In *Escherichia coli*, the methyl-accepting chemotaxis proteins (MCPs) (Kort *et al.*, 1975) are the receptors for attractants and repellents, and are subject to methyl-esterification on conserved glutamate side chains (Kleene *et al.*, 1977; Van der Werf & Koshland, 1977) located within their cytoplasmic domain. Binding of a repellent at the MCPs is believed to cause an increase in the rate of autophosphorylation of CheA, with subsequent increases in levels of CheY-P and CheB-P (Hess *et al.*, 1988; Ordal *et al.*, 1992). CheY-P binds to the switch to cause clockwise rotation of the flagella (Bourret *et al.*, 1990), whereas CheB-P demethylates the MCPs to restore the autophosphorylation of CheA to a prestimulus level (Lupas & Stock, 1989; Stewart *et al.*, 1990). Thus, the receptors play a dual role, one to facilitate excitation, which occurs upon the initial binding of attractants or repellents, and the other to bring about adaptation, which occurs upon the continued binding of a chemoeffectector. Phosphorylation reactions are involved in the excitation process, while methylation reactions are involved in adaptation.

MCPs are widespread among prokaryotes (Morgan *et al.*, 1993), and their presence in both eubacteria and archaea (Alam *et al.*, 1989; Yao & Spudich, 1993) is testimony to their ancient origin, which probably predates the separation of these two lines of descent. MCPs are also known to exist in the Gram-positive organism *Bacillus subtilis*. Biochemical evidence suggested that there were three MCPs, with molecular masses ranging from 77 to 97 kDa (Bedale *et al.*, 1988; Hanlon *et al.*, 1993). However, four *B. subtilis* genes encoding proteins homologous to *E. coli* MCPs have recently been cloned and characterized. These genes are located in three contiguous operons, and all have predicted molecular masses of 72 kDa. Interestingly, inactivation of two of these transducer-like proteins leads to no apparent loss of methylation and results in no observable defects in chemotaxis (Hanlon & Ordal, 1994).

Here we report the cloning, sequencing and characterization of a unique methyl-accepting protein from *B. subtilis*, designated TlpC (transducer-like protein). The corresponding gene was discovered in the course of a sequencing project seeking to uncover possible competence genes near the *comL* locus.

Abbreviation: MCP, methyl-accepting chemotaxis protein.
The GenBank accession number for the nucleotide sequence reported in this paper is X34005.
Table 1. Bacterial strains and plasmids used in the characterization of the B. subtilis tlpC gene

<table>
<thead>
<tr>
<th>Strain or plasmid</th>
<th>Relevant genotype or description</th>
<th>Comment/reference</th>
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<tbody>
<tr>
<td><strong>Strains</strong></td>
<td></td>
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<tr>
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<td></td>
</tr>
<tr>
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<td>K38</td>
<td>Harbours pGP1-2</td>
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<td>JM101</td>
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<td><strong>B. subtilis</strong></td>
<td></td>
<td></td>
</tr>
<tr>
<td>O11085</td>
<td>C8c' hisH2 metC trpF7</td>
<td>Ordal &amp; Goldman (1976)</td>
</tr>
<tr>
<td>O13054</td>
<td>O11085(pDW41), Cm'</td>
<td>This work</td>
</tr>
<tr>
<td><strong>Plasmids</strong></td>
<td></td>
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<tr>
<td>pBGSC6</td>
<td>Integration vector, Cm'</td>
<td>Bacillus Genetic Stock Center</td>
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<tr>
<td>pT7-6</td>
<td>E. coli expression plasmid, Ap'</td>
<td>Tabor &amp; Richardson (1985)</td>
</tr>
<tr>
<td>pGP1-2</td>
<td>Contains gene encoding T7 polymerase, Km'</td>
<td>Tabor &amp; Richardson (1985)</td>
</tr>
<tr>
<td>pGSM10</td>
<td>Contains map62 gene within a 6 kb Sall–EcoRI DNA fragment, Ap'</td>
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<td>1.9 kb TaqI fragment cloned into AccI site in pBluescriptSK-, Ap'</td>
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<td>pDW39 containing a 400 bp BglII–BanHI deletion</td>
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<tr>
<td>pDW41</td>
<td>0.8 kb Spbl–BglII fragment subcloned into pBGSC6</td>
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**METHODS**

**Bacterial strains and plasmids.** All bacterial strains and plasmids used in this study are described in Table 1.

**DNA sequence and analysis.** The 1.9 kb TaqI DNA fragment shown in Fig. 1 was sequenced on both strands to obtain an unambiguous consensus sequence. Sequencing was performed by the dideoxy chain termination method (Sanger et al., 1977). Protein alignments were performed using the AALIGN program from DNASTAR.

**Expression of TlpC.** The 1.9 kb TaqI fragment containing tlpC was modified by site-directed mutagenesis to create an additional TaqI restriction site which was proximally located just upstream of the potential ribosome-binding site. The corresponding 1.7 kb TaqI fragment which was isolated from pDW37 did not contain the adjacent terminator or promoter regions which might have interfered with the expression analysis. This insert was ultimately subcloned into the pT7-6 expression plasmid and transformed into E. coli strain K38 for expression using the T7 expression system of Tabor and Richardson (1985). Plasmid pDW40, containing a 400 bp C-terminal deletion of the TlpC gene in pT7-6, was expressed in parallel. The protein samples were electrophoresed on 10% (w/v) gels and 35S-labelled bands were visualized by autoradiography.

**Mutagenesis of tlpC.** A 0.8 kb Spbl–BglII fragment from tlpC was subcloned into pBGSC6, a plasmid which is unable to replicate in B. subtilis. The resulting plasmid, pDW41, was subsequently transformed into wild-type strain O11085. A single Campbell-like recombination event between homologous DNA resulted in the disruption of the tlpC gene, which was selected for by resistance to chloramphenicol. The integration event used to create mutant strain O13054 was confirmed by Southern blot analysis.

**Methylations.** In vivo methylation experiments have been described previously (Ullah & Ordal, 1981). To visualize poorly methylated proteins, an extended methylation was performed for 10 min with 25 μCi (925 kBq) [methyl-3H]methionine. The procedure used to isolate membranes has been described elsewhere (Goldman & Ordal, 1984). In vitro methylation reactions were performed essentially as described by Goldman & Ordal (1984) with slight modification, which included an increase in the addition of S-adenosyl-[methyl-3H]methionine to 20 μl. Reactions were incubated at room temperature for 3 h to achieve maximal labelling.

**Other procedures.** E. coli transformations were performed using the RhCl procedure of Hanahan (1985) and B. subtilis transformations were performed as described previously by Ordal et al. (1983). The immunoblot procedure has been described in detail elsewhere (Carpenter et al., 1992). Capillary assays have also been described previously (Ordal & Goldman, 1975). Assays which were performed to examine sporulation (Rudner et al., 1991) and competence (Ordal et al., 1983) have been described. To examine protein secretion, cells from the wild type O11085 and tlpC mutant strain O13054 were grown in L-broth until early- and mid-exponential growth was reached (40 and 120 Klett units), as well as early-stationary phase.

**Fig. 1.** Nucleotide and deduced amino acid sequence of tlpC. The predicted ribosome-binding site for the open reading frame corresponding to TlpC is underlined, and the stop codon is indicated with an asterisk. The putative promoter region is double underlined, and a predicted terminator from the upstream transcriptional unit is indicated by bold facing arrows. The location of relevant restriction sites which were used to construct the tlpC mutant are indicated above the DNA sequence.
Fig. 1. For legend see facing page.
were immediately precipitated on ice with 7% (w/v) TCA for 15 min. Following centrifugation and an acetone/ethanol wash, the protein pellets were resuspended in 1 × SDS solubilizer (62 mM Tris pH 6.8, 2% SDS, 10% glycerol, 5% β-mercaptoethanol). Equivalent amounts of protein were boiled for 5 min and electrophoresed by SDS-PAGE on 10% (w/v) polyacrylamide gels. Secreted proteins were detected by silver stain.

RESULTS

Nucleotide sequence and analysis of tlpC

DNA sequence analysis of a 1.9 kb TaqI fragment reveals a large open reading frame (ORF) which encodes a polypeptide of 573 amino acids, with a predicted molecular mass of 61.8 kDa (Fig. 1). A putative ribosome-binding site (RBS) is located only four nucleotides upstream of the start codon ATG and seven nucleotides upstream of the alternative start codon TTG and displays strong similarity to the consensus RBS sequence (TAAGGAGG) of B. subtilis. This spacing is shorter than the reported optimal length of 8–9 nucleotides, and might therefore be expected to reduce the translational yield of this protein (Vellonoweth & Robinowitz, 1992). The upstream nucleotides encompass a putative εD consensus promoter element which closely resembles the consensus sequence of CTAAA...N16...CCGATAT (Mirel et al., 1992). Although an obvious transcriptional terminator is not located after this gene product, designated TlpC, it is very likely that this gene is monocistronic since the immediately adjacent nucA gene is specific for competence (Vosman et al., 1988). Because the transcription of genes involved with the physiological process of competence does not coincide with the observed expression of TlpC, it follows that the transcriptional regulation of tlpC must be unique.

In order to verify that this proposed ORF encodes a protein of the predicted size, a 17 bp TaqI fragment containing the entire tlpC gene which was deleted for the adjacent transcriptional elements was subcloned from pDW39 into the E. coli expression plasmid pT7-6. The resulting plasmid pDW39 was then introduced into E. coli strain K38. Expression of the subcloned DNA produced a radiolabelled protein of 63 kDa, which is in good agreement with the predicted molecular mass (Fig. 2, lane 1). However, several lower molecular mass bands of strong intensity were co-expressed. To demonstrate that the 63 kDa radiolabelled band corresponds to the expression of TlpC, a 400 bp C-terminal deletion of the tlpC gene was constructed. Expression of the resulting fragment produced the expected shift of 15 kDa in the expression profile (Fig. 2, lane 2). It is suspected that these lower molecular mass bands result from degradation or additional internal start sites that are recognized in E. coli.

Homology to known proteins

The amino acid sequence of this predicted protein exhibited homology to the MCPs from E. coli (Bollinger et al., 1984; Krikos et al., 1983; Russo & Koshland, 1983; Boyd et al., 1983), as well as to chemotactic transducer proteins from other organisms, including FrzCD from Myxococcus xanthus (McCleary et al., 1990), McpA from Caulobacter crescentus (Alley et al., 1992), HtrI from Halobacterium halobium (Yao & Spudich, 1993) and, more strikingly, MCPs from B. subtilis. A hydrophathy profile of TlpC revealed two hydrophobic segments in the N-terminal region of TlpC. These segments are characteristic of transmembrane regions and their location is typical of MCPs (Fig. 3). On comparing various MCPs, the region of high conservation was found to be localized within the C-terminal domain (Fig. 4), with no detectable homology in the N-terminal region. An amino acid alignment between TlpC and a representative E. coli transducer Tar showed 30.0% identity in a 297 amino acid overlap (Fig. 4). The similarity between TlpC and B. subtilis McpA was higher (38.3% identity) and extended through a 358 amino acid overlap. This similarity is not as extensive as within previously characterized MCPs, which exhibit an overall 57–64% amino acid identity among them that includes the N-terminal, extra-membrane region (Hanlon & Ordal, 1994; Fig. 4). Moreover, there are two regions of TlpC that are much more similar to McpA from B. subtilis than to Tar from E. coli (see underlined residues in Fig. 4).

The putative methylation sites also reflect a greater similarity with the B. subtilis MCPs, compared with E. coli transducers (Fig. 4). Three of the four predicted sites appear to be conserved, while none are in the locations found in Tar (Fig. 4). By contrast, the molecular mass of TlpC is similar to that of the E. coli MCPs, which range from 58 to 60 kDa (Taylor & Lengeler, 1990), and considerably less than the 72 kDa observed for the four MCP or MCP-type genes sequenced thus far from B. subtilis (Hanlon & Ordal, 1994).

Interestingly, a search of the TlpC protein sequence against sequences in the GenBank also identified significant homology to HlyB of Vibrio cholerae, with the two proteins sharing 23.8% amino acid identity which extends the entire length of the two proteins (data not shown). HlyB from V. cholerae is a 60.3 kDa putative outer membrane associated protein which is required for the secretion of haemolysin (Aim & Manning, 1990).

Characterization of a null mutant in tlpC

In order to examine the role of TlpC in B. subtilis, a mutation was created in the tlpC ORF using an integration plasmid pDW41, which contains an SpôI–BglII DNA fragment that is internal to the tlpC gene. Transformation and homologous recombination into wild type strain OI1085 resulted in the chromosomal disruption of tlpC to create mutant strain OI3054. The fidelity of the gene disruption was confirmed by Southern blot analysis (data not shown).

A standard in vivo methylation reaction which was performed on the wild-type and corresponding mutant strains did not detect any visible differences in the methylation profiles. However, under conditions requiring an extended methylation with an increased amount of
Hydropathy profile of TlpC. The algorithm of Kyte and Doolittle was used with a window span of 19. Hydropathy values are shown on the vertical axis. The dashed line shows the threshold hydropathy value for known membrane-spanning segments of the Rhodobacter viridis photosynthetic reaction centre L submit. Vertical lines represent increments of 20 amino acids.

[methyl-$^3$H]methionine, a noticeably methylated protein migrating at approximately 63 kDa on SDS-PAGE was present in wild type strain OI1085 but not in OI3054 (Fig. 5). As observed from the fluorogram, this methylated protein does not correspond to the major MCPs of B. subtilis, which are grossly overexposed. An in vitro methylation was subsequently performed which also demonstrated that this membrane-bound protein was able to be methylated, albeit poorly (data not shown). In addition, it was determined that the chemotactic methyltransferase, CheR, was required for the methylation of this previously uncharacterized TlpC protein, since this protein is unmethylated in a methyltransferase mutant strain (data not shown).

An immunoblot analysis of membranes prepared from strains OI1085 and OI3054 was performed using the E. coli anti-Trg antibody, which has been shown to cross-react with the B. subtilis MCPs (Nowlin et al., 1985). The results presented in Fig. 6 demonstrate that the E. coli antibody cross-reacts with TlpC in wild-type membranes, while no cross-reactivity is observed in membranes prepared from the mutant strain OI3054. Cross-reactivity is also observed with the H3 MCP in both strains, which has an apparent molecular mass of 76 kDa on SDS-polyacrylamide gels. Although the E. coli Trg antibody cross-reacts with the other B. subtilis transducers, the recognition is substantially weaker than observed with H3 and often difficult to detect by immunoblot analysis. The results obtained thus far indicate that TlpC is a methylated integral membrane protein with strong homology to chemotactic transducers from other organisms, but is not one of the previously identified MCPs that have been biochemically characterized in B. subtilis.

All 20 amino acids and many sugars are attractants for B. subtilis, while a diverse array of compounds serve as repellents (Ordal & Goldman, 1976). A broad-based survey was undertaken to determine whether TlpC was involved in chemotaxis. Capillary assays were performed on the OI3054 mutant strain to quantify chemotaxis towards all 20 amino acids, and a variety of sugars which included glucose, fructose, maltose, mannose, methyl a-glucoside, sorbitol and sucrose. All amino acids were assayed at previously determined apparent $K_D$ concentrations (Ordal et al., 1979), while sugars were assayed at concentrations generating maximal accumulation in a capillary assay (‘peak concentrations’) (Ordal et al., 1979). Several repellents which included butyrate, 2,6-dibromophenol, indole, quinacrine and sodium cyanide were also examined (data not shown) (Ordal & Goldman, 1976). The results from these experiments demonstrated that the OI3054 mutant strain was chemotactically wild-type toward all of the compounds tested, suggesting that TlpC may not be involved in chemotaxis.

The lack of an observed chemotactic phenotype prompted us to explore the possibility that the TlpC protein was somehow involved in another cellular process which utilizes the TlpC receptor to recognize an appropriate stimulus and cytoplasmically transduce the signal received by this protein using a two component regulatory system homologous to CheA and CheY. Several assays were therefore performed to examine the processes of protein secretion, competence, and sporulation in B. subtilis. The inactivation of the tlpC gene produced no observable defects for any of these processes.

DISCUSSION

This paper reports the nucleotide sequence of the tlpC gene, which encodes a predicted 618 kDa polypeptide, in agreement with results obtained using a T7 expression system in E. coli. The amino acid sequence of TlpC suggests that this B. subtilis protein should be involved in the chemotactic signal transduction process, based upon its strong homology to chemotactic transducers from other organisms, including the MCPs from E. coli ('Tar,
D. W. HANLON and OTHERS

Fig. 5. In vivo protein methylation. Methylation were performed for 10 min with 25 µl [methyl-\(^{3}H\)]methionine per sample. Lane 1, wild-type strain OI1085; lane 2, tlpC mutant OI3054. The arrowhead indicates the position of TlpC.

Fig. 6. Immunoblot analysis. The cross-reacting E. coli anti-Trg antibody was used to detect TlpC among total membrane proteins. Lane 1, OI1085; lane 2, OI3054. The arrowhead indicates the position of TlpC.

Tap, Trg and Tar (Bollinger et al., 1984; Krikos et al., 1983; Russo & Koshland, 1983; Boyd et al., 1983), FtuCD from M. xanthus (McCleary et al., 1990), MCPA from C. crescentus (Alley et al., 1992), Htrl from H. halobium (Yao & Spudich, 1993), and the MCPs (McpA and McpB) and transducer-like proteins (TlpA and TlpB) from B. subtilis (Hanlon & Ordal, 1994). In addition, the hydropathy profile predicts two hydrophobic membrane spanning regions for TlpC, which is biochemically supported by its partition in the membrane fraction. Based upon the E. coli model, it would appear that these transmembrane regions separate two domains of the protein: an N-terminal extracellular binding region, which might interact with extracellular effectors, and a C-terminal domain, which would be responsible for interacting with several chemotaxis proteins to cytoplasmically transduce the signal received by the receptor and ultimately control the swimming behaviour of the bacterium.

The initial prediction that the TlpC protein would be involved in chemotaxis stems from the observed immunogenic cross-reactivity of this protein with the E. coli Trg antibody, in addition to the ability of TlpC to become methylated both in vivo and in vitro, although at a much reduced level compared to the previously biochemically characterized MCPs (Goldman & Ordal, 1984; Goldman et al., 1982; Hanlon & Ordal, 1994). Furthermore, the transcription of this gene appears to be regulated by the \(\sigma^{B}\) form of RNA polymerase, in agreement with the regulation of the major MCPs from E. coli transducers and the predicted methylation sites of TlpC, respectively. The asterisk in parenthesis indicates the predicted site in McpA and McpB that is not present in TlpC. The underlining indicates regions where the overall similarity of TlpC is considerably greater to McpA than to Tar.
also mediate these taxes. Only after the remaining MCP genes have been cloned and inactivated will it be possible to create a strain containing only tlpC. Only then should it be possible to investigate what taxes, if any, TlpC mediates. It also may be that we have not tested the appropriate chemoeffectors for this receptor. However, based upon previous studies which demonstrate that all amino acids and many sugars are attractants (Ordal et al., 1977, 1979), while several compounds serve as repellents (Ordal & Goldman, 1976), it seems peculiar that this potential chemotactic receptor would not recognize any of these chemoeffectors tested. Finally, it is possible that TlpC might carry out other non-chemotactic functions.

Recently, we have cloned, sequenced, and characterized four genes encoding proteins of 72 kDa, which are homologous to chemotactic transducers from other organisms. Two of these genes encode major MCPs of B. subtilis, based upon the loss of methylated bands visualized on SDS-polyacrylamide gels in the corresponding mutant strains. In addition, these transducers are responsible for recognizing various sugar or amino acid attractants. However, inactivation of the other two transducer-like proteins (TlpA and TlpB) had no apparent effect upon the MCP methylation profiles. Furthermore, no chemotactic defect was observed in the absence of these transducer-like proteins for any amino acid, sugar or repellent tested (Hanlon & Ordal, 1994). Thus, TlpC is not the only MCP-type protein whose function is obscure.

It is noteworthy that TlpC has three of the four predicted methylation sites of McpA and McpB (and TlpA and TlpB) but none of the sites identified in Tar. Furthermore, TlpC has additional regions of similarity with McpA and McpB that are not found in Tar (Fig. 4). This suggests that other, unique, proteins might interact with the B. subtilis MCPs, proteins that are not found in E. coli. Three candidates have been identified thus far [CheC, CheD (M. Rosario, J. Kirby & G. Ordal, unpublished) and CheV (Frederick & Helman, 1994; Rosario et al., 1991)].

These similarities also indicate TlpC's closer relationship to the B. subtilis MCPs, compared to the E. coli MCPs. However, there is no detectable similarity between TlpC and the N-terminal regions of McpA, McpB, TlpA and TlpB, which are very similar to each other. This similarity among the last four proteins is believed to reflect the requirement to bind similar members of a family of chemoeffect/binding protein complexes rather than the chemoeffectors directly (Hanlon & Ordal, 1994). The lack of similarity between TlpC and the other proteins, along with its smaller molecular mass, indicates that it performs other functions.

The fact that TlpC is similar in size to the E. coli MCPs leads to speculation about the possible evolutionary divergence between the B. subtilis and E. coli transducers. It is conceivable that TlpC is closely related to the ancestor of the B. subtilis transducers which are involved in chemotaxis and has itself descended from an E. coli-like transducer. After the evolutionary lines that gave rise to B. subtilis and E. coli diverged, the ancestor of TlpC may have given rise to the larger chemotactic transducers of B. subtilis.

REFERENCES


transducers of *Escherichia coli* are composed of discrete structural and functional domains. *Cell* 33, 615–622.


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