PorH, a new channel-forming protein present in the cell wall of *Corynebacterium efficiens* and *Corynebacterium callunae*

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*Corynebacterium callunae* and *Corynebacterium efficiens* are close relatives of the glutamate-producing mycolata species *Corynebacterium glutamicum*. The properties of the pore-forming proteins, extracted by organic solvents, were studied. The cell extracts contained channel-forming proteins that formed ion-permeable channels with a single-channel conductance of about 2 to 3 nS in 1 M KCl in a lipid bilayer assay. The corresponding proteins from both corynebacteria were puriﬁed to homogeneity and were named PorH<sub>C.call</sub> and PorH<sub>C.eff</sub>.

Electrophysiological studies of the channels suggested that they are wide and water-ﬁlled. Channels formed by PorH<sub>C.call</sub> are cation-selective, whereas PorH<sub>C.eff</sub> forms slightly anion-selective channels. Both proteins were partially sequenced. A multiple sequence alignment search within the known chromosome of *C. efficiens* demonstrated that it contains a gene that fits the partial amino acid sequence of PorH<sub>C.eff</sub>. PorH<sub>C.call</sub> shows high homology to PorH<sub>C.eff</sub>. PorH<sub>C.eff</sub> is encoded in the bacterial chromosome by a gene that is localized within the vicinity of the porA gene of *C. efficiens*. PorH<sub>C.eff</sub> has no signal sequence at the N terminus, which means that it is not exported by the Sec-secretion pathway. The structure of PorH in the cell wall of the corynebacteria is discussed.

**INTRODUCTION**

In 2002, three glutamic-acid-producing coryneform strains, belonging to the genus *Corynebacterium*, were isolated from soil and vegetable samples. Phylogenetic studies, based on 16S rRNA analysis, demonstrated that the nearest relatives of these strains were *Corynebacterium glutamicum* and *Corynebacterium callunae*, which are known as glutamic-acid-producing species. The most signiﬁcant characteristics of the newly found strains, named *Corynebacterium efficiens*, was the production of acid from dextrin (Fudou et al., 2002). *C. glutamicum* is used for industrial production of L-glutamate, L-lysine and other amino acids through fermentation processes (Udaka, 1960; Gutmann et al., 1992; Keilhauer et al., 1993; Sahm et al., 1996; Eggeling & Sahm, 1999). The range of temperature for the growth of most corynebacteria is between 30 and 37 °C, with the exception of *C. efficiens* (Fudou et al., 2002) which can grow up to 45 °C. This feature is beneﬁcial from an economic point of view; the need for a cooling system in industrial fermenters is reduced using this bacterium, which means that the costs for the production of L-glutamic acid could be reduced.

*C. efficiens*, *C. callunae* and *C. glutamicum* share similar cell-wall composition. The cell wall of mycolata contains a second layer consisting of covalently bound mycolic acids and extractable lipids (Barksdale, 1981; Goodfellow et al., 1976; Minnikin, 1987; Ochi, 1995) in addition to the thick peptidoglycan layer. The mycolic acids are 2-branched, 3-hydroxylated fatty acids and variable in chain length. The cell wall of corynebacteria contains mycolic acids with a chain length of about 22–38 carbon atoms, whereas other members of the mycolata contain much longer mycolic acids (Minnikin, 1987; Yano & Saito, 1972; Minnikin et al., 1990; Holt et al., 1994; Brennan & Nikaido, 1995). The mycolic acid layer represents a permeability barrier (Liu et al., 1995, 1996; Nikaido et al., 1993), similar to the outer membrane of Gram-negative bacteria. To overcome this barrier, channel-forming proteins, so-called porins, are necessary to allow the passage of hydrophilic solutes. With respect to the transport of amino acids over this barrier, it is of particular importance to characterize the hydrophilic pathways in the cell wall of corynebacteria.

The first porin identified in the cell wall of a member of the
mycolata consisted of a 59 kDa cell-wall protein with a mean single-channel conductance of 2.7 nS in 1 M KCl from *Mycobacterium chelonae* (Trias *et al.*, 1992; Trias & Benz, 1993). For this bacterium it has been demonstrated that the permeability of the cell wall for hydrophilic solutes is slightly lower than that of *Pseudomonas aeruginosa* and much lower than that of *Escherichia coli* (Jarlier & Nikaido, 1990; Trias & Benz, 1993). This could explain why members of the mycolata have a low susceptibility towards certain antibiotics. Since the discovery of the first cell-wall channel, several porins have been identified and characterized in members of the mycolata (Costa-Riu *et al.*, 1998, 1999, 2000, 2001; Costa-Riu *et al.*, 2003b). Common to most of them is the formation of wide and water-filled pores that are cation-selective due to negative charges (Trias & Benz, 1993, 1994; Riess *et al.*, 1998; Lichtinger *et al.*, 1998, 1999, 2001).

PorA from *C. glutamicum* was the first pore-forming protein of the corynebacteria that was characterized. The channel is cation-selective with a single-channel conductance of about 5.5 nS in 1 M KCl and it is formed by an oligomer of a small 45 aa polypeptide that is encoded without a leader sequence (Lichtinger *et al.*, 1998, 2001). Another porin, PorB, of 99 aa, was found after deleting the porA gene from the *C. glutamicum* chromosome (Costa-Riu *et al.*, 2003a, b). PorB forms anion-selective channels with a single-channel conductance of about 700 pS in 1 M KCl in lipid-bilayer experiments. To extend the knowledge of channel-forming proteins of corynebacteria, we screened these strains and growth conditions.

**METHODS**

**Bacterial strains and growth conditions.** *C. efficiens* AI 12310 (obtained from DSMZ, Braunschweig, Germany) was routinely grown in BHI medium (Difco) and *C. callunae* ATCC 15991 (obtained from DSMZ) was grown in double yeast tryptone (2 × YT; BIO 101) medium, both at 30 °C.

**Isolation and purification of channel-forming proteins.** For the isolation of the channel-forming proteins from *C. efficiens* AI 12310 and *C. callunae* ATCC 15991, a method was used that has been described previously for the isolation and purification of PorA of *C. glutamicum* (Lichtinger *et al.*, 1999). It is based on the extraction of whole cells with organic solvents and avoids the substantial loss of material caused by sucrose density centrifugation of the cell envelope to separate the cytoplasmic membrane from the cell-wall fraction. For the extraction procedure 200 ml cells was grown to an OD_{600} of 10 and harvested by centrifugation (10 000 r.p.m. for 10 min in a Beckman J2-21M/E centrifuge). The cells were washed twice in 10 mM Tris/HCl (pH 8). The washed and centrifuged cells were extracted twice with organic solvent, a 1:2 mixture of chloroform/methanol in a proportion of 1 part cells and 5–8 parts chloroform/methanol. The duration of the extraction was about 3 h at room temperature with stirring in a closed tube to avoid loss of chloroform. Cells and the chloroform/methanol solution were centrifuged for 15 min (10 000 r.p.m. in a Beckman J2-21M/E centrifuge). The pellet of cells was discarded. The supernatant contained the channel-forming activity. It was mixed in a ratio of 1 part supernatant to 9 parts ether and kept overnight at −20 °C. The precipitated protein was dissolved in a solution containing 0.5% LDAO (N,N-dimethyldodecylamine-N-oxide) and 10 mM Tris/HCl (pH 8), and inspected for channel-forming activity. The protein was subjected to fast protein liquid chromatography (FPLC) across a HitTrap-Q column (Amersham Pharmacia Biotech). The column was washed first with a buffer containing 0.4% LDAO and 10 mM Tris/HCl (pH 8), and then the protein was eluted with 0.4% LDAO in 10 mM Tris/HCl (pH 8) using a linear gradient between 0 and 1 M NaCl.

**SDS-PAGE.** SDS-PAGE was performed with Tricine-containing gels (Schägger & von Jagow, 1987). The gels were stained with coomassie brilliant blue (Neuhoff *et al.*, 1988) or silver (Blum *et al.*, 1987). Before separation, the samples were all incubated for 3 min at 100 °C with loading buffer (containing 0.5% LDAO (N,N-dimethyldodecylamine-N-oxide) and 10 mM Tris/HCl (pH 8)). SDSPAGE was used for identification and purification of the channel-forming activity from the organic solvent extracts of whole *C. efficiens* cells.

**Peptide sequencing.** The precipitated protein pellet resulting from the active FPLC fractions or preparative SDS-PAGE was dissolved in 100 µl 70% (v/v) formic acid containing 10% (w/v) CNBr (Merck) and incubated in the dark at room temperature for 14 h (Gross, 1967). After lyophilization, the CNBr peptides were dissolved in 20% (v/v) formic acid and separated by reversed-phase-HPLC (SYCAM), using a Luna C-18 column, 150 × 1 mm, with a flow rate of 40 µl min⁻¹ and a 120 min gradient from 100% A [0–1% (v/v) trifluoroacetic acid in water] to 80% B (0–1% trifluoroacetic acid in acetoniitrile). Collected fractions were subjected to amino acid sequence analysis on a 492 protein sequencer (Applied Biosystems) using the conditions recommended by the manufacturer. The major sequences for the precipitated protein pellet of *C. callunae* were DLSLADNLDYDSTFGKNIAGTAL and IPDLIKGIAFENFGDLAETT; the main sequence for the *C. efficiens* protein was DLSLILDSDFATLGKN.

**Lipid bilayer experiments.** The methods used for black lipid bilayer experiments have been described previously (Benz *et al.*, 1978; Benz, 2003). The experimental set-up consisted of a Teflon cell with two water-filled compartments connected by a small circular hole. The hole had an area of about 0.4 mm². Membranes were formed across the hole using a 1% solution of diphytanoyl phosphatidylcholine (PC; Avanti Polar Lipids) dissolved in n-decane. The temperature was maintained at 20 °C during all experiments. All salts were obtained from Merck (analytical grade). They were used unbuffered. The electrical measurements were performed using Ag/AgCl electrodes (with salt bridges) connected in series to a voltage source and a home-made current-to-voltage converter made with a Burr Brown operational amplifier. The amplified signal was monitored on a storage oscilloscope (Tektronix 7633) and recorded on a strip chart or tape recorder.

The zero-current membrane potentials were measured as described previously (Benz *et al.*, 1979). The membranes were formed in a 100 mM KCl solution containing a predetermined protein concentration so that the membrane conductance increased about 100-
1000-fold within 10–20 min after membrane formation. At this time the instrumentation was switched to the measurements of the zero-current potentials and the salt concentration on the cis side of the membrane was raised by adding small amounts of concentrated salt solutions. The polarity was connected to the trans side. The zero-current membrane potential reached its final value between 2 and 5 min.

**Effect of negatively charged groups attached to the channel mouth.** Negative charges at the pore mouth result in substantial ionic-strength-dependent surface potentials at the pore mouth that attract cations and repel anions. Accordingly, they influence both single-channel conductance and zero-current membrane potential. A quantitative description of the effect of charges on the single-channel conductance may be given by the following considerations. The first one is based on the Debye–Hückel theory describing the effect of charges in an aqueous environment. The second treatment was proposed by Nelson & McQuarrie (1975) and describes the effect of charges on the surface of a membrane and does not consider charges attached to a channel. However, this does not represent a serious restriction of its use and we assume here that the charges are localized at the PorH channel. In case of a negative charge, \( q \), in an aqueous environment, a potential \( \Phi \) is created that is dependent on the distance, \( r \), from the charge:

\[
\Phi = \frac{q q^+ \frac{\varepsilon}{\varepsilon_0}}{4 \pi \varepsilon_0 \varepsilon_0 r} = \frac{c c^+ R T}{2 F^2 c^+} \tag{1}
\]

where \( \varepsilon_0 = 8.85 \times 10^{-12} \text{ F m}^{-1} \) and \( \varepsilon = 80 \) are the absolute dielectric constant of vacuum and the relative constant of water, respectively, and \( l_0 \) is the so-called Debye length that controls the decay of the positive potential (and that of the accumulated positively charged ions) in the aqueous phase:

\[
\rho_D^2 = \frac{\varepsilon \varepsilon_0 R T}{2 F^2 c^+} \tag{2}
\]

where \( c \) is the bulk aqueous salt concentration, \( R \) is 8.3 J mol\(^{-1}\) K\(^{-1}\), \( T \) is 293 K and \( F \) is 96485.3 As mol\(^{-1}\) (\( R T F^2 = 25.2 \text{ mV} \) at 20 °C). The potential \( \Phi \) created by a negative charge on the surface of a membrane is twice that of equation (1) caused by the generation of an image force on the opposite side of the membrane (Nelson & McQuarrie, 1975; Benz et al., 1994). The concentration of the monovalent cations near the charge increases because of the negative potential. Their concentration is in both cases (Debye–Hückel or Nelson–McQuarrie) dependent on the potential \( \Phi \) and given by:

\[
c^+ = c^0 e^{-\frac{\varepsilon r}{c^+}} \tag{3}
\]

Similarly, the anion concentration \( c^- \), near the charge decreases according to:

\[
c^- = c^0 e^{\frac{\varepsilon r}{c^-}} \tag{4}
\]

In the following situation we assume that the negative charge is attached to the channel. In such a case its conductance is limited by the accumulated positively charged ions and not by their bulk aqueous concentration. The cation concentration (equation 3) at the mouth of the pore can now be used for calculation of the effective conductance-concentration curve:

\[
G(c) = G_0 c^+ \tag{5}
\]

where \( G_0 \) is the concentration-independent conductance of the channel.

### RESULTS

**Purification of PorH\(_{C.\text{call}}\) and PorH\(_{C.\text{eff}}\)**

Proteins within the organic solvent extract of whole \( C.\text{callunae} \) and \( C.\text{efficiens} \) cells were precipitated with ether in the cold. The precipitate was dissolved in the detergent LDAO and inspected for channel-forming activity using the lipid bilayer assay. The detergent solution had a high channel-forming activity, and channels with a conductance between 2 and 6 nS in 1 M KCl were formed under these conditions. Purification of the channel-forming proteins from \( C.\text{callunae} \) and \( C.\text{efficiens} \) was performed by FPLC across a HiTrap Q column. Fig. 1(a), lane 2 shows the protein composition of the organic solvent extract of \( C.\text{callunae} \) that was applied to the column. The column was first washed with buffer and then eluted with buffer supplemented with increasing concentration of NaCl. Pure 6 kDa protein was eluted at an NaCl concentration of 0.25 M. The 6 kDa protein of \( C.\text{efficiens} \) was not completely pure after FPLC across a HiTrap Q column. Final purification was achieved by preparative SDS-PAGE of the precipitated organic solvent extract that contained the channel-forming activity (see Fig. 1b).

**Single channel analysis of PorH\(_{C.\text{call}}\) and PorH\(_{C.\text{eff}}\)**

Fig. 2(a) shows a single-channel recording of a PC membrane in the presence of the pure 6 kDa protein of \( C.\text{callunae} \), which was added to a black membrane in a concentration of about 10 ng ml\(^{-1}\). The single-channel

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**Fig. 1.** (a) Tricine (10 %) SDS-PAGE of the \( C.\text{callunae} \) PorH purification procedure. The gel was stained with colloidal Coomassie. Lanes: 1, low molecular mass marker; 2, 15 μl ether-precipitated extract dissolved in 0-4 % LDAO, treated for 10 min at 100 °C with 5 μl sample buffer; 3, 15 μl fraction 17 from the Hitrap-Q FPLC column, treated for 10 min at 100 °C with 5 μl sample buffer. (b) 12 % Tricine (12 %) SDS-PAGE of \( C.\text{efficiens} \) PorH obtained by elution of the 6 kDa band from preparative SDS-PAGE. The gel was stained with silver. Lanes: 1, low molecular mass marker; 2, 15 μl ether-precipitated extract dissolved in 0-4 % LDAO, treated for 10 min at 100 °C with 5 μl sample buffer; 3, 3 μg pure 6 kDa protein solubilized for 10 min at 100 °C with 5 μl sample buffer.
PorH C.eff. The insets display the single-channel recording of single-channel events (left-hand side maximum in Fig. 2b) in PorH C.call and 2 proteins from PC/n-decane membranes in the presence of the pure 6 kDa proteins from C. callunae and C. efficiens. P(G) is the probability that a given conductance increment G is observed in the single-channel experiments. It was calculated by dividing the number of fluctuations with a given conductance increment by the total number of conductance fluctuations. The aqueous phase contained 1 M KCl and 10 ng cell-wall proteins ml⁻¹. The applied membrane potential was 20 mV at 20 °C. The mean single-channel conductance was 3.0±0.4 nS for 139 single-channel events in PorH C.call and 2.3±0.3 nS for 126 single-channel events (left-hand side maximum in Fig. 2b) in PorH C.eff. The insets display the single-channel recording of PC/n-decane membranes in the presence of the pure 6 kDa proteins from C. callunae (a) and C. efficiens (b).

40 mV (see below). Channels formed by PorH C.eff had a very similar lifetime compared to those formed by PorH C.call as the single-channel recording of Fig. 2(b) clearly indicates. The only exception was the occurrence of two maxima in the histogram of the single-channel distribution (see Fig. 2b). These two maxima (2-3 and 4-7 nS in 1 M KCl) most probably reflect the reconstitution of two channels at once, because the conductance of the right-side maximum was twice of that of the left side.

Single-channel experiments were also performed with salts other than KCl to obtain some information on the size of the channels formed by PorH C.call and PorH C.eff and their ion selectivity. The results are summarized in Table 1. The conductance sequence of the different salts within the channel formed by PorH C.call was RbCl≈KCl≈K acetate > NaCl > LiCl > N(CH3)4Cl > N(C2H5)4Cl, which means that the single-channel conductance followed approximately the aqueous mobility of the different cations in the aqueous phase. Presumably, this means that the influence of cations on the conductance of the channel in different salt solutions was more substantial than that of anions (Table 1), suggesting a cation selectivity of the channel. Table 1 also shows the mean single-channel conductance, G, of PorH C.call as a function of the KCl concentration in the aqueous phase. Similarly, as in the case of many porin channels of Gram-positive bacteria (Trias & Benz, 1993, 1994; Riess et al., 1998; Lichtinger et al., 1999), the conductance was not a linear function of the KCl concentration, which is characteristic for the presence of net charges in or near the channel (Trias & Benz, 1994; Lichtinger et al., 1999).

Table 1 demonstrates that the single-channel conductance of the channels formed by PorH C.eff was in the same range as that measured for PorH C.call. However, it seems that the ion selectivity of PorH C.eff was somewhat different because the conductance of the channels in LiCl was higher than in K-acetate (Table 1). Furthermore, the conductance of salts containing tetraalkylammonium ions was more or less independent of the size of the cation. These results suggested that PorH C.eff could form anion-selective channels. Zero-current membrane potential measurements were performed in the presence of KCl gradients to check such a possibility. Fivefold KCl gradients (100 versus 500 mM) were established across lipid bilayer membranes which contained about 100–1000 PorH C.eff or PorH C.call channels. The measurements with PorH C.eff resulted in an asymmetry potential of about −6 mV at the more dilute trans side (mean of four measurements). This result indicated some preferential movement of chloride over potassium ions through the PorH C.eff channel at neutral pH. Similar experiments with PorH C.call resulted in an asymmetry potential of about 28 mV at the more dilute side. The zero-current membrane potentials were analysed using the Goldman–Hodgkin–Katz equation (Benz et al., 1979). The ratio of the potassium permeability, Pk, divided by the chloride permeability, PCl, was about 0.7 and 7 for PorH C.eff and...
Table 1. Mean single-channel conductance, $G$, of PorHC$_{\text{call}}$ and PorHC$_{\text{eff}}$ in different salt solutions

The membranes were formed of PC dissolved in n-decane. The aqueous solutions were unbuffered and had a pH of 6, unless otherwise indicated. The concentration of PorHC$_{\text{call}}$ and PorHC$_{\text{eff}}$ was about 10 ng ml$^{-1}$. Note that the mean single-channel conductance of PorHC$_{\text{eff}}$ always corresponded to the left-side maximum of the histograms. The applied voltage was 20 mV and the temperature was 20 °C. The mean single-channel conductance, $G$, was calculated from at least 80 single events. NM, Not measured.

<table>
<thead>
<tr>
<th>Salt</th>
<th>Concentration (M)</th>
<th>PorHC$_{\text{call}}$ $G$ (nS)</th>
<th>PorHC$_{\text{eff}}$ $G$ (nS)</th>
</tr>
</thead>
<tbody>
<tr>
<td>LiCl</td>
<td>1.0</td>
<td>1.25</td>
<td>1.50</td>
</tr>
<tr>
<td>NaCl</td>
<td>1.0</td>
<td>1.75</td>
<td>NM</td>
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<tr>
<td>KCl</td>
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<td>NM</td>
<td>0.025</td>
</tr>
<tr>
<td>KCl</td>
<td>0.03</td>
<td>0.35</td>
<td>0.075</td>
</tr>
<tr>
<td>KCl</td>
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<td>0.55</td>
<td>0.45</td>
</tr>
<tr>
<td>KCl</td>
<td>0.3</td>
<td>1.10</td>
<td>0.70</td>
</tr>
<tr>
<td>KCl</td>
<td>1.0</td>
<td>3.0</td>
<td>2.3</td>
</tr>
<tr>
<td>KCl</td>
<td>3.0</td>
<td>7.0</td>
<td>6.5</td>
</tr>
<tr>
<td>RhCl</td>
<td>1.0</td>
<td>3.0</td>
<td>NM</td>
</tr>
<tr>
<td>N(CH$_3$)$_4$Cl</td>
<td>1.0</td>
<td>1.0</td>
<td>1.8</td>
</tr>
<tr>
<td>N(C$_2$H$_5$)$_4$Cl</td>
<td>1.0</td>
<td>0.70</td>
<td>1.7</td>
</tr>
<tr>
<td>KCH$_3$COO (pH 7)</td>
<td>1.0</td>
<td>2.0</td>
<td>1.0</td>
</tr>
</tbody>
</table>

PorHC$_{\text{call}}$, respectively, which indicated a small anion selectivity for PorHC$_{\text{eff}}$ and cation selectivity for PorHC$_{\text{call}}$ (see also Discussion).

Voltage dependence

In single-channel recordings, channels formed by PorHC$_{\text{call}}$ and PorHC$_{\text{eff}}$ exhibited some flickering at higher voltages, i.e. they showed rapid transitions between open and closed configurations. The voltage-dependent closure of the channels was studied in detail in multi-channel experiments. The channel-forming protein was added at a concentration of 500 ng ml$^{-1}$ to one side of a black PC/n-decane membrane (to the cis side). After 30 min, about 50 channels were reconstituted into the membrane. At that time different potentials were applied to the cis side of the membrane: first 60 mV and then −60 mV. These experiments were repeated with 70, 80 and 90 mV. For both positive and negative potentials applied to the cis side of the membrane the current decreased in an exponential fashion. This result indicated a symmetric response of PorHC$_{\text{eff}}$ to the voltage applied to the membranes. Similar experiments were performed with PorHC$_{\text{call}}$ and a symmetrical response to the applied voltage was also observed (data not shown).

The voltage-dependence experiment, and similar ones, were analysed in the following way. The membrane conductance ($G$) as a function of voltage, $V_m$, was measured when the closing of channels reached an equilibrium, i.e. after the exponential decay of the membrane current following the voltage step $V_m$. $G$ was divided by the initial value of the conductance ($G_0$, a linear function of the voltage) obtained immediately after the onset of the voltage. The data in Fig. 3(a) (closed circles and squares, for PorHC$_{\text{eff}}$ and PorHC$_{\text{call}}$, respectively) correspond to the symmetric voltage-dependence of the two cell-wall channels (mean of four membranes) when the proteins were exclusively added to the cis side. The results suggest that PorHC$_{\text{eff}}$ exhibited a somewhat higher voltage-dependence than PorHC$_{\text{call}}$. The voltage-dependence of the data of Fig. 3(a) was analysed assuming a Boltzmann distribution between the number of open and closed channels, $N_o$ and $N_c$, respectively (Ludwig et al., 1986). This analysis allowed the calculation of the number of gating charges, $n$ (number of charges involved in the gating process), and the midpoint potential, $V_0$ (potential at which the number of open and closed channels is identical), from a semi-logarithmic plot of the ratio $N_o/N_c$, which is given by:

$$N_o/N_c = (G - G_{\text{min}})/(G_0 - G)$$

where $G$ in this equation is the conductance at a given membrane potential, $V_m$, and $G_0$ and $G_{\text{min}}$ are the conductance at zero voltage and very high potentials, respectively. The open to closed ratio of the channels, $N_o/N_c$, is given by:

$$N_o/N_c = \exp[-nF(V_m - V_0)/RT]$$

where $F$ (Faraday’s constant: 96485·3 C mol$^{-1}$), $R$ (gas constant: 8·3 J mol$^{-1}$ K$^{-1}$) and $T$ (absolute temperature: 293 K) are standard symbols, $n$ is the number of gating charges moving through the entire transmembrane potential gradient for channel gating (i.e. a measure for the strength of the interaction between the electric field and the open channel) and $V_0$ is the potential at which 50 % of the total number of channels are in the closed configuration (i.e. $N_o/N_c = 1$). Semi-logarithmic plots of the data given in Fig. 3(a) using least-squares fits (see Fig. 3b) show that they could be fitted to straight lines. The slope of the lines was such that an e-fold change of $N_o/N_c$ occurred when the
voltage was changed by about 16 mV (PorH C.call) or 14 mV (PorH C.eff). This means that the number of gating charges is approximately \( n = 1.6 \) in the first case and \( n = 1.8 \) in the latter case (because \( RT/F = 25.2 \) mV; see Fig. 3b). The broken numbers could mean that the gating charges do not move through the entire membrane thickness. Whereas the voltage dependence (the slope of the lines of Fig. 3a) was approximately similar for both channels, the midpoint potential \( V_0 \) (i.e. \( N_o/N_c = 1 \)) differed somewhat for PorH C.eff (\( V_0 \approx \pm 50 \) mV) and PorH C.call (\( V_0 \approx \pm 80 \) mV) (see Fig. 3b).

**Partial sequencing of the 6 kDa channel-forming proteins of *C. callunae* and *C. efficiens* and identification of *porH C.eff* within the chromosome of *C. efficiens*

The 6 kDa channel-forming proteins of *C. callunae* and *C. efficiens* were subjected to partial sequencing from the N-terminal end of the mature proteins after CNBr treatment using Edman degradation. Three stretches of 22 and 23 aa (*C. callunae*) and 18 aa (*C. efficiens*) were resolved. Multiple sequence alignments were performed with the translated known nucleotide sequence of the complete *C. efficiens* genome (NCBI reference sequence accession number NC_004369). The NCBI BLAST translation tool (Basic Local Alignment Search Tool; Zhang & Madden, 1997; Altschul et al., 1990) showed that the 18 aa stretch of *C. efficiens* is part of a 57 aa hypothetical protein of *C. efficiens* (DDBJ/EMBL/GenBank accession no. AJ871586; see Fig. 4a), which we named PorH C.eff. Interestingly, it exhibits only the inducer methionine at the N-terminal end, but no N-terminal extension, which suggests that translation and assembly of the protein could be very similar to that of PorA of *C. glutamicum* (Lichtinger et al., 2001). The gene *porH C.eff* consists of 174 bp and encodes a 57 aa acidic polypeptide (6 aspartic and glutamic acids compared to 2 lysines) without a leader sequence. This means that PorH C.eff is not transported out of the cytoplasmic membrane using the Sec apparatus as many other proteins from Gram-positive bacteria are (Freudl, 1992; Lichtinger et al., 2001). A search within the chromosome of *C. efficiens* demonstrates that *porH* and the gene encoding *PorA* of *C. efficiens* are localized very close to one another (see Fig. 4b). The genes encoding both proteins are only separated by 77 bp and there is no indication of a transcription terminator between them. Thus it seems very likely that both proteins share a common mode of export to the cell wall in *C. efficiens* and presumably also in *C. glutamicum* because the chromosome of the latter also contains the *porH C.glut* gene that has a high degree of homology to *porH C.eff*. Comparison of the two amino acid stretches (22 and 23 aa) derived from sequencing of PorH C.call with the sequence of PorH C.eff and PorH C.glut suggests that the proteins are highly homologous (see Fig. 4a). PorH C.call is also an acidic protein (8 aspartic and glutamic acids compared to 2 lysines of the partial sequence). The interesting feature of the channels formed by the two homologous proteins is the observation that one protein forms slightly anion-selective channels (PorH C.eff) and the other forms highly cation-selective channels (PorH C.call). This means presumably that their
arrangement in the channel-forming complexes may be responsible for their selectivity (see Discussion).

**DISCUSSION**

**The cell walls of *C. efficiens* and *C. callunae* contain ion-permeable channels formed by the 6 kDa PorH proteins**

In previous studies we identified different cell-wall channels in *C. glutamicum* (Lichtinger et al., 1998, 2001; Costa-Riu et al., 2003a, b). PorAC.glut forms a highly conductive cation-selective channel. Its deletion resulted in a much higher resistance of this bacterium to neutral or positively charged antibiotics, which indicates a lower permeability of the cell wall in the deletion mutant (Costa-Riu et al., 2003a). Nevertheless, growth of the mutant strain was only slightly impaired, in particular in rich medium. A search for another cell-wall channel revealed the existence of the anion-selective PorB.glut channel (Costa-Riu et al., 2003a, b). This result indicates that the cell wall of *C. glutamicum* contains several types of channels, as is the case in the outer membrane of Gram-negative bacteria (Benz, 2001) and in the Gram-positive *Rhodococcus equi*, which is also a member of the mycolata (Riess et al., 2003). In this study, we inspected the cell walls of *C. efficiens* and *C. callunae*, which are closely related to *C. glutamicum*, for the presence of cell-wall channels using the lipid bilayer technique. In organic solvent extracts of whole cells, channels were observed for both organisms that had a molecular mass of about 6 kDa, but were not identical to the well studied PorAC.glut channels. The channel-forming proteins of *C. efficiens* and *C. callunae* were purified to homogeneity and were named PorH.C.eff and PorH.C.call, respectively. Partial N-terminal sequencing of the proteins after CNBr cleavage resulted in three amino acid stretches that allowed the identification of the porH gene within the chromosome of *C. efficiens*. This gene encodes a 57 aa polypeptide without a leader extension, but it starts with the inducer methionine, which could be cleaved either during maturation or by CNBr. PorH.C.call is highly homologous to PorH.C.eff and the chromosome of *C. glutamicum* also contains a homologue gene of a similar protein PorH.C.glut (see Fig. 4; DDBJ/EMBL/GenBank accession no. AJ871585), which will be described in detail in a future study. The lack of an N-terminal leader extension suggested that PorH.C.eff is not transported via the Sec apparatus out of the cell to reach the cell wall. This is the same situation as for PorA.C.glut and considering the genes within the flanking regions of porA and porH it seems likely that their gene products share the same mode of translation, export and assembly, which represents a yet unknown secretion mechanism (Lichtinger et al., 2001).

**Effects of negative charges on the channel properties of PorH.C.call**

The channels formed by PorH.C.call and by PorH.C.eff differ somewhat in their ionic selectivity. PorH.C.eff forms slightly anion-selective channels despite the fact that the protein is overall acidic (6 negative charges compared to 2 positive ones). Thus it seems that the lysine in position 6 of the mature protein plays a crucial role in the selectivity of the channel because it is absent in the primary sequence of the highly homologous PorH.C.call. The data in Table 1 demonstrate that the single-channel conductance of the channels formed by PorH.C.call is not a linear function of the bulk aqueous concentration. Instead, we observed a dependence of the single-channel conductance on the square root of the salt concentration in the aqueous phase. This means, (i) that the cation specificity of PorH.C.call is not related to the presence of a binding site because saturation would be expected, and (ii) that negative charges are involved in ion selectivity as we and others have demonstrated previously for a variety of membrane channels (Menestrina & Antolini,
The precise number of charges involved in the charge effect is somewhat difficult to determine because of the use of either Nelson–McQuarrie or Debye–Hückel methods, which results in a difference in the potential of a factor of two. In one case the charge is in an aqueous environment (i.e. the charge is $q$) and in the other the charge on the surface of the membrane creates an image charge on the other side (i.e. the charge is $2q$). The decay of the potential in the aqueous phase is, on the other hand, independent from the localization of the charge, which means that the diameter of the channels is precise.

**Arrangement of** $\text{PorH}_{\text{C,call}}$ **and** $\text{PorH}_{\text{C,eff}}$ **in the cell wall**

$\text{PorH}_{\text{C,call}}$ and $\text{PorH}_{\text{C,eff}}$ have a rather small molecular mass of about 6 kDa, similar to that of $\text{PorA}_{\text{C,glut}}$ or $\text{PorB}_{\text{C,glut}}$. In general, the molecular masses of cell-wall porins are rather small compared to those of Gram-negative bacterial porins, which range between 30 and 60 kDa (Benz, 1994; Riess et al., 1998). This suggests that the cell-wall channels are formed by oligomers. This has been demonstrated for the subunit of the cation-selective channel of $M.\text{smegmatis}$, which has a molecular mass of about 20 kDa (Niederweis et al., 1999; Stahl et al., 2001) and forms an octamer in the cell wall (Faller et al., 2004). The monomers within the 3D structure of the octamer are arranged in a β-sheet structure similar to that of Gram-negative bacterial porins. However, such an arrangement is rather unlikely for the $\text{PorH}_{\text{C,call}}$ and $\text{PorH}_{\text{C,eff}}$ oligomers. Secondary structure predictions suggest that a stretch of about 28 aa (see Fig. 4a) of both proteins form amphipathic α-helices with about eight windings and a length of 4-2 nm in the mycolic acid layer (see Fig. 6). The arrangement is such that all hydrophilic amino acids are localized on one side of the helix and all hydrophobic ones are on the other side. Comparison of the helical wheels from the two organisms indicates that positively and negatively charged amino acids are balanced for $\text{PorH}_{\text{C,eff}}$ whereas the monomer of $\text{PorH}_{\text{C,call}}$ contains an excess of two negatively charged amino acids. It is noteworthy that this agrees well with the selectivity of both channels (see above). Secondary structure predictions for

![Fig. 5. Single-channel conductance of $\text{PorH}_{\text{C,call}}$ as a function the KCl concentration in the aqueous phase (■). The solid line represents the fit of the single-channel conductance data with the Nelson & McQuarrie (1975) formula (equations (1)–(5)), assuming the presence of negative point charges (1–6 negative charges; $q = -2.85 \times 10^{-19} \text{ As}$) at the channel mouth and assuming a channel diameter of 2.2 nm. $G_m$ mean single-channel conductance. The broken (straight) line shows the single-channel conductance of the cell-wall channel that would be expected without point charges. It corresponds to a linear function between channel conductance and bulk aqueous concentration.](image)

![Fig. 6. Schematic prediction of the $\text{PorH}_{\text{C,call}}$ and $\text{PorH}_{\text{C,call}}$ secondary structures. Both molecules can form α-helices with eight windings corresponding to an overall length of 4-2 nm based on secondary structure predictions of the primary sequence shown in Fig. 4(a) between the two vertical bars. Residues of the heptameric repeats are labelled in the sequence as a–g. The hydrophobic residues are located at positions a, e and d, indicating that they may be oriented towards the mycolic acids (indicated by oval rings). The hydrophilic residues are localized at the positions b, f, c and g and may face the channel lumen. Created with the help of Helical Wheel Java Applet (www.site.uottawa.ca/~turcotte/resources/HelixWheel/).](image)
the homologous porin PorH_{C,glut} of C. glutamicum likewise point to amphipathic \( \alpha \)-helices (data not shown).

This means that the arrangement of these cell-wall channels is different to MspA of \( M.\) smegmatis (Fallier et al., 2004). It is possible that the arrangement of PorH_{C,cell} and PorH_{C,eff} is associated with the thickness of the cell wall and the length of the mycolic acids of different mycolata. Thus, especially long mycolic acids have been found in mycobacteria and tsukamurellae (60–90 carbon atoms); they are medium-sized in gordonae, nocardiae and rhodococci (about 36–66 carbon atoms) and small in corynebacteria (22–38 carbon atoms) (Yano & Saito 1972; Minnikin et al., 1974, 1982; Minnikin 1987, 1991; Daffé et al., 1990; Holt et al., 1994; Ochi, 1995; Brennan & Nikaido 1995; Liu et al., 1995, 1996; Yassin et al., 1997). This means presumably that the cell walls of corynebacteria are much thinner than those of other mycolata, which is in agreement with structural studies (Marienfeld et al., 1997; Puech et al., 2001). Smaller polypeptides arranged as \( \alpha \)-helices are presumably sufficient to span the mycolic acid layer of corynebacteria. However, this may be tentative and further investigation of the cell-wall proteins of actinomycetes may be necessary to understand the structure and function of the cell-wall channels of the mycolata.

ACKNOWLEDGEMENTS

The authors would like to thank Christian Andersen for helpful discussions and help with the secondary structure predictions of the proteins. This work was supported by grants from the Deutsche Forschungsgemeinschaft (Be 865/9-5) and by the Fonds der Chemischen Industrie.

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