A conserved residue, PomB-F22, in the transmembrane segment of the flagellar stator complex, has a critical role in conducting ions and generating torque

Takashi Terauchi,† Hiroyuki Terashima,† Seiji Kojima and Michio Homma

Correspondence
Michio Homma
 reigning homma@cc.nagoya-u.ac.jp

Division of Biological Science, Graduate School of Science, Nagoya University, Chikusa-Ku, Nagoya 464-8602, Japan

Bacterial flagellar motors exploit the electrochemical potential gradient of a coupling ion (H\(^+\) or Na\(^+\)) as their energy source, and are composed of stator and rotor proteins. Sodium-driven and proton-driven motors have the stator proteins PomA and PomB or MotA and MotB, respectively, which interact with each other in their transmembrane (TM) regions to form an ion channel. The single TM region of PomB or MotB, which forms the ion-conduction pathway together with TM3 and TM4 of PomA or MotA, respectively, has a highly conserved aspartate residue that is the ion binding site and is essential for rotation. To investigate the ion conductivity and selectivity of the Na\(^+\)-driven PomA/PomB stator complex, we replaced conserved residues predicted to be near the conserved aspartate with H\(^+\)-type residues, PomA-N194Y, PomB-F22Y and/or PomB-S27T. Motility analysis revealed that the ion specificity was not changed by either of the PomB mutations. PomB-F22Y required a higher concentration of Na\(^+\) to exhibit swimming, but this effect was suppressed by additional mutations, PomA-N194Y or PomB-S27T. Moreover, the motility of the PomB-F22Y mutant was resistant to phenamil, a specific inhibitor for the Na\(^+\) channel. When PomB-F22 was changed to other amino acids and the effects on swimming ability were investigated, replacement with a hydrophilic residue decreased the maximum swimming speed and conferred strong resistance to phenamil. From these results, we speculate that the Na\(^+\) flux is reduced by the PomB-F22Y mutation, and that PomB-F22 is important for the effective release of Na\(^+\) from PomB-D24.

INTRODUCTION

Some ion channels and transporters that exist in cell membranes can selectively translocate only a particular ion. The high ion specificity of an ion channel or transporter is extremely important for signal transduction, membrane excitability and the homeostasis of organisms. Each selective ion transporter, which is coupled to a sodium ion, such as LeuT, NtpK or NhaA, possesses an ion binding pocket. A particular ion and/or a transport substrate interacts with the ion binding pocket, induces a conformational change, and is then translocated to the opposite side across the membrane (Gouaux & Mackinnon, 2005; Yamashita et al., 2005; Hunte et al., 2005; Murata et al., 2005, 2008). For example, in the Na\(^+\)-driven V-type ATPase of Enterococcus hirae, the transmembrane complex Vo, which conducts Na\(^+\) (or Li\(^+\)), is composed of a membrane rotor ring (K-ring) comprising oligomers of NtpK and a single copy of the Ntp1 subunit. It has been suggested that the cavity size of the K-ring binding pocket contributes to the ion specificity, that five residues (I\(^{61}\), T\(^{64}\), Q\(^{65}\), Q\(^{110}\), E\(^{139}\)) of NtpK are involved in the Na\(^+\) binding to the K-ring, and that the essential glutamate E\(^{139}\) is conserved in the homologous subunits of H\(^+\)-driven V-ATPase (Murata et al., 2005, 2008). Bacterial flagellar motors are rotary motors which convert the electrochemical potential difference of a coupling ion (H\(^+\) or Na\(^+)\) across the cytoplasmic membrane into torque, which rotates the flagellum. Escherichia coli and Salmonella use H\(^+\) as the coupling ion, whereas Vibrio and alkaliphilic Bacillus use Na\(^+\) (Kojima & Blair, 2004; Terashima et al., 2008).

Each flagellar motor is composed of a stator and a rotor. The stator serves as a torque-generating unit and is thought to work by interacting with the rotor. MotA and MotB are stator proteins in the H\(^+\)-driven motor of E. coli and Salmonella, while PomA and PomB, which are orthologues
of MotA and MotB, are found in the Na\textsuperscript{+}-driven motor of Vibrio spp. (Asai et al., 1997; Dean et al., 1984; Stader et al., 1986). Only the Na\textsuperscript{+}-driven motor of Vibrio spp. requires additional motor proteins, MotX and MotY, for torque generation (Okabe et al., 2001; Okunishi et al., 1996). PomA and PomB (MotA and MotB) are membrane proteins and form an A\textsubscript{2}:B\textsubscript{2} heterohexamer (Kojima & Blair, 2004; Sato & Homma, 2000a, b; Yorimitsu et al., 2004). PomA (MotA) has four transmembrane (TM) segments, whereas PomB (MotB) has only a single TM segment (Asai et al., 1997; Chun & Parkinson, 1988; Zhou et al., 1995). The C-terminal half of PomB (MotB) associates with the peptidoglycan layer and at least 11 PomA/B (MotA/B) complexes assemble around the rotor (Kojima et al., 2009; Leake et al., 2006; Reid et al., 2006). The coupling ion is taken through an ion-conducting pathway formed in the PomA/B (MotA/B) complex (Blair & Berg, 1990; Sato & Homma, 2000b). The ion influx induces a conformational change of the stator complex, which causes an interaction between PomA (MotA) and the rotor component FliG, and it has been inferred that the torque is generated by that interaction (Kojima & Blair, 2001; Lloyd & Blair, 1997; Yorimitsu et al., 2002; Zhou & Blair, 1997; Zhou et al., 1998a). The ion-conducting pathway is thought to be formed mainly by the third and fourth TM segments of PomA (MotA) and the single TM segment of PomB (MotB) (Braun & Blair, 2001; Braun et al., 2004; Sudo et al., 2009b; Yakushi et al., 2004). PomB (MotB) has a completely conserved aspartate residue (PomB-D24 for Vibrio, MotB-D32 for E. coli) which is essential for torque generation, and is a binding site of the coupling ion (Sudo et al., 2009a; Zhou et al., 1998b). Recently, it has been shown that this essential aspartate residue in PomB can be transferred to the TM segment of PomA. The transferred residue of PomA-N194D, which is a mutation in TM4, is able to partially rescue the motility defect in PomB-D24N, which suggests that PomA-N194 and PomB-D24 form an Na\textsuperscript{+} binding pocket for the coupling ion (Terashima et al., 2010).

Studies using chimeric proteins between H\textsuperscript{+}-type MotA/B of Rhodobacter sphaeroides or E. coli and Na\textsuperscript{+}-type PomA/B of Vibrio alginolyticus suggest that the B subunit is important for determining the ion specificity of the stator complex (Asai et al., 2000, 2003). In Bacillus subtilis, two types of stator complexes, MotA/B as the H\textsuperscript{+} type and MotP/S as the Na\textsuperscript{+} type, assemble around a single flagellar base, and the ion dependence of the functional hybrid stator complex (MotA/S or MotP/B) suggests the importance of the B subunit for determining the coupling ion (Ito et al., 2005). It has been reported that exchanging only three amino acids between MotB and MotS in B. subtilis can convert the ion specificity from the H\textsuperscript{+} type to the Na\textsuperscript{+} type and vice versa (Terahara et al., 2008). However, it remains unclear how the ion specificity is determined and how the coupling ion is coordinated by residues in the ion binding pocket, which then releases the ion from the binding pocket into the cytoplasm.

To investigate how the ion is selectively recognized in the stator complex and is released from it, we focused here on residues close to the essential aspartate residue of PomB. We constructed mutants in which the conserved residue in the H\textsuperscript{+}-type stator was changed to the corresponding residue in the Na\textsuperscript{+}-type stator, and the effects on motility were analysed. Thus we found a residue involved in determining the ion specificity and/or the ion release from PomB-D24.

**METHODS**

**Bacterial strains, plasmids and growth conditions.** The bacterial strains and plasmids used in this study are shown in Table 1. Site-directed mutagenesis of pomA or pomB was done using the QuikChange procedure (Stratagene). V. alginolyticus was cultured in VC broth (0.5 % (w/v) Bacto tryptone, 0.5 % (w/v) yeast extract, 0.4 % (w/v) K\textsubscript{2}HPO\textsubscript{4}, 3 % (w/v) NaCl, 0.2 % (w/v) glucose) or in VPG500 medium (1 % (w/v) Bacto tryptone, 0.4 % (w/v) K\textsubscript{2}HPO\textsubscript{4}, 500 mM NaCl, 0.5 % (w/v) glycerol) at 30 °C. E. coli was cultured in LB broth (1 % (w/v) Bacto tryptone, 0.5 % (w/v) yeast extract, 0.5 % (w/v) NaCl). Chloramphenicol was added to a final concentration of 2.5 μg ml\textsuperscript{-1} for V. alginolyticus and 25 μg ml\textsuperscript{-1} for E. coli.

**Swimming assay in semisolid agar.** VPG500 semisolid agar [1 % (w/v) Bacto tryptone, 0.4 % (w/v) K\textsubscript{2}HPO\textsubscript{4}, 500 mM NaCl, 0.5 % (w/v) glycerol, 0.25 % (w/v) Bacto agar] containing 0.02 % (w/v) arabinose was used for motility assays of V. alginolyticus. A 1 μl aliquot of each overnight culture was spotted onto VPG500 semisolid agar containing 0.02 % (w/v) arabinose or VPG500 semisolid agar containing 0.02 % (w/v) arabinose and 200 μM phenamil, and was incubated at 30 °C for the desired time.

**Introduction of plasmids into V. alginolyticus.** Transformation of Vibrio cells was carried out using electroporation, as described previously (Kawagishi et al., 1994).

**Measurement of swimming speed for Vibrio cells.** Overnight cultures were inoculated into VPG500 medium containing 0.02 % (w/v) arabinose at a 100-fold dilution. Cells were incubated at 30 °C for 4 h and then collected by centrifugation at 2000 g for 5 min. Cells were resuspended in TMN (50 mM Tris/HCl, pH 7.0, 5 mM MgCl\textsubscript{2}, 5 mM glucose, total ion strength 500 mM NaCl and KCl), TMN0 (Na\textsuperscript{+} 0 mM, K\textsuperscript{+} 500 mM), TMN5 (Na\textsuperscript{+} 5 mM, K\textsuperscript{+} 495 mM), TMN10 (Na\textsuperscript{+} 10 mM, K\textsuperscript{+} 490 mM), TMN20 (Na\textsuperscript{+} 20 mM, K\textsuperscript{+} 480 mM), TMN50 (Na\textsuperscript{+} 50 mM, K\textsuperscript{+} 450 mM), TMN100 (Na\textsuperscript{+} 100 mM, K\textsuperscript{+} 400 mM), TMN300 (Na\textsuperscript{+} 300 mM, K\textsuperscript{+} 200 mM) or TMN500 (Na\textsuperscript{+} 500 mM, K\textsuperscript{+} 0 mM) buffer. The suspensions were centrifuged and then resuspended in the same TMN buffer, and cells were diluted to 1:50 in the same TMN buffer and kept at room temperature for 15 min. Swimming of the cells was observed using dark-field microscopy immediately after the addition of serine to a final concentration of 20 mM to make the cells swim smoothly. Swimming speeds were determined from analysis of at least 20 individual cells. To investigate the effect of phenamil on swimming, cells were suspended in TMN300 buffer and phenamil was added to a final concentration of 0.2, 5, 10, 20, 50 or 100 μM. After the cells were exposed to phenamil for 15 s, swimming cells were recorded and then measured by using software for motion analysis (Move-tr/2D; Library Co.).

**Immunoblotting.** Cells were resuspended in SDS loading buffer and boiled at 95 °C for 5 min, and then were subjected to SDS-PAGE and immunoblotting as described previously (Yorimitsu et al., 1999). The
antibody to PomA (PomA1312) has been reported previously (Yorimitsu et al., 1999) and the antibody to PomB (PomBc2-B0455) was prepared as follows: an N-terminally truncated PomB variant consisting of residues 59–315 (PomBc2) with a His6-tag fused at its C terminus was constructed, and was overexpressed in BL21(DE3) cells from plasmid pTSK36, a derivative of pET22b. Cells were disrupted and a soluble fraction was isolated by ultracentrifugation. His-tagged PomBc2 was purified from this soluble fraction by using a HisTrap column followed by a HiTrap Q column (GE Healthcare). Purified PomBc2 was separated by SDS-PAGE, stained with Coomassie blue R250 and excised for immunization. The rabbit anti-PomBc2 antibody (PomBC2B0455) was produced by Biogate Co. Horseradish peroxidase-linked goat anti-rabbit IgG (Santa Cruz) was used as the secondary antibody.

RESULTS

Motility of cells producing PomB-L35V/S38A/E41S or PomB-L35V in Na⁺-free buffer

MotA/B and MotP/S of B. subtilis are the stators for the H⁺- and Na⁺-driven motors, respectively. When conserved residues in the H⁺- or Na⁺-type motors were exchanged between MotB and MotS (MotB-V35L + A38S + S41Q or MotS-L41V + S44A + Q47S), MotA/B was converted to the Na⁺-driven type, whereas MotP/S was converted to the H⁺-driven type (Terahara et al., 2008). Therefore, we substituted the corresponding residues of the Na⁺-type Vibrio PomB with those of the H⁺-type E. coli MotB (PomB-L35V + S38A + E41S or PomB-L35V) (Fig. 1). The swimming speeds of cells producing PomB-L35V or PomB-L35V + S38A + E41S were measured in buffer containing 0–300 mM NaCl (Fig. 2). The maximum swimming speed of cells producing PomB-L35V decreased to approximately 85% of the wild-type value. The maximum swimming speed of cells producing PomB-L35V + S38A + E41S decreased to approximately 50% of the wild-type value. However, in sodium-free buffer, cells producing PomB-L35V + S38A + E41S or PomB-L35V were not able to swim, and the swimming speed profiles were dependent on Na⁺ concentration (Fig. 2).

Motility of mutants converted from an Na⁺- to an H⁺-type residue

To investigate further the mechanism of the ion translocation and specificity in the stator complex, we focused on the residues that are conserved in the TM segments of the Na⁺-type stator proteins but not in those of the H⁺-type proteins, or on some residues around the boundary of the TM segments, because they may function as the entrance for ion conductance. We targeted the residues PomA-N194, PomB-F22 and PomB-S27, and replaced them with the corresponding amino acid of the H⁺-type protein (PomA-N194Y, PomB-F22Y and PomB-S27T) (Fig. 1). The swimming speeds of cells expressing PomA-N194Y, PomB-F22Y and PomB-S27T were measured in buffer containing 0–500 mM NaCl (Fig. 3). All mutants were able to swim in the presence of NaCl but not in Na⁺-free buffer, suggesting that the ion specificity was not converted. The maximum swimming speed of cells producing PomA-N194Y decreased to approximately 50% of the wild-type value. The maximum swimming speed of cells producing PomB-F22Y was almost the same as that of the wild-type; however, these cells were unable to swim in the presence of 5 mM NaCl and appeared to have a swimming threshold between 5 and 10 mM NaCl (Fig. 3b). The swimming speed of cells expressing PomB-S27T decreased to approximately 60% of the wild-type value. The amount of each mutant protein expressed from the plasmid was not affected by any of the mutations (data not shown).

To investigate whether the phenotype is affected by combinations of the mutations, mutants producing PomA-N194Y/PomB-F22Y, PomB-F22Y + S27T and PomB-F22Y + L35V were constructed, and their swimming speeds were measured at 0–50 mM NaCl (Fig. 4). These combination mutants were not able to swim in Na⁺-free buffer, suggesting that their ion specificity was not converted. Production of PomA-N194Y/PomB-F22Y and PomB-F22Y + S27T conferred swimming ability in buffer containing 5 mM Na⁺, but PomB-F22Y + L35V did not, indicating that PomA-N194Y and PomB-S27T suppressed the threshold phenotype of PomB-F22Y. Cells producing PomB-F22Y + L35V were also observed.

Table 1. Bacterial strains and plasmids used in the study

<table>
<thead>
<tr>
<th>Strain or plasmid</th>
<th>Genotype or description</th>
<th>Reference</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>V. alginolyticus strains</strong></td>
<td></td>
<td></td>
</tr>
<tr>
<td>NMB191</td>
<td>VIO5 pomAB (Mot⁺)</td>
<td>Yorimitsu et al. (1999)</td>
</tr>
<tr>
<td>sp2</td>
<td>NMB191, up-motile phenotype when PomAB is expressed</td>
<td>Terashima et al. (2010)</td>
</tr>
<tr>
<td><strong>E. coli strain</strong></td>
<td></td>
<td></td>
</tr>
<tr>
<td>JM109</td>
<td>recA1 endA1 gyrA96 thi hsdR17 supE44 relA1 Δ(lac-proAB) (F' traD36 proAB lacPl lacZAM15)</td>
<td>Yanisch-Perron et al. (1985)</td>
</tr>
<tr>
<td><strong>Plasmids</strong></td>
<td></td>
<td></td>
</tr>
<tr>
<td>pBAD33</td>
<td>Cm' PBAD</td>
<td>Guzman et al. (1995)</td>
</tr>
<tr>
<td>pHFAB</td>
<td>pma and pomB in pBAD33</td>
<td>Fukuoka et al. (2005)</td>
</tr>
</tbody>
</table>
required an Na\(^{+}\) concentration between 10 and 20 mM NaCl to exhibit swimming.

**Motility of various PomB-F22 mutants**

The phenotype of the PomB-F22Y mutant suggested that the mutation may affect ion conduction or torque generation. We carried out site-directed mutagenesis to replace Phe22 of PomB with various amino acid residues, K, D, L, W, Y, A, S and N. The swimming speed for each mutant was then measured in buffer containing 0–500 mM Na\(^{+}\) (data not shown). Except for the F22K and F22D mutants, the other six mutants exhibited motility at 500 mM NaCl. F22L and F22W showed nearly the same Na\(^{+}\) dependence and swimming speed as the wild-type. On the other hand, F22A had an Na\(^{+}\) threshold to exhibit swimming between 5 and 10 mM NaCl, similar to F22Y (Fig. 5a), and F22S and F22N had a threshold between 10 and 20 mM NaCl (Fig. 5b, c). The maximum swimming speeds of the F22L, F22W and F22Y mutants were almost the same as the original F22, while that of the F22A, F22S and F22N mutants decreased by approximately 50 % compared with F22. We also checked the swimming ability of the PomB-F22 mutants in semisolid agar containing 500 mM NaCl (Fig. 6a). Except for the F22L mutant, the swimming abilities in liquid and in semisolid agar for each mutant were comparable. The swimming ring size of F22L decreased to approximately 50 % of the wild-type value. These results show that various mutations of the F22 residue of PomB seem to affect motility in an Na\(^{+}\) concentration-dependent manner. Small hydrophobic (F22A) or hydrophilic (F22S and F22N, F22Y) residues showed a threshold of Na\(^{+}\) concentration to exhibit swimming (Fig. 5). However, large hydrophobic residues (F22L and F22W) did not show such a threshold (data not shown). The side-chain volume of Leu and Asn is
almost the same; however, the substitutions conferred different phenotypes. Thus, the hydrophobicity of F22 seems to be important for stator function through ion conduction.

Phenamil resistance of various PomB-F22 mutants

If a mutation affects the Na\(^+\)-dependent swimming property, it might also change the sensitivity to an Na\(^+\) channel blocker or a specific inhibitor of Na\(^+\)-driven motors such as phenamil. We checked the motilities of various PomB-F22 mutants in the presence of 200 \(\mu\)M phenamil by using semisolid agar containing 500 mM NaCl (Fig. 6b). The F22K and F22D mutants did not show swimming expansion even in the absence of phenamil. F22A showed a similar swimming expansion profile to that of the wild-type, while F22L and F22Y showed a slightly larger swimming expansion than the wild-type. F22W, F22S and F22N showed an even larger swimming expansion than F22L and F22Y. We next measured the swimming speeds of cells producing PomB-F22W, F22S, F22N and F22Y in buffer containing 300 mM Na\(^+\) with a final concentration of 0–100 \(\mu\)M phenamil (Fig. 7). Mutants producing F22W or F22Y were able to swim in the presence of 100 \(\mu\)M phenamil, but the swimming speed of cells decreased with increasing phenamil concentration. On the other hand, the motility of cells producing F22S or F22N remained at the same level, even at higher concentrations of phenamil. F22S and F22N showed strong resistance to phenamil. These results suggest that replacement of Phe22 with a large hydrophobic (W) or hydrophilic residues (S and N, Y) weakens the interaction with phenamil.

Conversion of the ion specificity in the up-motile strain

When PomA-N194Y, PomB-F22Y or PomB-S27T was produced in the sp2 strain, which gives an increased motility phenotype (Terashima et al., 2010), PomA-N194Y conferred slight swimming ability (mean ± SD 1.8 ± 0.76 \(\mu\)m s\(^{-1}\)) even in Na\(^+\)-free buffer (see Supplementary Movie), but the wild-type and PomB-F22Y and PomB-S27T mutants did not (data not shown). Because we suspected possible contamination with Na\(^+\) from the VPG500 broth, we washed the cells twice with Na\(^+\)-free buffer. Cells producing PomA-N194Y conferred only slight swimming ability, even after the additional washes. In 0 mM Na\(^+\) buffer with phenamil or carbonyl cyanide m-chlorophenylhydrazone (CCCP), this mutant was no longer able to confer motility. From these results, we were not able to determine which ion was used to rotate the flagellar motor by PomA-N194Y. However, the wild-type PomA/B was not able to confer motility at all by using the standard protocol with two washes. Therefore, we speculate that PomA-N194Y may use a different ion, such as H\(^+\), to rotate the flagellar motor; alternatively, the PomA-N194 stator may be driven by an extremely low Na\(^+\) concentration.

DISCUSSION

It has been proposed that the highly conserved aspartate residue (PomB-D24) binds the coupling ion and forms an ion binding pocket with PomA-N194 (Sudo et al., 2009a; Terashima et al., 2010). If the ion binding pocket is not the correct size for the coupling ion or if residues of the ion binding pocket are not correctly aligned to interact with the coupling ion, the conformational change of the
The stator complex followed by the binding and release of the coupling ion will probably not occur. In other words, if the Na\(^{+}\) binding pocket of PomA/B becomes properly coordinated to H\(^{+}\) by mutagenesis, we should be able to produce an H\(^{+}\)-driven PomA/B complex. It has been shown clearly that the ion specificity can be changed by replacing some residues of MotB around the putative periplasmic entrance of the ion (Terahara et al., 2008).

Therefore, we changed the corresponding residues of PomB, but this had no effect on ion selectivity. Other amino acid residues of the periplasmic surface may be important for determining ion binding and specificity. Unfortunately, we could not identify the periplasmic surface residues which are involved in ion binding and specificity. However, we found that PomA-N194 may be important for ion specificity and may create an ion binding

---

**Fig. 4.** Swimming speeds of the mutant stators combined with PomB-F22Y. Swimming speeds of cells producing PomA/PomB (a), PomA/PomB-L35V (b), PomA-N194Y/PomB-F22Y (c), PomA/PomB-F22Y+S27T (d) or PomA/PomB-F22Y+L35V (e) were measured as described in the legend of Fig. 2 in buffer containing 0–50 mM NaCl.
some periplasmic surface residues may also contribute to the ion specificity. This means that the recognition mechanism for an ion is not simple and that multiple sites are necessary to determine the specificity, as discussed below.

In this study, we found that PomA-N194Y confers the ability to swim in an Na\(^+\)-free buffer in the increased motility strain sp2. However, we could not determine what the coupling ion is or whether the Na\(^+\)-type PomA/B has been converted to the H\(^+\) type. Attenuated total reflection Fourier transform infrared spectroscopy has shown that the PomA/B complex has at least three Na\(^+\) binding carboxyl residues. One of the Na\(^+\) binding carboxyl residues is the essential aspartate, PomB-D24, and the others are as yet unidentified (Sudo et al., 2009a). We suggest that other as-yet-unidentified Na\(^+\) binding sites may contribute to determining the ion specificity and/or to promoting ion flow by efficient binding of the ions. Because PomA-N194 is thought to be the residue that forms the ion binding pocket with PomB-D24, the dramatic decrease of the swimming speed of cells expressing PomA-N194Y may derive from a slow flux of Na\(^+\) because of inefficient recognition or binding of ions. The corresponding residue

![Fig. 5. Swimming speeds of various PomB-F22 mutants.](image)

Swimming speeds of cells producing F22A (a), F22S (b) or F22N (c) were measured as described in the legend of Fig. 2 in buffer containing 0–50 mM NaCl.

![Fig. 6. Effects of phenamil on the swimming abilities of the various PomB-F22 mutants in semisolid agar.](image)

(a) Cells were inoculated on 0.25 % agar VPG plates and were incubated at 30 °C for 5 h. (b) Cells were inoculated on 0.25 % agar VPG plates containing 200 μM phenamil and were incubated at 30 °C for 24 h.
of the $H^+$-type MotA is conserved as tyrosine. This may imply that the tyrosine and/or asparagine contributes to the ion specificity ($H^+$ or $Na^+$) of the flagellar motor. We think that PomA-N194 might be one of the most important residues for ion specificity, although there are probably other residues that contribute. NtpK, which is a V-ATPase rotor ring component, coordinates $Na^+$ with the essential carboxyl group of E139, the carbonyl group of Q65 and Q110, the hydroxyl group of T64 and the main chain carbonyl group of L61 (Murata et al., 2005).

Therefore, we speculate that the ion binding pocket of PomA/B is composed of residues other than PomB-D24 and PomA-N194 that coordinate $Na^+$ ions. So, to generate an $H^+$-driven PomA/B complex, the introduction of two or more mutations with PomA-N194Y in TM4 may be required in other TM regions (TM1–3) of PomA.

It has been reported that the PomA-D31C mutant cells require a higher $Na^+$ concentration (greater than 19 mM $NaCl$) to exhibit swimming motility (Kojima et al., 2000).

Fig. 7. Effects of phenamil on the swimming abilities of the various PomB-F22 mutants. Swimming speeds of cells producing PomB (a), PomB-F22Y (b), F22W (c), F22S (d) or F22N (e) were measured as described in the legend of Fig. 2 in buffer containing 300 mM $NaCl$ and various concentrations of phenamil.
When PomA-D31 was substituted to charge-inverted or large side-chain amino acids, the Na\(^+\) thresholds of those mutants were even higher, above 50 mM NaCl. It has been speculated that the efficiency of Na\(^+\) flow is increased by the negative charge at D31 and that Na\(^+\) ions may be recruited by this negative charge. The motility of cells producing PomB-F22Y was decreased at low Na\(^+\) concentration but did not change at high Na\(^+\) concentration compared with the wild-type. We thus hypothesized that the F22Y mutation affects ion flux or torque generation. F22L, F22W and F22Y conferred almost the same maximal swimming speed as the wild-type, while the F22A, F22S and F22N mutants were decreased to approximately 50% of the wild-type value. The F22A, F22S and F22N mutants also showed a threshold of Na\(^+\) concentration for swimming motility. On semisolid agar containing 500 mM NaCl, except for the F22L mutant, all swimming ring sizes among the TM regions between the two PomA subunits, might be involved in the release of Na\(^+\) from PomB-D24. It has been suggested that PomA-D148 and PomB-P16 contribute to forming a high-affinity phenamil binding site at the inner face of the PomA/PomB complex.

PomB-F22Y would be on nearly the opposite helix face from PomB-D24 according to helical wheel modelling. However, a cross-linking study of MotA/B proposed that one MotA and one MotB subunit form an ion binding pocket that and the carboxyl group of MotB-D32 (corresponding to PomB-D24) directs ions to the pocket, although MotB-Y30 (corresponding to PomB-F22) is thought to face the other MotA subunit (Braun et al., 2004). In the cross-linking study of TolQR, which are inner-membrane proteins of the Tol–Pal system that show homology with MotA/B and PomA/B, it has been proposed that TolR rotates between two TolQ subunits (Zhang et al., 2009). The size of the swimming ring of the F22L mutant was decreased to approximately 50% of the wild-type value on semisolid agar, suggesting that torque might be reduced. The aromatic ring at position F22 might be important to generate maximal torque. In the F22Y mutant, the hydroxyl group of Tyr might lead to the motility defect under low Na\(^+\) conditions. We speculate that the Na\(^+\) flux might be reduced by the replacement of F22 in PomB with hydrophilic residues.

### Diagram

![Model of the ion flux pathway.](image)

**Fig. 8.** Model of the ion flux pathway. Asp24 of PomB forms an Na\(^+\) binding site which is suggested to make an ion binding pocket with Asn194 of PomA. Cys31 of PomB and Ala39 of MotB form a pair of amino acids for the H\(^+\) pocket with Asn194 of PomA. Cys31 of PomB and Ala39 of MotB form a pair of amino acids for the H\(^+\) pocket with Asn194 of PomA.

### references

- Sudo et al., 2009a, b; Terashima et al., 2010.
- Tao et al., 2010.
- Kojima et al., 1999.
- Jaques et al., 1999.
On the basis of our results, combined with previous studies, we propose a model for the ion flux pathway through MotA/B and PomA/B ion channels (Fig. 8). First, the ion passes through the periplasmic side of a channel pore, a part of which is formed by Leu183 of PomA and Cys31 of PomB, or Met206 of MotA and Ala39 of MotB (Sudo et al., 2009b). Next, the ion binds to the pocket that is formed mainly by Asn194 of PomA and Asp24 of PomB, or by Tyr217 of MotA and Asp32 of MotB (Sudo et al., 2009b; Terashima et al., 2010). Finally, an event to generate torque starts, and the ion is released from the ion binding pocket to the cytoplasm, and at this stage, Phe22 of PomB or Tyr30 of MotB might be important. In this study, we introduced mutations into TM4 of PomA or into the TM of PomB. To convert from the Na\(^+\) to the H\(^+\) type, mutations need to be introduced in residues of PomA TM1, 2 or 3, and the mutations need to be combined.

ACKNOWLEDGEMENTS

This work was supported in part by grants-in-aid for scientific research from the Ministry of Education, Science, and Culture of Japan, the Japan Science and Technology Corporation (to M. H.) and the Japan Society for the Promotion of Science (to H.T.).

REFERENCES


Edited by: P. W. O'Toole