

Random mutagenesis of the *pomA* gene encoding a putative channel component of the Na⁺-driven polar flagellar motor of *Vibrio alginolyticus*

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PomA and PomB are integral membrane proteins and are essential for the rotation of the Na⁺-driven polar flagellar motor of *Vibrio alginolyticus*. On the basis of their similarity to MotA and MotB, which are the proton-conducting components of the H⁺-driven motor, they are thought to form the Na⁺-channel complex and to be essential for mechanochemical coupling in the motor. To investigate PomA function, random mutagenesis of the *pomA* gene by using hydroxylamine was carried out. We isolated 37 non-motile mutants (26 independent mutations) and most of the mutations were dominant; these mutant alleles are able to inhibit the motility of wild-type cells when greatly overexpressed. The mutant PomA proteins could be detected by immunoblotting, except for those with deletions or truncations. Many of the dominant mutations were mapped to the putative third or fourth transmembrane segments, which are the most conserved regions. Some mutations that showed strong dominance were in highly conserved residues. T186I is the mutation of a polar residue located in a transmembrane segment that might be involved in ion translocation. P199L occurred in a residue that is thought to mediate conformational changes essential for torque generation in MotA. These results suggest that PomA and MotA have very similar structures and roles, and the basic mechanism for torque generation will be similar in the proton and sodium motors.

Keywords: flagella, sodium ion, *Vibrio*, motor, *pomA*

INTRODUCTION

Bacterial flagella are the organelles responsible for motility. At the base of each filament, a rotary motor is embedded in the cytoplasmic membrane, and bacteria can swim by rotating their helical flagellar filaments. The motor is powered by the electrochemical gradient of a specific ion, H⁺ or Na⁺, across the cytoplasmic membrane (Blair, 1995; Imae & Atsumi, 1989). The study of the flagellar motor has been intensively done in the H⁺ motors of *Escherichia coli* and *Salmonella typhimurium*. These studies have focused mainly on five core proteins involved in the motor function. In the rotor part of the motor, three soluble proteins, FliG, FliM and FliN, are the components for force generation,

flagellar assembly and controlling the direction of motor rotation (Yamaguchi *et al.*, 1986; Sockett *et al.*, 1992; Irikura *et al.*, 1993). Together they form a complex, called the 'switch complex' or 'C-ring' (Francis *et al.*, 1994). Among them, FliG has a direct role in force generation (Lloyd *et al.*, 1996). The stator part of the motor, two integral membrane proteins, MotA and MotB, are the components essential for force generation (Dean *et al.*, 1984; Stader *et al.*, 1986; Block & Berg, 1984; Blair & Berg, 1988). They have four and one transmembrane segments, respectively (Zhou *et al.*, 1995; Chun & Parkinson, 1988), and form a H⁺-conducting channel complex responsible for coupling ion translocation to force generation (Blair & Berg, 1990; Stolz & Berg, 1991; Sharp *et al.*, 1995a; Garza *et al.*, 1995, 1996). The MotA/MotB channel complex is believed to be anchored to the cell wall by the peptidoglycan-binding domain of MotB (Chun & Park-

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Abbreviation: TM, transmembrane.

inson, 1988; Blair *et al.*, 1991; De Mot & Vanderleyden, 1994).

Intensive mutational analysis of MotA, MotB and FliG of *E. coli* revealed some critical residues involved in torque generation. It was shown that most of the dominant mutations occurred in the transmembrane domains of MotA and MotB (Blair & Berg, 1991; Blair *et al.*, 1991). In particular, Asp32 of MotB, a conserved acidic residue in the membrane segment, was suggested to be the residue conveying protons (Zhou *et al.*, 1998a). Other recent mutational analyses indicated that three charged residues of FliG predicted to be on one surface, Arg281, Asp288, Asp289, and two cytoplasmic charged residues of MotA, Arg90 and Glu98, are involved in torque generation (Lloyd & Blair, 1997; Zhou & Blair, 1997). It was speculated that these charged residues of FliG and MotA might engage in electrostatic interactions with each other (Zhou *et al.*, 1998b).

The Na⁺-driven motor has some advantages for study compared with the H⁺-driven type. Sodium-motive force can be manipulated more easily than proton-motive force, and amiloride and its analogues work as specific inhibitors of the motor (Sugiyama *et al.*, 1988; Atsumi *et al.*, 1990). It was thought that the inhibitor interacted with the Na⁺-channel components in the motor. Four proteins essential for torque generation, PomA, PomB, MotX and MotY, were recently identified in the polar flagellar motor of *Vibrio alginolyticus* (Asai *et al.*, 1997; Okunishi *et al.*, 1996). PomA and PomB are homologous to MotA and MotB, and have four and one transmembrane segments, respectively. *Rhodobacter sphaeroides* MotA, which is the H⁺-motor component (Shah & Sockett, 1995), is very similar to PomA and contains the same number of residues (Asai *et al.*, 1997). Therefore, PomA and PomB are thought to form a Na⁺-channel complex in the motor. Recently, mutations which cause the resistance to the specific inhibitor, phenamil (an amiloride analogue), were identified in PomA and PomB, supporting the suggestion that these proteins are Na⁺-motor-specific channel components (Kojima *et al.*, 1999). On the other hand, both MotX and MotY, which have been identified in *Vibrio parahaemolyticus* (McCarter, 1994a, b) and have putative single transmembrane segments, are not homologous to the proton-type motor proteins, except that MotY has a peptidoglycan-binding motif in the C-terminal region, as do MotB and PomB. MotX was also inferred to be the Na⁺-channel component of the motor because overproduction of MotX is lethal to *E. coli* in proportion to the external Na⁺ concentration and because this lethality is reversed by the addition of amiloride (McCarter, 1994a).

Thus, the H⁺ motor and the Na⁺ motor have some similar and some distinct aspects. We hypothesize that the basic mechanism for torque generation will be common in the H⁺-driven and Na⁺-driven motors. If so, residues critical for motor function will also be common between the two types of motors. In this study, we carried out random mutagenesis of the *pomA* gene in order to identify residues responsible for the function of PomA.

METHODS

Bacterial strains, growth conditions and media. *V. alginolyticus* VIO5 (Laf⁻ PomA⁺) and VIO586 (Laf⁻ PomA⁻) were used as the host strains to express the wild-type and mutant *pomA* genes (the Laf phenotype is the presence of lateral flagella) (Okunishi *et al.*, 1996, Asai *et al.*, 1997). For DNA manipulation, we used the *E. coli* strain DH5 α (Grant *et al.*, 1990). *V. alginolyticus* cells were cultured in VC medium (0.5% polypeptone, 0.5% yeast extract, 0.4% K₂HPO₄, 3% NaCl, 0.2% glucose) at 30 °C and *E. coli* cells were cultured in LB medium (1% tryptone, 0.5% yeast extract, 0.5% NaCl) at 37 °C. For swarm assays, *Vibrio* cells were inoculated on 0.25% agar VPG plates (0.25% agar in VPG medium containing 1% polypeptone, 0.4% K₂HPO₄, 3% NaCl, 0.5% w/v, glycerol). When necessary, chloramphenicol was added to a final concentration of 2.5 μ g ml⁻¹ for *Vibrio* cells and 25 μ g ml⁻¹ for *E. coli* cells.

Plasmids. For isolation of *pomA* mutants, the *pomA* gene in the *Bam*HI fragment of plasmid pYA301 was subcloned into pSU21, a chloramphenicol-resistant vector (Bartolomé *et al.*, 1991), and named pMK101. The *Bam*HI fragment in pMK101 was inserted in the opposite orientation to the *lac* promoter in pSU21. This *Bam*HI fragment was also cloned in the reverse orientation and the resultant plasmid was named pMK201.

Isolation of *pomA* mutants. Plasmid pMK101 was treated with 2 M hydroxylamine in 0.1 M potassium phosphate (pH 6.0), 1 mM EDTA for 4 h at 50 °C. After the treatment, plasmids were diluted in 10 mM Tris/HCl (pH 7.5), 1 mM EDTA, and dialysed overnight to remove hydroxylamine. Then, plasmids were precipitated with ethanol and transformed into the *pomA* mutant VIO586. We selected Pom⁻ (polar flagellar motility defective) transformants from the chloramphenicol-resistant and swarm-deficient ones as described previously (Okunishi *et al.*, 1996). The Pom⁻ phenotype was confirmed by isolating mutant plasmids and retransforming them into VIO586.

Dominance. To assay the dominance of the plasmid-borne *pomA* mutants, each plasmid was transformed into the PomA⁺ strain VIO5. Transformants were inoculated on a 0.25% agar VPG plate and incubated for 6 h at 30 °C. The diameters of the swarms of each mutant were measured and their mean diameter was normalized to the diameter of the swarm formed on the same plate by VIO5/pMK201(PomA⁺) cells. The relative swarm size of each mutant was obtained from at least three independent experiments, and the dominance was determined from the mean value of them. The swarm size of wild-type cells was 0.92 \pm 0.06 cm. The mutants were categorized into four types; severely dominant (+++; 0–20% of wild-type swarm size), strongly dominant (++; 21–45% of wild-type), slightly dominant (+; 46–70% of wild-type) and recessive (–; 71–100% of wild-type).

DNA manipulations and sequencing. Routine DNA manipulations were carried out according to standard procedures (Sambrook *et al.*, 1989). Restriction endonucleases and other enzymes for DNA manipulations were purchased from Takara Shuzo and New England Biolabs. The nucleotide sequence was determined by the dideoxy chain termination method using the ABI PRISM Dye Terminator Cycle Sequencing Ready Reaction Kit and the ABI PRISM 377 DNA sequencer (Perkin Elmer).

Electroporation. Transformation of *Vibrio* cells by electroporation was carried out as described previously (Kawagishi *et al.*, 1994).

Immunoblots of PomA. Immunoblotting was carried out as described previously (Nishioka *et al.*, 1998). Cells were

harvested and suspended in distilled water at an OD_{660} of 10. The suspension was electrophoresed through a 10% SDS-PAGE gel. For the detection of the mutant PomA proteins, we used an anti-PomA peptide antibody (PomA91), which was generated against peptides derived from three segments of PomA with an additional cysteine at the N terminus to keyhole limpet haemocyanin; 1, CKKDIALTDERHTQGTVFRAFGDVAP (in the cytoplasmic domain between TM2 and 3); 2, CTTLYGAILSNMVFFPIADKLSLRDQET (in the TM4); 3, CQDQGNPRVIDSYLKNYLNEGK (in the C-terminal cytoplasmic domain).

RESULTS

Isolation of PomA mutants

We first subcloned the *pomA* gene from the plasmid pYA301 (*pomA*⁺, Km^r) into the vector pSU21 (Cm^r), because transformation of *Vibrio* cells with the Cm^r vector was more efficient than with the Km^r vector. Random mutagenesis of the *pomA* gene was carried out by treating the resultant plasmid, pMK101 (*pomA*⁺, Cm^r), with hydroxylamine. The mutagenized plasmids were introduced into the *pomA* mutant VIO586, which has non-motile polar flagella, and each transformant was inoculated on semisolid agar plates. Approximately 1% of the Cm^r clones obtained were deficient for swarming in this screen, and we isolated 43 mutants by this procedure. These mutants were classified into two groups: (I) cells completely impaired in polar flagellar motility on semisolid agar (Pom⁻; 37 clones), and (II) cells that swarm much more slowly than wild-type (6 clones). Fig. 1 shows typical swarms of the type I

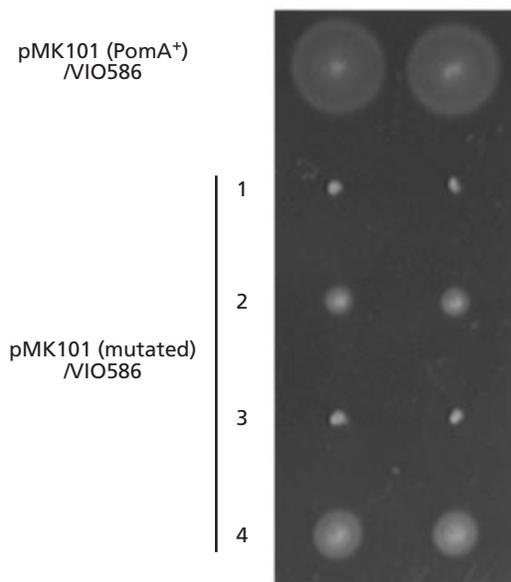


Fig. 1. PomA mutant phenotypes. Fresh colonies of the *pomA* mutant (VIO586) containing plasmid pMK101 were inoculated on 0.25% agar VPG plates containing chloramphenicol and incubated at 30 °C for 4 h. Colonies 1 and 3 are examples of type I mutants (immotile) and colonies 2 and 4 are the examples of type II mutants (slow swarming).

mutants (alleles 1 and 3) and type II mutants (alleles 2 and 4). We expected that type II mutants might swim slowly. However, when each of them was grown in liquid broth and examined under the microscope, only a small fraction of the cells were swimming, at the same speed as wild-type cells, and most cells were immotile. All of the type II mutants showed this phenotype. On the other hand, all of the type I mutants were completely immotile when grown in broth and observed under the microscope. We characterized the type I mutants further.

Positions of *pomA* mutations

The nucleotide changes in all the type I *pomA* alleles were determined by sequencing. The results are summarized in Table 1. In six mutants (alleles 3, 7, 23, 24, 26 and 37) we could not find any nucleotide changes in the *pomA* coding region. These mutations might occur in regions that affect the expression of *pomA*. Nucleotide changes in the other mutants were of the type expected for hydroxylamine mutagenesis (GC to AT transitions). The mutants were grouped into four categories (Table 1). Deletions or terminations were found in ten mutant alleles. Single and double amino acid substitutions were found in 16 and 5 mutants, respectively. Double mutations were detected mainly in the cytoplasmic domain, and interestingly, two were in adjacent residues. On the other hand, it is noteworthy that most of the single mutations were mapped to the putative third or fourth transmembrane segments, which are highly conserved between PomA and MotA of *R. sphaeroides* or *E. coli* (Asai *et al.*, 1997) (Fig. 2). Actually, all of the mutated residues in the single mutants, except for Ser193, are conserved in MotA. Five mutations were found in residues that also gave a dominant, swarm-deficient phenotype when mutated in *motA* in *E. coli*. These residues are Gly8, Gly154, Thr186 and Pro199 (mutations in MotA were G6S, G6D, G176S, T209W and P222L, respectively). Most of the single mutations were substitutions of a non-charged residue by a polar or charged one, and others were substitutions by residues with large side chains.

Dominance of *pomA* mutations

Next, we investigated the dominant-negative effects of the mutant PomA proteins. All the type I mutant *pomA* alleles were introduced into VIO5 (*pomA*⁺) cells, and fresh transformants were inoculated on semisolid agar plates. None of the mutant plasmids caused any significant reduction in swarm size in this assay (data not shown). The *pomA* fragment in pMK101 is inserted in the opposite orientation to the *lac* promoter, and so although the protein is expressed at levels sufficient to complement a *pomA* defect, it is not expected to be overexpressed (for discussion of an analogous construct expressing *motY*, see Okunishi *et al.*, 1996). To determine whether higher-level expression of mutant *pomA* alleles *in trans* from multicopy plasmids in PomA⁺ cells might affect the dominance of the mutation, we reversed the orientation of the wild-type and all the

Table 1. Nucleotide and amino acid changes of PomA mutants

Nucleotide changes were identified as described in Methods. Dominance was determined by swarm size relative to that of wild-type (see Fig. 4). Loop₁₋₂ is the region between TM1 and TM2 (periplasm), loop₂₋₃ is the region between TM2 and TM3 (cytoplasm), and loop₃₋₄ is the region between TM3 and TM4 (periplasm). NE; not examined.

Allele number/type	Base change	Amino acid change	Dominance	Location
Deletion				
2	Δ262–472	Frameshift	–	Loop ₂₋₃ –TM3
Nonsense mutations				
11, 15, 19, 25	C160T	Q54Termination	–	Loop ₂₋₃
28	C412T	Q138Termination	–	Loop ₂₋₃
16	C676T	Q226Termination	+	C-terminus
4	C685T	Q229Termination	+	C-terminus
34	C694T	R232Termination	–	C-terminus
31	C578T/C694T	S193F/R232Termination	NE	TM4/C-terminus
Single amino acid substitutions				
10	G22A	G8S	++	TM1
27	G23A	G8D	++	TM1
22	G460A	G154R	+	TM3
6	G461A	G154E	+	TM3
36	G470A	G157D	+++	TM3
21	(C345T)/C473T	(G115G)/T158I	+++	TM3
17	C484T	L162F	+++	TM3
33	G526A	G176R	++	Loop ₃₋₄
13	G527A	G176E	+++	Loop ₃₋₄
1, 29	C557T	T186I	++	TM4
32	C578T	S193F	–	TM4
30	C596T	P199L	+++	TM4
5	(C594T)/C596T	(F198F)/P199L	NE	TM4
14	G662A	G221D	–	C-terminus
8	C739T	R247C	+	C-terminus
Double amino acid substitutions				
35	C260T/C406T	A87V/H136Y	+++	Loop ₂₋₃ /loop ₂₋₃
9	C391T/C395T	L131F/T132M	–	Loop ₂₋₃ /loop ₂₋₃
18, 20	G404A/G507A	R135Q/M169I	+++	Loop ₂₋₃ /TM3
12	G657A/G658A	M219I/D220N	++	C-terminus/C-terminus
No mutation detected in <i>pomA</i>				
3, 7, 23, 24, 26, 37			NE	

mutant *pomA* genes, placing them downstream of the *lac* promoter (the resultant plasmid containing wild-type *pomA* is named pMK201). These mutant plasmids were introduced into VIO586 (PomA[–]) and VIO5 (PomA⁺) cells and each transformant was inoculated on semisolid agar plates.

As shown in Fig. 3(a), *pomA* in pMK201 complemented the PomA[–] phenotype of VIO586, indicating that function is normal when the PomA protein is expressed from this plasmid. Most of the mutant PomA remained nonfunctional in this assay. Exceptions were G176R and S193F, which were slightly motile, suggesting that these two mutations might be suppressed by overexpression

of the proteins. As shown in Fig. 3(b), most of the mutant proteins reduced the swarming ability of VIO5 (PomA⁺) cells when they were overexpressed from the plasmids. To quantify the dominance of each mutant, the swarm assays were repeated, and relative swarm sizes for at least three measurements were averaged. The data are summarized in Fig. 4. Deleted or truncated PomA mutants exhibited recessive or slightly dominant phenotypes. On the other hand, most of the single or double mutants showed dominant effects. The strength of dominance was ranked as described in Methods (Table 1). The mutations in the transmembrane segments showed the strongest dominance (+++ or ++), consistent with the results of MotA mutagenesis.

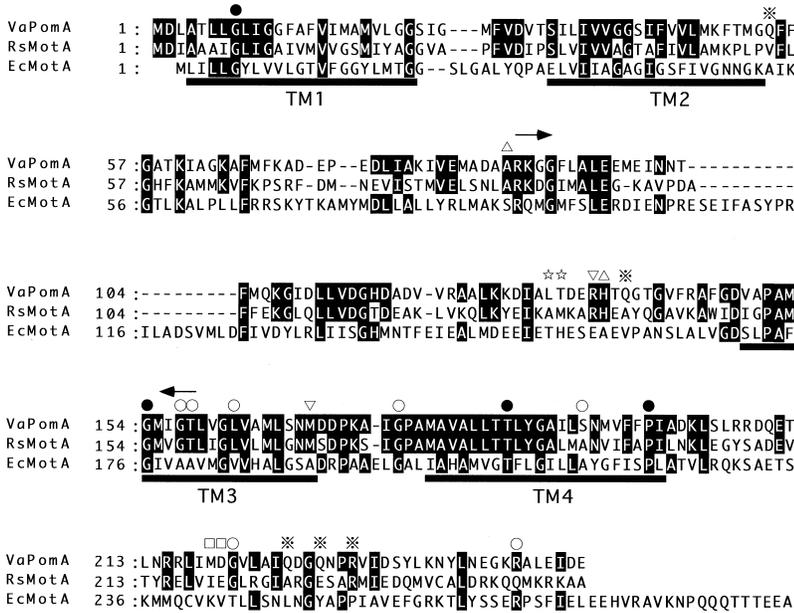


Fig. 2. Amino acid alignments of PomA and sites of mutations isolated in this study. Mutated residues are marked by symbols. ✖ show sites of nonsense mutations, and arrows show the deletion in the allele 2 mutant. Circles show the sites of single mutations and paired symbols (Δ , ∇ , \square or \star) show sites of double mutations. Residues giving dominant mutations in both PomA and MotA of *E. coli* are marked by a black circle. Abbreviations: VaPomA, *V. alginolyticus* PomA; RsMotA, *R. sphaeroides* MotA; EcMotA, *E. coli* MotA. White letters in black boxes show residues identical to PomA.

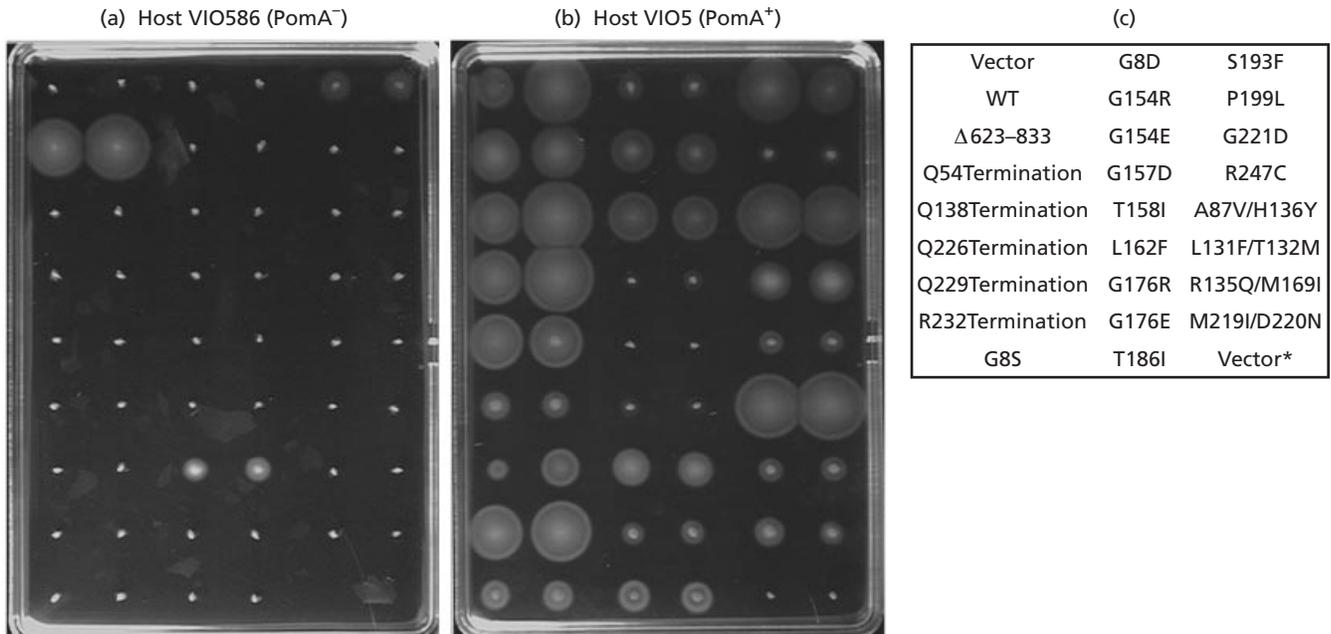


Fig. 3. Swarming abilities of the PomA mutants. Two fresh colonies of the *pomA* mutant (VIO586) (a) or the wild-type Pom⁺ strain (VIO5) (b) each carrying the mutant *pomA* genes on a multicopy plasmid were inoculated on 0.25% agar VPG plates containing chloramphenicol and incubated at 30 °C for 6 h. The mutations are identified in panel (c). In (a) WT stands for VIO586/pMK201 and 'vector' stands for VIO586/pSU21; in (b) WT stands for VIO5/pMK201 and 'vector' stands for VIO5/pSU21. 'Vector*' stands for VIO586/pSU21 and is only shown in (b), as a non-motile control.

Expression of mutant PomA

To detect the mutant proteins expressed from the plasmid pMK201, we performed immunoblots to the cell suspensions of the mutants by using a polyclonal anti-PomA peptide antibody (Fig. 5). We could detect PomA bands of the expected size (25 kDa) in all the strongly (++) or severely (+++) dominant mutants.

We observed some small differences in the amounts of the proteins between the mutants. In addition to the 25 kDa band (arrow in Fig. 5), we detected a band at 45 kDa, in both the wild-type and the mutants. The significance of this band is discussed later. We could not detect the PomA protein in the wild-type strain itself (vector in Fig. 5a and b), or in recessive (-) or slightly dominant (+) mutants (for example, G154R in Fig. 5b);

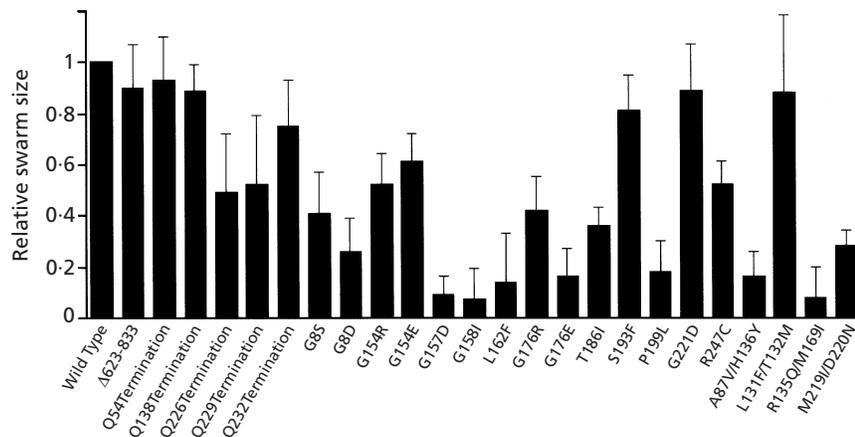


Fig. 4. Dominance of the PomA mutants. Swarm assays of the mutants, as shown in Fig. 3(b), were repeated at least three times and the swarm diameters of each mutant were normalized to that of the wild-type strain (VIO5/pMK201). The relative swarm size obtained from each experiment was averaged and is indicated on the figure with error bar.

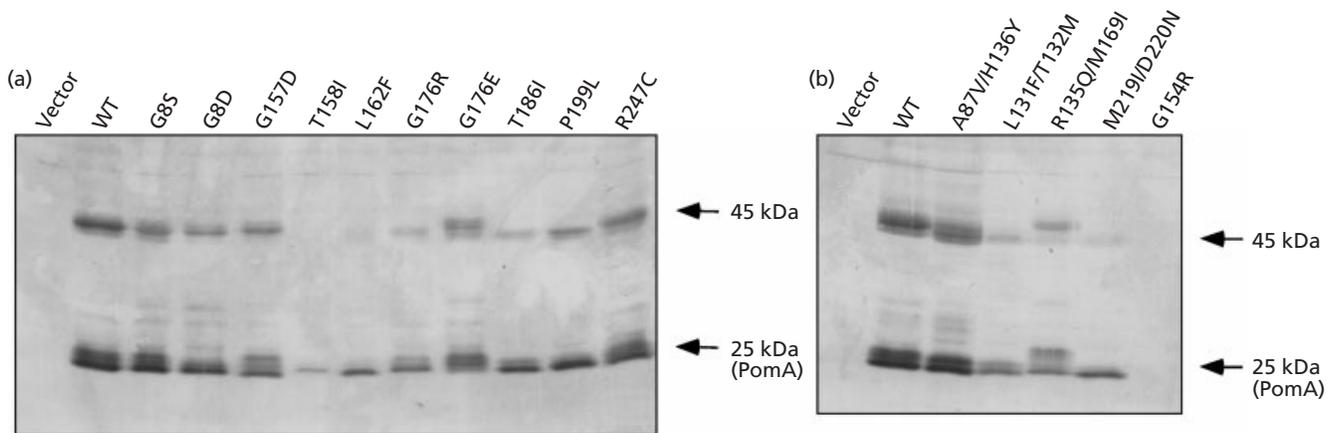


Fig. 5. Western-blot analysis of the mutant PomA proteins. PomA was not detected in any of the other mutants (data not shown). Cells transformed by the plasmids pMK201 were harvested and suspended in distilled water. This suspension was subjected to SDS-PAGE and immunoblotting with the anti-PomA peptide antibody.

other data not shown), except for R247C and L131F/T132M. All of the deleted or truncated mutant proteins could not be detected. These mutant proteins might be degraded or synthesized in very small amounts. L131F/T132M, which was detected but not dominant, might have some defect in assembling into the appropriate position in the motor.

In some mutants, the PomA bands were found at positions different from the wild-type PomA. The T158I protein was observed at a higher position than wild-type, and in the G176E and R135Q/M169I mutants, both the 25 kDa and 45 kDa bands were at significantly higher positions. Some structural change caused by these mutations might affect the mobility of the proteins in electrophoresis.

DISCUSSION

Isolation of *pomA* mutations

PomA is the homologue of the MotA protein, which is believed to be the channel component essential for

rotation of the H⁺-driven motor. PomA should have similar functions in the Na⁺-driven motor. To identify the residues of PomA essential for torque generation, we carried out random mutagenesis of the *pomA* gene by hydroxylamine. We isolated 37 non-motile mutants and identified 26 independent mutations in the *pomA* gene. Most of the mutants with single or double amino acid substitutions showed severe or strong dominance, and these mutant PomA proteins expressed from multicopy plasmids could be detected by immunoblotting. These results suggest that the mutant proteins which exhibit dominance are expressed and inserted into the motor but do not function properly, that is, they seem to have defects in torque generation. On the other hand, recessive and weakly dominant mutants could not be detected by immunoblotting. We also could not detect the wild-type level of PomA (Fig. 5a, b, lanes 1), so mutant proteins might be synthesized in very small amounts, although they do not significantly affect the torque generation when expressed in PomA⁺ cells. Therefore we mainly discuss the strongly dominant mutations in the subsequent sections.

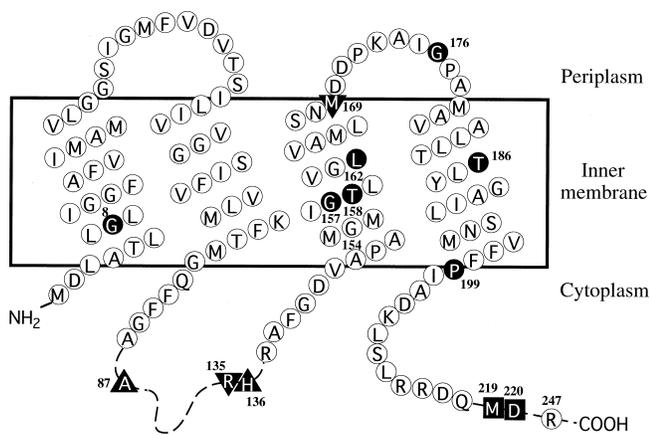


Fig. 6. Hypothetical transmembrane region of PomA. The residues altered in strongly and severely dominant mutants are shown by black symbols. The residues altered in slightly dominant mutants are marked by the residue number with white symbols. Dominant double mutants are shown by a pair of squares or triangles. Recessive mutants are not marked.

Localization of the dominant mutations

The dominant mutations were localized to the putative third or fourth transmembrane segments (Fig. 6), which are highly conserved between PomA and MotA. These transmembrane segments might be more important for function than other regions of the protein. Most of the mutations introduced amino acids with charged or large side-chains. According to the tryptophan-scanning mutagenesis of MotA (Sharp *et al.*, 1995b), helices 3 and 4 of MotA were more sensitive to bulky Trp substitutions than were helices 1 and 2, suggesting that helices 3 and 4 might be more fully surrounded by other protein segments that cannot accommodate the Trp side chain. Therefore, substitutions in TM3 or TM4 of PomA might affect conformation or interfere with the interaction between PomA and other channel components such as PomB, MotX and MotY, and consequently disrupt the arrangement of the channel complex, which would no longer function properly in the motor.

Several dominant double mutants were isolated and mapped to the cytoplasmic domain. M219I/M220N were mutated in residues that adjoin each other, suggesting that this region might be involved in protein-protein interaction or be important to protein conformation. It will be necessary to separate these mutations to determine which confers the Pom⁻ phenotype, or whether both are needed.

Comparison between PomA and MotA

Most of the dominant mutations isolated in this study occurred in the residues conserved in MotA proteins. Especially we found five mutations in residues that also gave a dominant, swarm-deficient phenotype when mutated in *motA* in *E. coli*. The mutations G8S, G8D (TM1) and P199L (TM4) correspond to G6S, G6D and

P222L, respectively, isolated in *E. coli* MotA (Blair & Berg, 1991). These residues are also highly conserved in MotA homologues (Fig. 2). They would not have a direct role in ion translocation but rather a structural role. Zhou & Blair (1997) focused on, and investigated, this proline residue (Pro222 in *E. coli* MotA) by intensive mutagenesis: they speculated that Pro222 might function to mediate conformational changes in MotA that couple the events occurring on the membrane and cytoplasmic domain during energy conversion. Pro151 of PomA is another Pro residue located in the putative third TM segment and is highly conserved among MotA homologues. Mutations of this residue were not isolated in this study, but according to the mutational analysis of the corresponding residue in *E. coli* MotA (Zhou & Blair, 1997), it would have a role similar to that of Pro199 in PomA. The G154R mutation was identical to a chromosomal mutation in PomA of VIO586 (Y. Asai, I. Kawagishi, E. Sockett & M. Homma, unpublished). This residue corresponds to Gly176 in *E. coli* MotA, and mutation G176S of MotA severely impaired motility (Blair & Berg, 1991).

There are no charged residues in the TM segments of PomA, although some polar residues exist there. These residues might be expected to interact with ions in an ion channel. Among the polar residues, dominant mutations were isolated in Thr158 (TM3) and Thr186 (TM4). Thr186 is highly conserved in MotA homologues, and might have an important role in ion translocation. Thr158 is also conserved in MotA of *R. sphaeroides*, and T158I mutations exhibited the strongest dominance (Fig. 4). In *E. coli* MotA, the non-motile dominant mutation A180V was isolated in the corresponding residue. So a protein carrying the T158I mutation might affect the ion translocation or impede the rotation of the motor, acting as a 'brake' because of its bulky side chain. In this study we could not isolate the Na⁺-motor-specific dominant mutations. This suggests that PomA has very similar profile to MotA as a channel component. In other words, PomA might mainly constitute the Na⁺ channel pore structure, and Na⁺-selectivity might not be determined by PomA alone.

Expression of mutant PomA

Some mutations of PomA affected the electrophoretic mobility of the protein. The T158I, G176E and R135Q/M169I proteins were detected at a position slightly above the wild-type protein on gels. This altered mobility might reflect differences in conformation or other modifications. In addition to the PomA bands (25 kDa), we observed bands at approximately 45 kDa in both wild-type and mutant PomA. We suggest that this band might represent a different conformation of PomA or an interaction of PomA with itself or with other proteins, which persist even in the presence of SDS (T. Yorimitsu, K. Sato, Y. Asai, I. Kawagishi & M. Homma, unpublished). The 45 kDa bands of G176E and R135Q/M169I were also found at the upper position, supporting this proposal. In some mutants, the 45 kDa bands were weaker. It will be necessary to examine more

systematically the conditions that affect the appearance of the 45 kDa band.

We think that the basic mechanism of torque generation in the flagellar motor will be common, independent of the coupling ion, H^+ or Na^+ . On the other hand, it is not known how the ion selectivity of the motor is determined, or what is the function of the additional motor genes, *motX* and *motY*, specific for the Na^+ motor. To answer these questions, it will be necessary to investigate interactions between the motor components. In the case of Na^+ -type F_0F_1 ATPase of *Propionigenium modestum*, an H^+ -type *E. coli* ($F_1-\delta$)/ Na^+ -type *P. modestum* ($F_0+\delta$) hybrid ATPase showed that the F_0 part is exclusively responsible for the recognition of the coupling ion (Kaim & Dimroth, 1993, 1994). Such hybrid studies, for example *Rhodobacter* MotA expressed in a *pomA*-deleted *Vibrio* strain, are now in progress in our laboratory. We hope that further analysis of the common structure between the Na^+ system and H^+ system will lead us to the essential points of the torque-generating mechanism.

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